Cladosporium prattiae NRRL B-64423 (FJI-L7-BK-DG1)

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MLST scheme used: ITS region

Score:902 bits(488), Expect:0.0, Identities:498/503(99%), Gaps:0/503(0%)

Query  12   ACCTGCGGAGGGATCATTACAAGTGAACAACCCTTCGGGGCCTGTCTCATAACCCTTTGT  71   Cladosporium prattiae NRRL B-64423 (FJI-L7-BK-DG1)
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  6    ACCTGCGGAGGGATCATTACAAGTGAACAACCCTTCGGGGCCTGTCTCATAACCCTTTGT  65   Cladosporium austrohemisphaericum CBS140482

Query  72   TGTCCGACCATGTTGCCTCCGGGGCGACCCTGCCTCCGGGCGGGGGCTCCGGGTGGACAC  131
            |||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||||
Sbjct  66   TGTCCGACCATGTTGCCTCCGGGGCGACCCTGCCTTCTGGCGGGGGCTCCGGGTGGACAA  125

Query  132  TTCAAACTCTTGCGTAACTTTGCAGTCTGAGTAAATTTAGTTAATAAATTAAAACTTTCA  191
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  126  TTCAAACTCTTGCGTAACTTTGCAGTCTGAGTAAATTTAATTAATAAATTAAAACTTTCA  185

Query  192  ACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGT  251
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  186  ACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGT  245

Query  252  GAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATTC  311
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  246  GAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATTC  305

Query  312  CGGGGGGCATGCCTGTTCGAGCGTCATTTCACCACTCAAGCCTCGCTTGGTATTGGGCAA  371
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  306  CGGGGGGCATGCCTGTTCGAGCGTCATTTCACCACTCAAGCCTCGCTTGGTATTGGGCAA  365

Query  372  CGCGGTCCGCCGCGTGCCTCAAATCGACCGGCTGGGTCTTCTGTCCCCTAAGCGTTGTGG  431
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  366  CGCGGTCCGCCGCGTGCCTCAAATCGACCGGCTGGGTCTTCTGTCCCCTAAGCGTTGTGG  425

Query  432  AAACTATTCGCTAAAGGAGGTTCGGGAGGCTACGCCGTAAAACAACCCCATTTCTAAGGT  491
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  426  AAACTATTCGCTAAAGGTGGTTCGGGAGGCTACGCCGTAAAACAACCCCATTTCTAAGGT  485

Query  492  TGACCTCGGATCAGGTAGGGATA  514
            |||||||||||||||||||||||
Sbjct  486  TGACCTCGGATCAGGTAGGGATA  508


 MLST scheme used: tef1-α

 Score:1450 bits(785), Expect:0.0, Identities:871/914(95%), Gaps:0/914(0%)

 Query  67   TGCGCTATCCTTATTATCGCTGCCGGCACTGGTGAGTTCGAGGCTGGTATCTCCAAGGAC  126  Cladosporium prattiae NRRL B-64423 (FJI-L7-BK-DG1)
             ||||| || || || || || ||||| ||||||||||||||||| ||||||||||||||||||||
 Sbjct  1    TGCGCCATTCTCATCATTGCCGCCGGTACTGGTGAGTTCGAGGCCGGTATCTCCAAGGAC  60   Cladosporium cucumerinum strain MUCL 10092

 Query  127  GGCCAGACCCGTGAGCACGCTCTTCTCGCCTACACCCTCGGTGTCAAGCAGCTCATCGTC  186
             || |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
 Sbjct  61   GGTCAGACCCGTGAGCACGCTCTTCTCGCCTACACCCTTGGTGTCAAGCAGCTCATCGTT  120

 Query  187  GCCATCAACAAGATGGACACCACCAAGTGGTCTGAGGACCGTTACCAGGAGATCATCAAG  246
             ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
 Sbjct  121  GCCATCAACAAGATGGACACCACCAAGTGGTCTGAGGCCCGTTACCAGGAGATCATCAAG  180

 Query  247  GAGACCTCCACCTTCATCAAGAAGGTCGGCTTCAACCCCAAGCACGTCCCCTTCGTCCCG  306
             |||||||||   ||||||||||||||||||||||||||||||||||| |||||||| ||
 Sbjct  181  GAGACCTCCGGTTTCATCAAGAAGGTCGGCTTCAACCCCAAGCACGTTCCCTTCGTGCCC  240

 Query  307  ATCTCCGGTTTCAACGGTGACAACATGATCGAGGTTTCCACCAACTGCCCCTGGTACAAG  366
             |||||||| |||||||||||||||||||| || ||||||||||||||||||||||||||||
 Sbjct  241  ATCTCCGGCTTCAACGGTGACAACATGATCGACGTCTCCACCAACTGCCCCTGGTACAAG  300

 Query  367  GGTTGGGAGAAGGAGACCAAGGCCAAGGCCACCGGCAAGACCCTCCTCGAGGCCATTGAC  426
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
 Sbjct  301  GGTTGGGAGAAGGAGACCAAGGCCAAGGCCACCGGCAAGACCCTTCTCGAGGCCATTGAC  360

 Query  427  GCCATCGAccccccccAGCCGTCCCACCGACAAGCCCCTCCGTCTTCCCCTCCAGGACGTC  486
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
 Sbjct  361  GCCATCGACCCCCCCCAGCCGTCCCACCGACAAGCCCCTCCGTCTTCCCCTCCAGGATGTC  420

 Query  487  TACAAGATCGGTGGTATTGGCACGGTTCCCGTCGGTCGTGTCGAGACCGGTACCATCAAG  546
             |||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
 Sbjct  421  TACAAGATCGGTGGTATTGGCACGGTTCCCGTCGGTCGTGTCGAGACCGGTGTGATCAAG  480

 Query  547  GCCGGCATGGTCGTCACCTTCGCCCCCGCTGGTGTCACCACTGAGGTCAAGTCCGTCGAG  606
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct  481  GCCGGTATGGTCGTCACCTTCGCCCCCGCTGGTGTCACCACTGAGGTCAAGTCCGTCGAG  540

 Query  607  ATGCACCACGAGCAGCTTCCCGAGGGTCTCCCTGGTGACAACGTCGGTTTCAACGTCAAG  666
             |||||||||||||||||||||||||||| || ||||||||||||| ||||||||||||
 Sbjct  541  ATGCACCACGAGCAGCTTCCCGAGGGTCTTCCCGGTGACAACGTCGGCTTCAACGTCAAG  600

 Query  667  AACGTCTCCGTCAAGGAGATCCGTCGTGGCAACGTCACCGGTGACTCCAAGAACGACCCC  726
             |||||||||||||||||||||||||||||||||  |||||||||||||| |||||||
 Sbjct  601  AACGTCTCCGTCAAGGAGATCCGTCGTGGCAACGTTGCCGGTGACTCCAAGACCGACCCC  660

 Query  727  CCGAAGGGCTGCGACAGCTTCAACGCCCAGGTCATCGTCCTCAACCACCCCGGTCAGGTC  786
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Sbjct  661  CCCAAGGGCTGCGACAGCTTCAACGCCCAGGTCATCGTCCTCAACCACCCCGGTCAGGTC  720

 Query  787  GGCGCCGGCTACGCGCCCGTCCTCGACTGCCACACTGCTCACATTGCCTGCAAGTTCTCT  846
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
 Sbjct  721  GGCGCCGGCTACGCGCCCGTCCTCGACTGCCACACTGCTCACATTGCTTGCAAGTTCTCT  780

 Query  847  GAGCTCCTCGAGAAGATCGACCGTCGCTCTGGCAAGTCCATTGAGGCCTCCCCCAAGTTC  906
             |||||||||||||||| |||||||| || |||||||||| ||| ||  ||||||||||
 Sbjct  781  GAGCTCCTCGAGAAGATTGACCGTCGTTCCGGCAAGTCCATCGAGTCCGGCCCCAAGTTC  840

 Query  907  ATCAAGTCTGGTGACGCCGCCATCGTCAAGATGGTTCCCTCCAAGCCGATGTGCGTTGAG  966
             |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
 Sbjct  841  ATCAAGTCTGGTGACGCCGCCATCGTCAAGATGGTTCCCTCCAAGCCCATGTGCGTTGAG  900

 Query  967  GCCTTCACCGACTA  980
             ||||||||||||||
 Sbjct  901  GCCTTCACCGACTA  914
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MLST scheme used: ACT

Score:357 bits(193), Expect:6e-103, Identities:214/224(95.54%), Gaps:1/224(0%)

Query  14   GTGCAAGGCCGGTTTCGCCGGTGACGATGCGCCCAGAGCCGTTTTCCGTAAGTCTGAAGA  73   Cladosporium prattiae NRRL B-64423 (FJI-L7-BK-DG1)
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    GTGCAAGGCCGGTTTCGCCGGTGACGATGCGCCCAGAGCCGTTTTCCGTAAGTCTGAAGA  60   Cladosporium austrohemisphaericum CBS 140482

Query  74   CAACTGTTTCACCCGCCGTAGGATGCCGAGCTGACAGCATTGTAGCTTCCATTGTCGGTA  133
            || |||||| |||||||||| | ||||||||||||||||||||||||||||||||||||
Sbjct  61   CACCTGTTCCACCCGCCGTGGAATGCCGAGCTGACAGCATTGTAGCTTCCATTGTCGGTA  120

Query  134  GACCCCGTCACCATGGGTATGCACTCATCCTTTCCACCTCCTCCGCCGGGG-CCAATGTC  192
            |||||||||||||||||| ||||||||||||||||| |||||||||| || ||||||||
Sbjct  121  GACCCCGTCACCATGGGTACGCACTCATCCTTTCCACTTCCTCCGCCGAGGCCCAATGTC  180

Query  193  TAACCGCAGCGCAGTATCATGATCGGTATGGGTCAGAAGGACTC  236
            |||||||| |||||||||||||||||||| ||||||||||
Sbjct  181  TAACCGCAACGCAGTATCATGATCGGTATGGGCCAGAAGGACTC  224


MLST scheme used: rpb2

Score:965 bits(522), Expect:0.0, Identities:996/1226(81%), Gaps:27/1226(2%)

Query  1192  GATGACCGTGATCACTTCGGTAAGAAACGTCTCGATCTGGCTGGTCCCTTGATGGCGCAA  1251  Cladosporium prattiae NRRL B-64423 (FJI-L7-BK-DG1)
              ||||| |||||||| ||||| |||||| ||||||||||||||||||| ||||||||||
Sbjct  1      GATGATCGTGATCATTTCGGCAAGAAGCGTCTCGATCTGGCTGGTCCTTTGATGGCGCAA  60   Cladosporium iridis strain CBS 138.40

Query  1252  GTTTTCCGCATGAAGTGGACGCAGGTCGTCCGTGAATTGCGTCAGTACATGCACAAGATG  1311
              || |||||||||| ||||| ||||| || |||||  |||| || ||||||||||||||||
Sbjct  61    GTCTTCCGCATGAAATGGACACAGGTTGTTCGTGAGCTGCGACAATACATGCACAAGATG  120

Query  1312  ATTGAAGCACCCAATAAGGACCGAGGCAACA--GAGAATTCAGCATGGTGACGGCCATCA  1369
              ||||||||||||| |||||  ||   |||   |||||||||| ||||| || ||  | |
Sbjct  121   ATTGAAGCACCCAACAAGGA--GA---AACGGGGAGAATTCAGTATGGTAACCGCGGTGA  175

Query  1370  AACCGAGCATCATCACACAAGGTCTGCGGTACTGTTTGGCAACTGGAAACTGGGGTGATC  1429
              | || || |||||||| |||||||||| |||||| ||||||| || |||||||| ||||
Sbjct  176   AGCCTAGTATCATCACCCAAGGTCTGCGATACTGTCTGGCAACCGGCAACTGGGGCGATC  235

Query  1430  AGAAGAAGGCTGCATCGGCGAAGGCTGGTGTCAGTCAAGTGCTTAACAGATACACCTACG  1489
              | || |||||||||||| || || |||||||| ||||| ||||| |||||||||||| ||||
Sbjct  236   AAAAAAAGGCTGCATCAGCAAAAGCTGGTGTGAGTCAGGTGCTCAACAGATACACATACG  295

Query  1490  CCTCGACATTATCACATTTGCGACGCACAAACACACCTATCGGCCGAGATGGCAAGATTG  1549
              |||||||  | || |||||||||||| || ||||| || || || || ||||||||||| |
Sbjct  296   CCTCGACGCTTTCTCATTTGCGACGTACCAACACTCCCATTGGTCGTGATGGCAAGATCG  355

Query  1550  CCAAGCCGCGTCAACTGCATAACACTCACTGGGGTTTGGTCTGCCCAGCCGAGACCCCCG  1609
              | || || |||||   | || ||||||||||||||| |||||||||| ||||| || || |
Sbjct  356   CGAAACCACGTCAGTTACACAACACTCACTGGGGTCTGGTCTGCCCTGCCGAAACGCCAG  415

Query  1610  AAGGTCAAGCTTGTGGTCTCGTCAAGAACTTGAGTTTGATGTGCTTCGTGTCCGTTGGTA  1669
              |||| |||||||||||||||||||||| ||||| ||||||| ||||| || |||||||
Sbjct  416   AAGGCCAAGCTTGTGGTCTCGTCAAGAACCTGAGTCTGATGTGTTTCGTTTCTGTTGGTA  475

Query  1670  CACCAGGTGGGCCTTTGACAGATTTCATGCGTCAGCGCGACATGGAGCTTCTGGAGGAGT  1729
              | || || || ||  |||| || |||||||| ||||| |||||||||||| |||||||||
Sbjct  476   CGCCCGGCGGACCGCTGACCGACTTCATGCGCCAGCGTGACATGGAGCTTTTGGAGGAGT  535

Query  1730  ACGATCCAGTCATGAATCCCAACGCTACCAAGGTTTTCGTCAACGGTACATGGGTGGGTG  1789
              ||||||| || ||||| |||||||| |||||||| ||||||||||||||||||||| ||||
Sbjct  536   ACGATCCGGTGATGAACCCCAACGCCACCAAGGTCTTCGTCAACGGTACATGGGTCGGTG  595

Query  1790  TGCACAAGAAACGCATCACAGCTCATGGATGTCTTGCTCGACATCCGTCGCAAAGGCCTGA  1849
              |||||||||||| || || ||||||||  |||| |||||||||||||||| || ||||
Sbjct  596   TGCACAAGAACGCCTCGCAACTCATGGAAATCTTACTCGACATCCGTCGCAAGGGTCTGA  655

Query  1850  TCAGCTTCGAATGCACAATTATAAGAGATGTGCGCGATCGCGAGATCAAGATCTTCACAG  1909
              |||||||||||||||| || |||||||| |||||||| |||||||||||||||||||| |
Sbjct  656   TCAGCTTCGAATGCACCATCATAAGAGACGTGCGCGACCGCGAGATCAAGATCTTCACTG  715

Query  1910  ATGCTGGACGTGTCATGAGGCCTCTGTTCGTCGTCGATAACGACCCACGCAG---TCCC-  1965
              | || |||||||||||| | ||  |||||||||| || |||||||| |||||   |  |
Sbjct  716   ACGCCGGACGTGTCATGCGACCCTTGTTCGTCGTTGACAACGACCCTCGCAGCGATAGCG  775

Query  1966  A--ATCGCGGTACACTCATGCTCAAGCAAGACCA--TG-TGCAACGCTTGAGAGAGGACC  2020
              |  | || || | ||| |||||||||   || ||  || |||||| |   || || || |
Sbjct  776   AGGACCGTGGCAGACTTATGCTCAAGAGGGAGCACGTGATGCAACTCA--AG-GACGATC  832

Query  2021  TTGAGATTTTGGCCAGCGGTGATCTCGCTAAC--TAC-AGCGAGGAAGAACGCGACCAAA  2077
                |  ||| |||  || || ||  | |  |||  | | || ||||| || ||||||   |
Sbjct  833   AGGCTATTCTGGGTAGTGGCGAAAT-G--AACGGTGCGAGTGAGGAGGAGCGCGACGCCA  889

Query  2078  CCATCTTCGGCTGGAAGGGTCTCATCAAGAATGGTGTTGTCGAGTACCTCGACGCAGAGG  2137
              |||| |||||||||||||||||||||||  || || || || ||||||||||||||| |
Sbjct  890   CCATTTTCGGCTGGAAGGGTCTCATCAAGAGCGGAGTGGTTGAATACCTCGACGCAGAAG  949

Query  2138  AGGAGGAGACGGCCATGATCATCATGTCGCCCGATGATCTAGAGGAGCACCGGGCGGTCC  2197
              |||| ||||| |||||||||||||| | || || ||  | ||||| |||||    |||
Sbjct  950   AGGAAGAGACTGCCATGATCATCATGACACCTGACGACTTGGAGGACCACCGCCTAGTCA  1009

Query  2198  GCGAAGGCATAGAT-TGGGACGAACCTGTTCTGGACCCACACAGACGCATCAAGCCTAAA  2256
                 ||||| | ||| |  || ||||| | || |||| ||||| ||||||||||
Sbjct  1010  AGAAAGGCGT-GATGTACGAGGAACCAATCCTCGACCCGCACAGGCGCATCAAGCCCCG  1068

Query  2257  CCCAACCCTGCGATTCACAGGTGGACACATTGCGAGATTCATCCTTCGATGATTTTGGGC  2316
              || ||| |  || ||||||| ||||| || |||||||||||||| || ||||| |||||
Sbjct  1069  CCAAACTCGTCGGTTCACAGATGGACGCACTGCGAGATTCATCCGTCCATGATCTTGGGT  1128

Query  2317  ATTTGCGCGTCCATCATTCCTTTCCCCGATCACAACCAGTCGCCCCGTAACACATACCAA  2376
              || |||||||||||||||| |||||||| |||||||||| || |||||||| ||||||
Sbjct  1129  ATCTGCGCGTCCATCATTCCGTTCCCCGACCACAACCAGTCTCCTCGTAACACCTACCAA  1188

Query  2377  TCCGCCATGGGTAAGCAAGCCATGGG  2402
              || |||||||| |||||||| |||||
Sbjct  1189  TCTGCCATGGGCAAGCAAGCTATGGG  1214
```

MLST scheme used: tub2

Score:351 bits(190), Expect:9e-101, Identities:313/370(85%), Gaps:18/370(4%)

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Query  1    ATTAACA-TCCGC-AAAGGGCAATCAAATTGGTGCTGCATTCTGGCAGACCATCTCCGGC  58  Cladosporium prattiae NRRL B-64423 (FJI-L7-BK-DG1)
            ||||||| ||| | ||||||||||||||||||||||||||| ||||||||||||||||||
Sbjct  208  ATTAACATTCCTCAAAAGGGCAATCAAATTGGTGCTGCATTTTGGCAGACCATCTCCGGC  267  Cladosporium aciculare CBS 140488

Query  59   GAGCATGGCCTCGACGGCGCCGGCGTGTATGTACA-CAA-TGCATCAGGGCACGCGAAAA  116
            |||||||||||||||||| | |||||||||||  |  | | ||| | ||  ||||||  |
Sbjct  268  GAGCATGGCCTCGACGGCTCTGGCGTGTATGTTCCGCCATTGCGTGAGAACACGCGGGA-  326

Query  117  CCAC-CAG-CTGACA-C-CGCATAGGTACAACGGCACGTCTGACCTCCAGCTCGAGCGCA  172
            | || | | ||||||| | |||  |||||||| |||||||||| ||||||||||||||||
Sbjct  327  C-ACTCTGACTGACAACACGC--AGGTACAATGGCACGTCTGATCTCCAGCTCGAGCGCA  383

Query  173  TGAACGTGTACTTCAACGAGGTATGATCCAC--CGAGGCACCCGC-ATATGCACGCTCCA  229
            ||||||| |||||||||||||||| |  ||    |||||||| | | | |||||  |||
Sbjct  384  TGAACGTCTACTTCAACGAGGTATG-TGAACTTTCAGGCACCCACCAAACGCACGTCCCA  442

Query  230  AG-GCCA-CGCACTGACCCTATACCATTGTAGGCCTCTGGCAACAAATACGTTCCCCGTG  287
            || |||  ||| ||||| || ||||||   |||| |||||||||| ||||||||||||
Sbjct  443  AGTGCCTGCGCGCTGACTCTGTACCATCACAGGCTTCTGGCAACAAGTACGTTCCCCGTG  502

Query  288  CCGTCCTCGTCGACTTGGAGCCCGGCACCATGGACGCTGTTCGCGCCGGTCCCTTCGGCC  347
            |||||||||||||||||||||||| ||||||||||||| || |||||||||||||| |
Sbjct  503  CCGTCCTCGTCGACTTGGAGCCCGGTACCATGGACGCTGTCCGTGCCGGTCCCTTCGGTC  562

Query  348  AGCTCTTCCG  357
            ||||||||||
Sbjct  563  AGCTCTTCCG  572
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Cladosporium crawfordii NRRL B-64425 FKII-L3-CM-PAB1

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MLST scheme used: ITS region

Score:953 bits(516), Expect:0.0, Identities:516/516(100%), Gaps:0/516(0%)

Query  1    CTGCGGAGGGATCATTACAAGTGACCCCGGTCTTACCACCGGGATGTTCATAACCCTTTG  60  Cladosporium crawfordii NRRL B-64425 (FKII-L3-CM-PAB1)
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  125  CTGCGGAGGGATCATTACAAGTGACCCCGGTCTTACCACCGGGATGTTCATAACCCTTTG  184  Cladosporium perangustum CBS 125996

Query  61   TTGTCCGACTCTGTTGCCTCCGGGGCGACCCTGCCTTCGGGCGGGGGCTCCGGGTGGACA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  185  TTGTCCGACTCTGTTGCCTCCGGGGCGACCCTGCCTTCGGGCGGGGGCTCCGGGTGGACA  244

Query  121  CTTCAAACTCTTGCGTAACTTTGCAGTCTGAGTAAACTTAATTAATAAATTAAAACTTTT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  245  CTTCAAACTCTTGCGTAACTTTGCAGTCTGAGTAAACTTAATTAATAAATTAAAACTTTT  304

Query  181  AACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  305  AACAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATG  364

Query  241  TGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  365  TGAATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCCTGGTATT  424

Query  301  CCGGGGGGCATGCCTGTTCGAGCGTCATTTCACCACTCAAGCCTCGCTTGGTATTGGGCA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  425  CCGGGGGGCATGCCTGTTCGAGCGTCATTTCACCACTCAAGCCTCGCTTGGTATTGGGCA  484

Query  361  ACGCGGTCCGCCGCGTGCCTCAAATCGACCGGCTGGGTCTTCTGTCCCCTAAGCGTTGTG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  485  ACGCGGTCCGCCGCGTGCCTCAAATCGACCGGCTGGGTCTTCTGTCCCCTAAGCGTTGTG  544

Query  421  GAAACTATTCGCTAAAGGGTGTTCGGGAGGCTACGCCGTAAAACAACCCCATTTCTAAGG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  545  GAAACTATTCGCTAAAGGGTGTTCGGGAGGCTACGCCGTAAAACAACCCCATTTCTAAGG  604

Query  481  TTGACCTCGGATCAGGTAGGGATACCCGCTGAACTT  516
            ||||||||||||||||||||||||||||||||||||
Sbjct  605  TTGACCTCGGATCAGGTAGGGATACCCGCTGAACTT  640
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MLST scheme used: act

Score:390 bits(211), Expect:6e-113, Identities:221/226(98%), Gaps:0/226(0%)

Query  11   TATGTGCAAGGCCGGTTTCGCCGGTGACGATGCGCCCAGAGCCGTTTTCCGTAAGTTTGA  70  Cladosporium crawfordii NRRL B-64425 (FKII-L3-CM-PAB1)
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1    TATGTGCAAGGCCGGTTTCGCCGGTGACGATGCGCCCAGAGCCGTTTTCCGTAAGTTTGA  60  Cladosporium perangustum strain CBS 125996

Query  71   AGACACCTGTTTCGCCCCGCCTAGAACTTCCAGCTGACAGTAACATAGCTTCCATTGTCG  130
            |||||||||||||||||||||||||||||||||||| | ||||||||||||||||||||
Sbjct  61   AGACACCTGTTTCGCCCCGCCTAGAACTTCCAGCTGACAGTATCTTAGCTTCCATTGTCG  120

Query  131  GCAGACCCCGTCACCATGGGTATGCCCTCTTCCCGCAATTTCCGCCGTCGAGTTCAGAGA  190
            |||||||||||||||||||||||||||||||||||||||||||||||||| ||||| |||
Sbjct  121  GCAGACCCCGTCACCATGGGTATGCCCTCTTCCCGCAATTTCCGCCGTCGAGCTCAGATA  180

Query  191  TCTAACAATGGCGCAGTATCATGATCGGTATGGGTCAGAAGGACTC  236
            |||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  181  TCTAACAATGGCGCAGTATCATGATCGGTATGGGCCAGAAGGACTC  226
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MLST scheme used: tef1-α

Score:1472 bits(797), Expect:0.0, Identities:875/914(96%), Gaps:0/914(0%)

```
Query  88    TGCGCCATTCTCATCATTGCCGCCGGTACTGGTGAGTTCGAGGCTGGTATCTCCAAGGAT  147  Cladosporium crawfordii NRRL B-64425 (FKII-L3-CM-PAB1)
             ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Sbjct  1     TGCGCCATTCTCATCATTGCCGCCGGTACTGGTGAGTTCGAGGCCGGTATCTCCAAGGAC  60  Cladosporium cucumerinum MUCL 10092

Query  148   GGCCAGACCCGTGAGCACGCCTTCTCGCCTACACCCTCGGTGTGAAGCAGCTCATCGTC  207
             || |||||||||||||||| |||||||||||||||| ||||| |||||||||||||||
Sbjct  61    GGTCAGACCCGTGAGCACGCTCTTCTCGCCTACACCCTTGGTGTCAAGCAGCTCATCGTT  120

Query  208   GCCATCAACAAGATGGACACCACCAAGTGGTCTGAGGCCCGTTACCAGGAGATCATCAAG  267
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GCCATCAACAAGATGGACACCACCAAGTGGTCTGAGGCCCGTTACCAGGAGATCATCAAG  180

Query  268   GAGACCTCCGGTTTCATCAAGAAGGTCGGCTTCAACCCCAAGCACGTTCCCTTCGTCCCC  327
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Sbjct  181   GAGACCTCCGGTTTCATCAAGAAGGTCGGCTTCAACCCCAAGCACGTTCCCTTCGTGCCC  240

Query  328   ATCTCCGGCTTCAATGGTGACAACATGATCGACGTCTCCACCAACTGCCCCTGGTACAAG  387
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   ATCTCCGGCTTCAACGGTGACAACATGATCGACGTCTCCACCAACTGCCCCTGGTACAAG  300

Query  388   GGCTGGGAGAAGGAGACCAAGGCCAAGGCCACTGGCAAGACCCTCCTCGAGGCCATCGAC  447
             || |||||||||||||||||||||||||||| |||||||||||| |||||||||||| |||
Sbjct  301   GGTTGGGAGAAGGAGACCAAGGCCAAGGCCACCGGCAAGACCCTTCTCGAGGCCATTGAC  360

Query  448   GCCATTGAccccccccACCCGTCCCACCGACAAGGCCCTCCGTCTTCCCCTCCAGGATGTC  507
             ||||| |||||||||| ||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  361   GCCATCGACCCCCCCCAGCCGTCCCACCGACAAGCCCCTCCGTCTTCCCCTCCAGGATGTC  420

Query  508   TACAAGATTGGCGGTATCGGCACGGTTCCCGTCGGTCGTGTTGAGACCGGTATCATCAAG  567
             |||||||| || ||||| |||||||||||||||||||| ||||||||| | ||||||||||
Sbjct  421   TACAAGATCGGTGGTATTGGCACGGTTCCCGTCGGTCGTGTCGAGACCGGTGTGATCAAG  480

Query  568   GCCGGCATGGTCGTCACCTTCGCCCCCGCTGGTGTCACCACTGAGGTCAAGTCCGTCGAG  627
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GCCGGTATGGTCGTCACCTTCGCCCCCGCTGGTGTCACCACTGAGGTCAAGTCCGTCGAG  540

Query  628   ATGCACCACGAGCAGCTTCCCGAGGGTCTCCCCGGTGACAACGTCGGCTTCAACGTCAAG  687
             |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  541   ATGCACCACGAGCAGCTTCCCGAGGGTCTTCCCGGTGACAACGTCGGCTTCAACGTCAAG  600

Query  688   AACGTCTCCGTCAAGGAGATCCGTCGTGGCAACGTTGCCGGTGACTCCAAGAACGAcccc  747
             |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Sbjct  601   AACGTCTCCGTCAAGGAGATCCGTCGTGGCAACGTTGCCGGTGACTCCAAGACCGACCCC  660

Query  748   cccAAGGGCTGCGAGAGCTTCAACGCCCAGGTCATCGTCCTCAACCACCCCGGTCAGGTT  807
             ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   CCCAAGGGCTGCGACAGCTTCAACGCCCAGGTCATCGTCCTCAACCACCCCGGTCAGGTC  720

Query  808   GGTGCCGGTTACGCGCCCGTCCTCGACTGCCACACCGCCCACATTGCCTGCAAGTTCTCT  867
             || ||||| |||||||||||||||||||||||| || |||||||| ||||||||||||||
Sbjct  721   GGCGCCGGCTACGCGCCCGTCCTCGACTGCCACACTGCTCACATTGCTTGCAAGTTCTCT  780

Query  868   GAGCTCCTCGAGAAGATCGACCGCCGTACCGGCAAGTCCATGGAGGCCAGCCCCAAGTTC  927
             |||||||||||||||| ||||| ||| |||||||||||||| ||| || ||||||||||||
Sbjct  781   GAGCTCCTCGAGAAGATTGACCGTCGTTCCGGCAAGTCCATCGAGTCCGGCCCCAAGTTC  840

Query  928   ATCAAGTCTGGTGACGCTGCCATCGTCAAGATGGTTCCCTCCAAGCCCATGTGCGTTGAG  987
             |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841   ATCAAGTCTGGTGACGCCGCCATCGTCAAGATGGTTCCCTCCAAGCCCATGTGCGTTGAG  900

Query  988   GCCTTCACCGACTA  1001
             ||||||||||||||
Sbjct  901   GCCTTCACCGACTA  914
```

Waltergamsia balasubramanianii NRRL 64428 (FKII-L8-BK-P5)

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MLST scheme used: ITS region

Score:813 bits(440), Expect:0.0, Identities:497/524(95%), Gaps:5/524(0%)

Query  19    GGATCATTATAGAGTGT-AAAACTCCCAAACCTTTGTGAACATACCACTGTTGCTTCGGC  77   Waltergamsia balasubramanianii NRRL 64428 (FKII-L8-BK-P5)
              ||||||||||||||| |   ||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GGATCATTATAGAGTCTCTGAACTCCCAAACCTTTGTGAACATACCACTGTTGCTTCGGC  60   Waltergamsia citrina CBS 384.96

Query  78    GGCGTTCCTGGTGTCTCCGGGCGTCCAGGCTCGCACGCGCCGCCGAGGGTACCAAACTCT  137
              |||||||  ||||| ||||||| ||||||  |  ||||||||||||||||||||||||||
Sbjct  61    GGCGTTCTGGGTGTATCCGGGCATCCAGGGTTCCACGCGCCGCCGAGGGTACCAAACTCT  120

Query  138   TGCTTTTATAGCGGACTTCTGAGTACAAAAACATAAATGAATTAAAACTTTCAGCAACGG  197
              ||  |||||| ||||||||||||||  ||| ||| |||| ||||||||||||||||||||
Sbjct  121   TGTCTTTATATCGGACTTCTGAGTGAAAATACA-AAATAAATTAAAACTTTCAGCAACGG  179

Query  198   ATCTCTTGGCTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGC  257
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  180   ATCTCTTGGCTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGC  239

Query  258   AGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCACCAGTATTCTGGTGGG  317
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   AGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCACCAGTATTCTGGTGGG  299

Query  318   CATGCCTGTCCGAGCGTCATTTCAACCCTCAGGCCCGGCCTGGTGTTGGGGATTGGCCCT  377
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||  ||
Sbjct  300   CATGCCTGTCCGAGCGTCATTTCAACCCTCAGGCCCAGCCTGGTGTTGGGGATTGG--CT  357

Query  378   TCGCGGCCAGCCCCGAAATGCAGTGGCGGCCCTCCGC-AACTCCTCTGTGTAGTAGTAAT  436
              ||||||||| |||||||||||||||||||||||||| |||||||||||| ||||||  ||
Sbjct  358   TCGCGGCCACCCCCGAAATGCAGTGGCGGCCCTCCGCGAACTCCTCTGTGCAGTAGTGAT  417

Query  437   ACCTCGCTTTGGATAGTGGTTGCGCCTCGCCGTAAAACCTCCAACTTCTCAAGGTTGACC  496
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  418   ACCTCGCATTGGATAGTGGTTGCGCCTCGCCGTAAAACCTCCAACTTCTCAAGGTTGACC  477

Query  497   TCGGATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  540
              |||||||||||||||||||||||||||||||||||||||||||
Sbjct  478   TCGGATCAGGTAGGAATACCCGCTGAACTTAAGCATATCAATAA  521


MLST scheme used: rpb2

Score:1129 bits(611), Expect:0.0, Identities:707/755(94%), Gaps:0/755(0%)

Query  1603  CGACAGCTTCATAACACTCACTGGGGCTTGGTGTGCCCTGCTGAGACGCCTGAAGGCCAG  1662  Waltergamsia balasubramanianii NRRL 64428 (FKII-L8-BK-P5)
              || |||||||| |||||||| |||||  |||||||||| || |||||||| ||||| |||
Sbjct  1     CGGCAGCTTCACAACACTCATTGGGGACTGGTGTGCCCCGCCGAGACGCCCGAAGGTCAG  60   Waltergamsia alkalina culture CBS:741.94

Query  1663  GCTTGTGGTCTGGTGAAGAACTTGTCGTTGATGTGCTACGTTTCAGTTGGATCTCCCTCG  1722
              |||||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GCTTGTGGTCTCGTGAAGAATTTGTCGTTGATGTGCTACGTTTCAGTTGGATCTCCCTCG  120

Query  1723  GAGCCTCTCCTATCTTTCATGATAAGTCGTGGGATGGAGCTAATCGAGGAGTACGATCCA  1782
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GAGCCTCTCCTATCTTTCATGATAAGTCGTGGGATGGAGCTAATCGAGGAGTACGATCCA  180

Query  1783  TTAAGATTCCCCCACGCTACCAAGATCTTCATCAATGGTAGCTGGGTGGGCATTCACCAA  1842
              |||||||||||||||||||||||||||||| ||||| ||||||||||||||||||||||
Sbjct  181   TTAAGATTCCCCCACGCTACCAAGATCTTTATCAACGGTAGCTGGGTGGGCATTCACCAA  240

Query  1843  GAACCTAAGCAGCTCGTCGATCACTTGGTCGCGCTGCGTCGGTCCGCCCGAATGGCGCAT  1902
              ||||| |||||||||||||||||||||| || |||||||| || ||||| |||||||||
Sbjct  241   GAACCCAAGCAGCTCGTCGATCACTTGGTGGCACTGCGTCGTTCTGCCCGCATGGCGCAT  300

Query  1903  GAGGTTTCTCTTGTTCGTGACATTCGCGATCGAGAATTCAAGTTCTTCTCTGATGCGGGG  1962
              || || ||||||||||||| || || ||||||||||||||||||||||||||||||||||
Sbjct  301   GAAGTGTCTCTTGTTCGTGATATCCGTGATCGAGAATTCAAGTTCTTCTCTGATGCGGGC  360

Query  1963  CGCGTAATGCGTCCTGTCTTTACCGTGCGACAAGAGGAAGGTGAAATTGGTGATCCACCA  2022
              || || |||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  361   CGTGTGATGCGTCCTGTCTTCACCGTGCGACAAGAGGAAGGTGAAATTGGTGATCCACCA  420

Query  2023  AAGGGTTCCCTTGTCCTGACCAAGGACGACATCAGTAGGATTGATGAAGAGTACTGGCAC  2082
              |||||||| |||||| | ||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   AAGGGTTCACTTGTCTTAACCAAGGACGACATCAGTAGGATTGATGAAGAGTACTGGCAC  480

Query  2083  TCGGACAAGGAAGAATGGTTAAGGGGCTGGGACAAGCTTGTTGGCATTGGTTGCGTCGAG  2142
               ||||||||||||||||||||| ||||||||||||||| ||||| ||||| ||||||||
Sbjct  481   GCGGACAAGGAAGAATGGTTAAGAGGCTGGGACAAGCTCGTTGGTATTGGCTGCGTCGAA  540

Query  2143  TACCTGGATGCAGAAGAAGAGGAAACGGCCATGATCTGCATGACTCCGGAAGATTTGGAA  2202
              |||||||||||||||||||||| |||||||||||||||||||||| |||||| |||||
Sbjct  541   TACCTGGATGCAGAAGAAGAGGAGACGGCCATGATCTGCATGACTCCAGAAGATCTGGAA  600

Query  2203  TCGTACCGAATCCAACGACTTGGCTACGACGCCCCCGATGCCTACGAGGAGCTGGAGCCC  2262
              |||||||||| |||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  601   TCGTACCGAATTCAACGACTTGGCTACGACGCCCCCGATGCCTACGAGGAGCTCGAGCCC  660

Query  2263  AACAAGCGCTTGAAGACAAAGACCAACCCGACTACGCACATGTATACCCATTGCGAGATT  2322
              |||||||||||||||||||||||||||||||||||||||||| ||||| |||||||||
Sbjct  661   AACAAGCGCTTGAAGACAAAGACCAACCCGACTACGCACATGTACACCCACTGCGAGATT  720

Query  2323  CATCCCAGCATGATTCTCGGCATTTGTGCAAGCAT  2357
              |||||||||||||||| || ||||| || |||||
Sbjct  721   CATCCCAGCATGATTCTTGGTATTTGCGCTAGCAT  755
```

MLST scheme used: lsu

Score:1496 bits(810), Expect:0.0, Identities:833/844(99%), Gaps:2/844(0%)

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Query  2234  ATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCTCAGTAACGGCGAGTGAAGCGG  2293  Waltergamsia balasubramanianii NRRL 64428 (FKII-L8-BK-P5)
              ||||||||||||||||||||||||| ||||||||||||  ||||||||||||||||||||
Sbjct  1     ATCAATAAGCGGAGGAAAAGAAAC-AACAGGGATTGCCCTAGTAACGGCGAGTGAAGCGG  59  Waltergamsia hennebertii CBS 768.69

Query  2294  CAACAGCTCAAATTTGAAATCTGGCCCTCGGGTCCGAATTGTAATTTGTAGAGGATGTTT  2353
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  60    CAACAGCTCAAATTTGAAATCTGGCCCTTGGGTCCGAATTGTAATTTGTAGAGGATGTTT  119

Query  2354  CTGGCGACGTGTCTTCCGAGTTCCCTGGAACGGGACGCCATAGAGGGTGAGAGCCCCGTC  2413
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  120   CTGGCGACGTGTCTTCCGAGTTCCCTGGAACGGGACGCCATAGAGGGTGAGAGCCCCGTC  179

Query  2414  CGGTCGTACGCCTAGCCTCTGTGAAACTCCTTCGACGAGTCGAGTAGTTTGGGAATGCTG  2473
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  180   CGGTCGTACGCCTAGCCTCTGTGAAACTCCTTCGACGAGTCGAGTAGTTTGGGAATGCTG  239

Query  2474  CTCAAAATGGGAGGTATACGTCTTCTAAAGCTAAATACCGGCCAGAGACCGATAGCGCAC  2533
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240   CTCAAAATGGGAGGTATACGTCTTCTAAAGCTAAATACCGGCCAGAGACCGATAGCGCAC  299

Query  2534  AAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGGGTTAAATAGTACGTGAAAT  2593
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  300   AAGTAGAGTGATCGAAAGATGAAAAGCACTTTGAAAAGAGGGTTAAATAGTACGTGAAAT  359

Query  2594  TGCTGAAAGGGAAGCGTTTATGACCAGACTTGGGCTCGGTGAATCATCCGGCGTTCTCGC  2653
              |||||||||||||||| | ||||||||||||||||||||||||||||||||||||||||
Sbjct  360   TGCTGAAAGGGAAGCGCTCATGACCAGACTTGGGCTCGGTGAATCATCCGGCGTTCTCGC  419

Query  2654  CGGTGCACTTTGCCGGTCCAGGCCAGCATCAGCTCGCCTCGGGGGATAAAGGCTTCGGGA  2713
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  420   CGGTGCACTTTGCCGGTCCAGGCCAGCATCAGCTTGCCTCGGGGGATAAAGGCTTCGGGA  479

Query  2714  ATGTAGCTTCTTCGGAAGTGTTATAGACCGTTGCGTAATACCCTGGGGCGGGCTGAGGTA  2773
              |||||||||||||||||||||||||||||||| |||||| |||||||| ||||||||||
Sbjct  480   ATGTAGCTTCTTCGGAAGTGTTATAGACCGTTGTGTAATA-CCTGGGGCAGGCTGAGGTA  538

Query  2774  CGCGTTCTGCAAGGATGCTGGCGTAATGGTCATCAATGACCCGTCTTGAAACACGGACCA  2833
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  539   CGCGTTCTGCAAGGATGCTGGCGTAATGGTCATCAGTGACCCGTCTTGAAACACGGACCA  598

Query  2834  AGGAGTCGTCTTCGTATGCGAGTGTTCGGGTGTCAAACCCCTACGCGTAATGAAAGTGAA  2893
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  599   AGGAGTCGTCTTCGTATGCGAGTGTTCGGGTGTCAAACCCCTACGCGTAATGAAAGTGAA  658

Query  2894  CGTAGGAGAGAGCTTCGGCGCATCTCCGACCGATCCTGATGTTCTCGGATGGATTTGAGT  2953
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  659   CGTAGGAGAGAGCTTCGGCGCATCTCCGACCGATCCTGATGTTCTCGGATGGATTTGAGT  718

Query  2954  AAGAGCATACGGGGCCGGACCCGAAAGAAGGTGAACTATGCCTGTATAGGGTGAAGCCAG  3013
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  719   AAGAGCATACGGGGCCGGACCCGAAAGAAGGTGAACTATGCCTGTATAGGGTGAAGCCAG  778

Query  3014  AGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAATATGGG  3073
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  779   AGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAATATGGG  838

Query  3074  CATG  3077
              ||||
Sbjct  839   CATG  842
```

MLST scheme used: tef1-α

Score:1454 bits(787), Expect:0.0, Identities:803/811(99%), Gaps:0/811(0%)

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Query  112  TCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTCGCCTACACCCTCGGTGTCCGACAG  171  Waltergamsia balasubramanianii NRRL 64428 (FKII-L8-BK-P5)
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     TCCAAGGATGGCCAGACCCGTGAGCACGCTCTGCTCGCCTACACCCTCGGTGTCCGACAG  60  Waltergamsia alkalina CBS741.94

Query  172  CTCATTGTCGCCATCAACAAGATGGACACTGCTCAGTGGAAGGAGGCCCGTTACCTTGAG  231
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   CTCATTGTCGCCATCAACAAGATGGACACTGCTCAGTGGAAGGAGGCCCGTTACCTTGAA  120

Query  232  ATTATCAAGGAGACTTCCAACTTCATCAAGAAGGTCGGCTACAACCCCAAGACTGTTGCC  291
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121  ATTATCAAGGAGACTTCCAACTTCATCAAGAAGGTCGGCTACAACCCCAAGACTGTTGCC  180

Query  292  TTCGTCCCCATCTCCGGTTTCAACGGTGACAACATGCTTGAGCCTTCCACCAACTGCCCC  351
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  TTCGTCCCCATCTCCGGTTTCAACGGTGACAACATGCTTGAGCCTTCCACCAACTGCCCC  240

Query  352  TGGTACAAGGGCTGGGAGAAGGAGGGCAAGGGTGGCTCCAAGGTCACCGGAAAGACCATC  411
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  TGGTACAAGGGCTGGGAGAAGGAGGGCAAGGGTGGCTCCAAGGTCACCGGAAAGACCATC  300

Query  412  CTTGAGGCCATCGACGCCATCGAGCCCCCCAAGCGTCCTCTCGACAAGCCCCTCCGTCTT  471
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  CTTGAGGCCATTGACGCCATCGAGCCCCCCAAGCGTCCTCTCGACAAGCCCCTCCGTCTT  360

Query  472  CCCCTCCAGGATGTCTACAAGATCGGTGGTATTGGCACGGTGCCCGTCGGCCGTATCGAG  531
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  CCCCTCCAGGATGTCTACAAGATCGGTGGTATTGGCACGGTGCCCGTCGGCCGTATCGAG  420

Query  532  ACTGGTACCATCAAGCCCGGCATGGTCGTCACCTTCGCCCCTGCCAACGTCACCACTGAA  591
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  ACTGGTACCATCAAGCCCGGCATGGTCGTCACCTTCGCCCCTGCCAACGTCACCACTGAA  480

Query  592  GTCAAGTCCGTCGAGATGCACCACGAGCAGCTTCCCGAGGGTTTCCCCGGTGACAACGTT  651
             |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GTCAAGTCTGTCGAGATGCACCACGAGCAGCTTCCCGAGGGTTTCCCCGGTGACAACGTT  540

Query  652  GGTTTCAACGTGAAGAACGTCTCCGTCAAGGATATCCGCCGTGGTAACGTCGCTTCTGAC  711
             |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541  GGTTTCAACGTCAAGAACGTCTCCGTCAAGGATATCCGCCGTGGTAACGTCGCTTCTGAC  600

Query  712  TCCAAGAACGACCCCGCCGCTGGATGCGCCACCTTCAACGCCCAGGTCATTGTCCTGAAC  771
             |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  601  TCCAAGAACGACCCCGCCGCTGGATGCTCCACCTTCAACGCCCAGGTCATTGTCCTGAAC  660

Query  772  CACCCTGGTCAGGTCGGCCCCGGCTACGCTCCCGTCCTCGACTGCCACACTGCCCACATT  831
             ||||| ||||||||||||| ||||||| ||||||||||||||||||||||||||||||||
Sbjct  661  CACCCCGGTCAGGTCGGCCCTGGCTACGCCCCGTCCTCGACTGCCACACTGCCCACATT  720

Query  832  GCTTGCAAGTTCACCGAGATCCTTGAGAAGATCGACCGCCGTACCGGTAAGTCGGTTGAG  891
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721  GCTTGCAAGTTCACCGAGATCCTTGAGAAGATCGACCGCCGTACCGGTAAGTCGGTTGAG  780

Query  892  AACAACCCCAAGTTCATCAAGTCCGGTGACT  922
             |||||||||||||||||||||||||||||||
Sbjct  781  AACAACCCCAAGTTCATCAAGTCCGGTGACT  811
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Phaeophleospora burdickii NRRL 64430 (FKII-L3-CM-PAB3)

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MLST scheme used: ITS region

Score:1024 bits(554), Expect:0.0, Identities:562/565(99%), Gaps:3/565(0%)

Query  1    CCGTAGGGGTG-ACCTGCGGAGGGATCATTAAAATAGGCCGATAAGAAGGCACTCTCCCC  59  Phaeophleospora burdickii NRRL 64430 (FKII-L3-CM-PAB3)
            |||||  |||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11   CCGTA--GGTGAACCTGCGGAGGGATCATTAAAATAGGCCGATAAGAAGGCACTCTCCCC  68  Phaeophleospora eucalypticola CPC 26523

Query  60   TCGGGGAGAGGGCGGGCCGTATCCCACACCCTTTGTGAACCACAACTCTGTTGCTTCGGG  119
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  69   TCGGGGAGAGGGCGGGCCGTATCCCACACCCTTTGTGAACCACAACTCTGTTGCTTCGGG  128

Query  120  GGCGACCCTGCCGTCAGGCGGCGGTGCCCCCGGTGGCCTTCAACTAAACTCTGCATCTTT  179
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  129  GGCGACCCTGCCGTCAGGCGGCGGTGCCCCCGGTGGCCTTCAACTAAACTCTGCATCTTT  188

Query  180  TGCGTCGGAGTCTTTTAAAGAATTAAACAAAACTTTCAACAACGGATCTCTTGGTTCTGG  239
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  189  TGCGTCGGAGTCTTTTAAAGAATTAAACAAAACTTTCAACAACGGATCTCTTGGTTCTGG  248

Query  240  CATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATC  299
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  249  CATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATC  308

Query  300  ATCGAATCTTTGAACGCACATTGCGCCCCGTGGTATTCCGCGGGGCATGCCTGTTCGAGC  359
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  309  ATCGAATCTTTGAACGCACATTGCGCCCCGTGGTATTCCGCGGGGCATGCCTGTTCGAGC  368

Query  360  GTCATTTCACCACTCAAGCCTAGCTTGGTATTGGGCGCCGCGGCGATCTCCATCGCTGCG  419
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  369  GTCATTTCACCACTCAAGCCTAGCTTGGTATTGGGCGCCGCGGCGATCTCCATCGCTGCG  428

Query  420  CGCCTTAAAGTCTCCGGCTGAGCAGTCTGTCTCCGAGCGTTGTGACACATGTCGCTAGGG  479
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  429  CGCCTTAAAGTCTCCGGCTGAGCAGTCTGTCTCCGAGCGTTGTGACACATGTCGCTAGGG  488

Query  480  AGTGCAGGTCTGCCGCGGCCGTTAAATCTTTATCAAAGGTTGACCTCGGATCAGGTAGGG  539
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  489  AGTGCAGGTCTGCCGCGGCCGTTAAATCTTTATCAAAGGTTGACCTCGGATCAGGTAGGG  548

Query  540  ATACCCGCTGAACTTAAGCATATCA  564
            |||||||||||||||||||||||||
Sbjct  549  ATACCCGCTGAACTTAAGCATATCA  573


MLST scheme used: tef1-α

Score:708 bits(383), Expect:0.0, Identities:471/513(92%),  Gaps:8/513(1%)

Query  1    CATCGAGAAGTTCGAGAAGGTGAGTCGACACTCCTACACTGGCGGCGTTCAAATTTTCGC  60  Phaeophleospora burdickii NRRL 64430 (FKII-L3-CM-PAB3)
            ||||||||||||||||||||| ||||| ||||||||||||||||||||||||||||||||
Sbjct  1    CATCGAGAAGTTCGAGAAGGTAAGTCGGCACTCCTACACTGGCGGCGTTCAAATTTTCGC  60  Phaeophleospora eucalypticola CPC 26523

Query  61   TGCTTATCGTCCTCTGCTGGAGGGGCAAAATTTGGTGGGCTGGCGGTTGGTGGGGTGCGA  120
            |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TGCTTATCGCCCTCTGCTGGAGGGGCAAAATTTGGTGGGCTGGCGGTTGGTGGGGTGCGA  120

Query  121  GAATTTTGGCGCTTAGCCAGTTCCGGCCTCAGGCAATGACCTCATTCATCTCTACCACCA  180
            |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  121  GAATTTTGGCGCTTAGCCAGTTCCGGCCTCAGGCAATGACCTCATCCATCTCTACCACCA  180

Query  181  CCACCATCTTCACCACCGCCTCCGCCATTGGGCGTCGACGACAGACAT---ATCGTCTCG  237
            |||||| |  |||||||||||| ||| ||||| ||||||||||  ||   |||||||
Sbjct  181  CCACCA-C--CACCACCGCCTCTGCCTTTGGGGGTCGACGACAGCAATACCATCGTCTTT  237

Query  238  GCAAATGTCTTTGAATGCTTGGCTAACATTGCTGTCTCATAGGAAGCCGCTGAGCTCGGA  297
            |||||| | || |||||| ||||||| | |||||||||| ||||||||||||||||||||
Sbjct  238  GCAAATTTTTTGGAATGCCTGGCTAATAATGCTGTCTCACAGGAAGCCGCTGAGCTCGGA  297

Query  298  AAGGGTTCCTTCAAGTACGCGTGGGTGCTCGACAAGCTGAAGGCCGAGCGTGAGCGTGGT  357
            |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Sbjct  298  AAGGGTTCCTTCAAGTATGCGTGGGTGCTCGACAAGCTGAAGGCCGAGCGTGAGCGTGGT  357

Query  358  ATCACTATCGACATTGCGCTCTGGAAGTTCGAAACACCTAAGTATTATGTCCGTCAAAAA  417
            |||||||||||||||||||||||||||||||||||| || ||||| ||  ||| | ||
Sbjct  358  ATCACTATCGACATTGCGCTCTGGAAGTTCGAAACACCGAAATATTACGTGAGTCCACAA  417

Query  418  TCCCCCAAGACACCTCCAAAATAACGTGCTGACACATGCCCAGGTCACCGTCATTGACGC  477
            |   | | | || | ||||||||||||||| | ||||||||||||||||||||||||||||
Sbjct  418  TTTTC-A-GTCATCCCCAAAATAACGTGCTAATACATGCCCAGGTCACCGTCATTGACGC  475

Query  478  CCCAGGTCACCGTGATTTCATCAAGAACATGAT  510
            |||||||||||||||||||||||||||||||||
Sbjct  476  CCCAGGTCACCGTGATTTCATCAAGAACATGAT  508
```

MLST scheme used: lsu

Score:1642 bits(889), Expect:0.0, Identities:891/892(99%), Gaps:0/892(0%)

```
Query  2259  GCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCTAGTAACGGCGAGTGAA  2318  Phaeophleospora burdickii NRRL 64430 (FKII-L3-CM-PAB3)
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     GCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCTAGTAACGGCGAGTGAA  60  Phaeophleospora eucalypticola CPC 26523

Query  2319  GCGGCAACAGCTCAAATTTGAAATCTGGCGCAAGCCCGAGTTGTAATTTGTAGAGGATGC  2378
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GCGGCAACAGCTCAAATTTGAAATCTGGCGCAAGCCCGAGTTGTAATTTGTAGAGGATGC  120

Query  2379  TTCTGGGCAGCGGCCGTTCTAAGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCC  2438
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TTCTGGGCAGCGGCCGTTCTAAGTTCCTTGGAACAGGACGTCATAGAGGGTGAGAATCCC  180

Query  2439  GTATGTGACCGGCACGTACCCTCCACGTAGCTCCTTCGACGAGTCGAGTTGTTTGGGAAT  2498
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   GTATGTGACCGGCACGTACCCTCCACGTAGCTCCTTCGACGAGTCGAGTTGTTTGGGAAT  240

Query  2499  GCAGCTCTAAATGGGAGGTAAATTTCTTCTAAAGCTAAATACCGGCCAGAGACCGATAGC  2558
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   GCAGCTCTAAATGGGAGGTAAATTTCTTCTAAAGCTAAATACCGGCCAGAGACCGATAGC  300

Query  2559  GCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGGAAAGAGAGTTAAAAAGCACGTG  2618
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   GCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGGAAAGAGAGTTAAAAAGCACGTG  360

Query  2619  AAATTGTTGAAAGGGAAGCGCTTACAACCAGACTTCGTGGCGGTGTTCCGCCGGTCTTCT  2678
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   AAATTGTTGAAAGGGAAGCGCTTACAACCAGACTTCGTGGCGGTGTTCCGCCGGTCTTCT  420

Query  2679  GACCGGTCTACTCGCCGCCGCGAGGCCAGCATCGTCTGGGGCCGCCGGATAAGACCTTGG  2738
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   GACCGGTCTACTCGCCGCCGCGAGGCCAGCATCGTCTGGGGCCGCCGGATAAGACCTTGG  480

Query  2739  GAATGTAGCTTGCCTCGGTAAGTGTTATAGCCCATGGTGATGCGGCGTGCCTCGGGCGAG  2798
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GAATGTAGCTTGCCTCGGTAAGTGTTATAGCCCATGGTGATGCGGCGTGCCTCGGGCGAG  540

Query  2799  GTCCGCGCTTCGGCAAGGATGCTGGCGTAATGGTTGTCAGCGGCCCGTCTTGAAACACGG  2858
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   GTCCGCGCTTCGGCAAGGATGCTGGCGTAATGGTTGTCAGCGGCCCGTCTTGAAACACGG  600

Query  2859  ACCAAGGAGTCTAACATCTATGCGAGTGTTCGGGTGTCAAACCCCTACGCGTAATGAAAG  2918
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   ACCAAGGAGTCTAACATCTATGCGAGTGTTCGGGTGTCAAACCCCTACGCGTAATGAAAG  660

Query  2919  TGAACGGAGGTGGGAAGCGCAAGCTGCACCATCGACCGATCCTGATGTCCTCGGATGGAT  2978
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   TGAACGGAGGTGGGAAGCGCAAGCTGCACCATCGACCGATCCTGATGTCCTCGGATGGAT  720

Query  2979  TTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGA  3038
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   TTGAGTAAGAGCATAGCTGTTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGTGA  780

Query  3039  AGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAA  3098
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   AGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCAAA  840

Query  3099  TTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCCTGC  3150
             |||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  841   TTTGGGTATAGGGGCGAAAGACTGATCGAACCATCTAGTAGCTGGTTCCTGC  892
```

Spissiomyces californiae NRRL 64432 (FJII-L1-SW-P2)

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MLST scheme used: ITS region

Score:1003 bits(543), Expect:0.0, Identities:553/558(99%), Gaps:0/558(0%)

Query  1    CCTGCGGAAGGATCATTACCGAGTCCACGGGGCTTCGGCCCCCAAACTCCCACCCCTTGT  60  Spissiomyces californiae NRRL 64432 (FJII-L1-SW-P2)
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  11   CCTGCGGAAGGATCATTACCGAGTCCACGGGGCTTCGGCCCCCAAACTCCCACCCCTTGC  70  Neospissiomyces floridanus CPC 45908

Query  61   GTACCTTAACCCTTGTTGCTTTGGCGGGCCTGCGCGCCCTGAAAAAGCGCGCTGCCGGCT  120
            |||||||||| |||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct  71   GTACCTTAACCTTTGTTGCTTTGGCGGGCCTGCGCGCCCTGAAAAGGCGCGCTGCCGGCT  130

Query  121  TCTGCTGGCTCGTGCCCGCCAGAGGCCCTCCAAACTCCTGTTTTTACCGGTGTCGTCTGA  180
            |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  131  TCTGCTGGCTCGTGCCCGCCAGAGGCCCTCCAAACTCCTGTTTTTACCGGTGTTGTCTGA  190

Query  181  GCGTAAACATGAATATTAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  191  GCGTAAACATGAATATTAAAACTTTCAACAACGGATCTCTTGGTTCTGGCATCGATGAAG  250

Query  241  AACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  251  AACGCAGCGAAATGCGATAAGTAATGTGAATTGCAGAATTCAGTGAATCATCGAATCTTT  310

Query  301  GAACGCACATTGCGCCCTTTGGTATTCCGAAGGGCATGCCTGTTCGAGCGTCATTACACC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  311  GAACGCACATTGCGCCCTTTGGTATTCCGAAGGGCATGCCTGTTCGAGCGTCATTACACC  370

Query  361  CCTCAAGCTTTGCTTGGTATTGGGCCTCCGTCCGCCAGCGGACGGGCCTCGAAATCCTCG  420
            |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  371  CCTCAAGCTTTGCTTGGTATTGGGCCTTCGTCCGCCAGCGGACGGGCCTCGAAATCCTCG  430

Query  421  GCGGCGGCGCCCGGCTTTGAGCGTAGTAGAAATTCTCATCTCGCTTTGAAGGCCCGTGGC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  431  GCGGCGGCGCCCGGCTTTGAGCGTAGTAGAAATTCTCATCTCGCTTTGAAGGCCCGTGGC  490

Query  481  GTCTGCTTGCCGGACGACCCCCAATCTTTCTTCTAAGGTTGACCTCGGATCAGGTAGGGA  540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  491  GTCTGCTTGCCGGACGACCCCCAATCTTTCTTCTAAGGTTGACCTCGGATCAGGTAGGGA  550

Query  541  TACCCGCTGAACTTAAGC  558
            ||||||||||||||||||
Sbjct  551  TACCCGCTGAACTTAAGC  568



MLST scheme used: lsu

Score:821 bits(444), Expect:0.0, Identities:446/447(99%), Gaps:0/447(0%)

Query  2360  AGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAACAGCTCAGATTTGAAATCTGGCCCT  2419  Spissiomyces californiae NRRL 64432 (FJII-L1-SW-P2)
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     AGGGATTGCCTTAGTAACGGCGAGTGAAGCGGCAACAGCTCAGATTTGAAATCTGGCCCT  60  Neospissiomyces floridanus strain CPC 45908

Query  2420  TTCAGGGTCCGAGTTGTAATCTGTAGAGGATGCCTCGGCGTCGGCCCCGGTCTAAGTTCC  2479
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    TTCAGGGTCCGAGTTGTAATCTGTAGAGGATGCCTCGGCGTCGGCCCCGGTCTAAGTTCC  120

Query  2480  TTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTACGTGACCGGTGGCTCAGCCATGTG  2539
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TTGGAACAGGACGTCACAGAGGGTGAGAATCCCGTACGTGACCGGTGGCTCAGCCATGTG  180

Query  2540  AGGCTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGAGGTAAATTTCT  2599
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AGGCTCCTTCGACGAGTCGAGTTGTTTGGGAATGCAGCTCTAAATGGGAGGTAAATTTCT  240

Query  2600  TCTAAAGCTAAATATTGGCCAGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAA  2659
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TCTAAAGCTAAATATTGGCCAGAGACCGATAGCGCACAAGTAGAGTGATCGAAAGATGAA  300

Query  2660  AAGCACTTTGGAAAGAGAGTTAAAAAGCACGTGAAATTGTTGAAAGGGAAGCGCTTGCAA  2719
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AAGCACTTTGGAAAGAGAGTTAAAAAGCACGTGAAATTGTTGAAAGGGAAGCGCTTGCAA  360

Query  2720  CCAGACTTGCCCGCAGTTGCTCAACCGGTCTCTCGGCCGGTGTACTCTTCTGCGGTCAGG  2779
              ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  361   CCAGACTTGCCCGCAGTTGCTCAACCGGTCTCCCGGCCGGTGTACTCTTCTGCGGTCAGG  420

Query  2780  CCAGCATCAGTTCGGGCGGTCGGATAA  2806
              ||||||||||||||||||||||||||
Sbjct  421   CCAGCATCAGTTCGGGCGGTCGGATAA  447
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MLST scheme used: tub2

Score:1090 bits(590), Expect:0.0, Identities:751/829(91%), Gaps:9/829(1%)

```
Query  127  TTCGTTCCCCGTGCTGTTCTCATCGACTTGGAGCCTGGCACTATGGATGCCGTCCGTGCT  186  Spissiomyces californiae NRRL 64432 (FJII-L1-SW-P2)
            |||||||||||||||||||| ||||||||||| ||||||||||||||||||||||||||
Sbjct  1    TTCGTTCCCCGTGCTGTTCTCGTCGACTTGGAGCCGGGCACTATGGATGCCGTCCGTGCT  60  Spissiomyces ramosus CGMCC 3.17076

Query  187  GGTCCTTTCGGTCAACTCTTCCGCCCGGATAACTTCGTCTTCGGCCAGTCTGGTGCCGGT  246
            |||||||||||||||||||||||||| || ||||||||||||| ||||||||||||||||
Sbjct  61   GGTCCTTTCGGTCAACTCTTCCGCCCTGACAACTTCGTCTTCGGTCAGTCTGGTGCCGGT  120

Query  247  AACAACTGGGCCAAGGGTCACTACACCGAGGGTGCTGAGCTGGTCGACCAAGTCTTGGAC  306
            |||||||||||||||||||||||||||||||||||||||||||||| ||||||||| | ||
Sbjct  121  AACAACTGGGCCAAGGGTCACTACACCGAGGGTGCTGAGCTGGTGGACCAAGTCCTCGAT  180

Query  307  GTCGTACGTCGTGAGGCCGAGGGCTGTGACTGCCTCCAAGGCTTCCAGATCACCCACTCC  366
            ||||| |||||||||||| ||||||||||||||||||||| ||||||||||||||| |||||
Sbjct  181  GTCGTGCGTCGTGAGGCTGAGGGCTGTGACTGCCTCCAGGGCTTCCAGATCACTCACTCT  240

Query  367  CTCGGTGGTGGTACCGGTGCTGGTATGGGTACTCTTTTGATCTCCAAGATCCGCGAGGAG  426
            || |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  241  CTTGGTGGTGGTACTGGTGCCGGTATGGGTACTCTTTTGATCTCCAAGATCCGCGAGGAG  300

Query  427  TTCCCGGACCGCATGATGGCCACTTTCTCCGTTCTTCCCTCGCCCAAGGTGTCAGACACC  486
            |||||||| |||||||||||||||||||||||||||| ||||||||||||||| || ||
Sbjct  301  TTCCCGGATCGCATGATGGCCACTTTCTCCGTTCTTCCGTCGCCCAAGGTGTCCGATACA  360

Query  487  GTTGTTGAGCCATACAACGCTACCCTGTCCATCCACCAGCTGGTTGAGAACTCGGACGAG  546
            |||||||||||||||||||||||| || ||| | |||||||||||| ||||||||||||||
Sbjct  361  GTTGTTGAGCCATACAACGCTACTCTCTCCGTGCACCAGCTGGTGGAGAACTCGGACGAG  420

Query  547  ACCTTCTGTATCGACAACCAGGTATG-C-TACCTCATGTTCACGCGCTAGATTACACTG-  603
            || ||||| || |||||||||||| || | | ||||  || |||   ||||| | |||||
Sbjct  421  ACTTTCTGCATTGACAACCAGGTTTGTCGTCCCTCC-GT-CACAA-CTAGAGT-CACTGT  476

Query  604  -CTAA-ACCATTCAGGCCCTCTACGACATCTGCATGGGCACTCTCAAGCTCAGCAACCCC  661
             |||| || ||||||||||||||||||||| ||||||| | |||||||||||||| ||| |||
Sbjct  477  ACTAAGACTATTCAGGCCCTCTACGACATTTGCATGAGGACTCTCAAGCTCAACAATCCC  536

Query  662  ACCTATGGTGACCTGAACCACCTCGTCTCGGCGGTCATGTCTGGTGTCACCACTTGCCTC  721
            |||||||| ||| ||||||||||||||| || |||||||| ||||||||||||||||||
Sbjct  537  ACCTATGGCGACTTGAACCACCTCGTCTCTGCCGTCATGTCCGGTGTCACCACTTGCCTG  596

Query  722  CGCTTCCCCGGTCAGCTCAACTCCGATCTGCGCAAGCTTGCAGTCAACATGGTCCCCTTC  781
            || |||||||||||||||||||| ||||||||||||||| |||||||||| || |||
Sbjct  597  CGATTCCCCGGTCAGCTCAACTCTGATCTGCGCAAGCTTGCCGTCAACATGGTTCCATTC  656

Query  782  CCTCGTCTACACTTCTTCATGGTTGGCTTTGCTCCATTGACCAGCCGTGGCGCGTACTCC  841
            |||||||| |||||||||||||||||| ||||||||||||||||||||||| |||||
Sbjct  657  CCTCGTCTCCACTTCTTCATGGTTGGCTTCGCTCCATTGACCAGCCGTGGCGCGAACTCC  716

Query  842  TTCCGTGCCGTGACCGTGCCGGAGTTGACCCAGCAGATGTTCGACCCCAAGAACATGATG  901
            |||||||||||||||| |||||||||| || || || || ||||||||||||||||||||
Sbjct  717  TTCCGTGCCGTGACCGTTCCGGAGTTGACTCAACAAATCTTTGACCCCAAGAACATGATG  776

Query  902  GCCGCGTCTGACTTCCGAAACGGCCGCTACCTGACCTGCTCTGCTATCT  950
            || ||| |||||||||| ||||| || ||||| || ||||||||||||
Sbjct  777  GCTGCGGCTGACTTCCGCAACGGTCGTTACCTCACTTGCTCTGCTATCT  825
```

MLST scheme used: rpb2

Score:915 bits(495), Expect:0.0, Identities:509/516(99%), Gaps:0/516(0%)

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Query  1    ATGGCCCTTCTGGAAGAGTATGAACCGCGGAACGATCCAAACGCGACAAAAGTATTCGTC  60  Spissiomyces californiae NRRL 64432 (FJII-L1-SW-P2)
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  232  ATGGCCCTTCTGGAAGAGTATGAACCGCGGAACGATCCAAACGCGACAAAAGTATTCGTC  291  Neospissiomyces floridanus CPC 45908

Query  61   AATGGTGTCTGGGTAGGTGTCCATCGTGATCCGACACAGCTGGTATCAGTCGTAAAGGGT  120
            |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  292  AATGGTGTCTGGGTAGGTGTTCATCGTGATCCGACACAGCTGGTATCAGTCGTAAAGGGT  351

Query  121  CTGCGTGGAAGGACACTGGATCCTGAGATCAGTATGATCAGGGACATTCGTGATCGTGAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  352  CTGCGTGGAAGGACACTGGATCCTGAGATCAGTATGATCAGGGACATTCGTGATCGTGAA  411

Query  181  TTCAAGATCTTTACGGATGCTGGCAGGGTGTGTCGACCACTGTTCGTCATTGACAACGAC  240
            |||||||||||||| |||||||||||||||| || ||||||||||||||||||||||||
Sbjct  412  TTCAAGATCTTTACAGATGCTGGCAGAGTGTGTCGACCACTATTTGTCATTGACAACGAC  471

Query  241  CCGAGCAGTGCAAACAAAGGCAACTTGGTACTCAACAAGGCCCACATCGACAAGCTTCAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  472  CCGAGCAGTGCAAACAAAGGCAACTTGGTACTCAACAAGGCCCACATCGACAAGCTTCAG  531

Query  301  GCAGACAGGGAACTCGACACGTCTGGATGGACACAGAGAGAGATCCAGGAAGCAAATATA  360
            |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  532  GCAGACAGGGAACTCGACACGTCTGGATGGACACAGAGAGAGATTCAGGAAGCAAATATA  591

Query  361  GGCTGGAACTACCTATTGAAGGAGAAGGTCATTGAGTATCTGGACGCTGAGGAGGAGGAA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  592  GGCTGGAACTACCTATTGAAGGAGAAGGTCATTGAGTATCTGGACGCTGAGGAGGAGGAA  651

Query  421  ACCGCCATGATTGTGATGAGTCCAGACGACCTCGCCGATCATCACCGCGTGCGAGCGGGC  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  652  ACCGCCATGATTGTGATGAGTCCAGACGACCTCGCCGATCATCACCGCGTGCGAGCGGGC  711

Query  481  GAATCCATATTCGAAGATGATGCCGATCCGCATAAA  516
            |||||||||||||||||||||||||||||| |||
Sbjct  712  GAATCCATATTCGAAGATGATGCCGATCCGCACAAA  747
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MLST scheme used: ssu

Score:1879 bits(1017), Expect:0.0, Identities:1019/1020(99%), Gaps:0/1020(0%)

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Query  66    ACGGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATAGTACCTTACTA  125  Spissiomyces californiae NRRL 64432 (FJII-L1-SW-P2)
             || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1     ACAGTGAAACTGCGAATGGCTCATTAAATCAGTTATCGTTTATTTGATAGTACCTTACTA  60   Spissiomyces ramosus CGMMCC 3.17076

Query  126   CATGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAACCCCGACTTCGGAAGGG  185
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    CATGGATAACCGTGGTAATTCTAGAGCTAATACATGCTAAAAACCCCGACTTCGGAAGGG  120

Query  186   GTGTATTTATTAGATAAAAAACCAACGCCCTTCGGGGCTCCTTGGTGATTCATAATAACT  245
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GTGTATTTATTAGATAAAAAACCAACGCCCTTCGGGGCTCCTTGGTGATTCATAATAACT  180

Query  246   TAACGAATCGCATGGCCTTGAGCCGGCGATGGTTCATTCAAATTTCTGCCCTATCAACTT  305
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   TAACGAATCGCATGGCCTTGAGCCGGCGATGGTTCATTCAAATTTCTGCCCTATCAACTT  240

Query  306   TCGATGGTAGGATAGTGGCCTACCATGGTATCAACGGGTAACGGGGAATTAGGGTTCGAT  365
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   TCGATGGTAGGATAGTGGCCTACCATGGTATCAACGGGTAACGGGGAATTAGGGTTCGAT  300

Query  366   TCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAAT  425
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   TCCGGAGAGGGAGCCTGAGAAACGGCTACCACATCCAAGGAAGGCAGCAGGCGCGCAAAT  360

Query  426   TACCCAATCCCGACACGGGGAGGTAGTGACAATAAATACTGATACAGGGCTCTTTTGGGT  485
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   TACCCAATCCCGACACGGGGAGGTAGTGACAATAAATACTGATACAGGGCTCTTTTGGGT  420

Query  486   CTTGTAATTGGAATGAGTACAATTTAAATCCCTTAACGAGGAACAATTGGAGGGCAAGTC  545
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   CTTGTAATTGGAATGAGTACAATTTAAATCCCTTAACGAGGAACAATTGGAGGGCAAGTC  480

Query  546   TGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTTGCAGTTA  605
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   TGGTGCCAGCAGCCGCGGTAATTCCAGCTCCAATAGCGTATATTAAAGTTGTTGCAGTTA  540

Query  606   AAAAGCTCGTAGTTGAACCTTGGGCCTGGCTGGCCGGTCCGCCTCACCGCGTGTACTGGT  665
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AAAAGCTCGTAGTTGAACCTTGGGCCTGGCTGGCCGGTCCGCCTCACCGCGTGTACTGGT  600

Query  666   CCGGCCGGGCCTTTCCTTCTGGGGATCCGCATGCCCTTCACTGGGTGTGCCGGGGAACCA  725
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   CCGGCCGGGCCTTTCCTTCTGGGGATCCGCATGCCCTTCACTGGGTGTGCCGGGGAACCA  660

Query  726   GGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTTTGCTCGAATACATTAGC  785
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   GGACTTTTACTTTGAAAAAATTAGAGTGTTCAAAGCAGGCCTTTGCTCGAATACATTAGC  720

Query  786   ATGGAATAATAGAATAGGACGTGCGGTTCTATTTTGTTGGTTTCTAGGACCGCCGTAATG  845
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   ATGGAATAATAGAATAGGACGTGCGGTTCTATTTTGTTGGTTTCTAGGACCGCCGTAATG  780

Query  846   ATTAATAGGGATAGTCGGGGGTGTCAGTATTCAATTGTCAGAGGTGAAATTCTTGGATTT  905
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   ATTAATAGGGATAGTCGGGGGTGTCAGTATTCAATTGTCAGAGGTGAAATTCTTGGATTT  840

Query  906   ATTGAAGACTAACTACTGCGAAAGCATTCACCAAGGATGTTTTCATTAATCAGTGAACGA  965
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841   ATTGAAGACTAACTACTGCGAAAGCATTCACCAAGGATGTTTTCATTAATCAGTGAACGA  900

Query  966   AAGTTAGGGGATCGAAGACGATCAGATACCGTCGTAGTCTTAACCGTAAACTATGCCGAC  1025
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  901   AAGTTAGGGGATCGAAGACGATCAGATACCGTCGTAGTCTTAACCGTAAACTATGCCGAC  960

Query  1026  TAGGGATCGGGCGATGTTATCATTTTGACTCGCTCGGCACCTTACGAGAAATCAAAGTCT  1085
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  961   TAGGGATCGGGCGATGTTATCATTTTGACTCGCTCGGCACCTTACGAGAAATCAAAGTCT  1020
```

Neocatenulostroma huberii NRRL B-64422 (FJI-L3-BK-P2)

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MLST scheme used: ITS region

Score:942 bits(510), Expect:0.0, Identities:521/526(99%), Gaps:2/526(0%)

Query  2    ACCTGCGGAGGGATCATTACCGAGTGAGGGCCTCTGGCCCGACCTCCAACCCCATGTTAT  61   Neocatenulostroma huberii NRRL B-64422 (FJI-L3-BK-P2)
            |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Sbjct  24   ACCTGCGGAGGGATCATTACTGAGTGAGGGCCTCTGGCCCGACCTCCAACCCCATGTTAT  83   Neocatenulostroma germanicum CBS 539.88

Query  62   CCGACACTGTTGCCTCCGGGGCGACCCGGCCTGCCTTCGGGCG-TTCGGGGCCCCGGGTG  120
            | ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Sbjct  84   CTGACACTGTTGCCTCCGGGGCGACCCGGCCTGCCTTCGGGCGTTTCGGGGCCCCGGGTG  143

Query  121  GACCATTCAACTCTGCATCTTTGCGTCTGAGTAAATGATTGAATCAATCAAAACTTTCAA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  144  GACCATTCAACTCTGCATCTTTGCGTCTGAGTAAATGATTGAATCAATCAAAACTTTCAA  203

Query  181  CAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  204  CAACGGATCTCTTGGTTCTGGCATCGATGAAGAACGCAGCGAAATGCGATAAGTAATGTG  263

Query  241  AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTCC  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  264  AATTGCAGAATTCAGTGAATCATCGAATCTTTGAACGCACATTGCGCCCCTTGGTATTCC  323

Query  301  GAGGGGCATGCCTGTTCGAGCGTCATTACACCACTCAAGCCTCGCTTGGTATTGGGCGCC  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  324  GAGGGGCATGCCTGTTCGAGCGTCATTACACCACTCAAGCCTCGCTTGGTATTGGGCGCC  383

Query  361  GCGGTCCGCCGCGCGCCTCAATGTTTCCGGCTGAGCTCTCTGTCTCTAAGCGTTGTGGTT  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  384  GCGGTCCGCCGCGCGCCTCAATGTTTCCGGCTGAGCTCTCTGTCTCTAAGCGTTGTGGTT  443

Query  421  AAAACTATCCGCTTGCGAGATT-GGGGGCGTCTGGCCGTTAAACCATTACTCAAAGGTTG  479
            ||||||||||||||||||||  ||||||||||||||||||||||||||||||||||||||
Sbjct  444  AAAACTATCCGCTTGCGAGATCGGGGGGCGTCTGGCCGTTAAACCATTACTCAAAGGTTG  503

Query  480  ACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATA  525
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  504  ACCTCGGATCAGGTAGGGATACCCGCTGAACTTAAGCATATCAATA  549


MLST scheme used: lsu

Score:1646 bits(891), Expect:0.0, Identities:891/891(100%), Gaps:0/891(0%)

Query  2227  TAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCTAGTAACGGCGAGT  2286  Neocatenulostroma huberii NRRL B-64422 (FJI-L3-BK-P2)
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1      TAAGCATATCAATAAGCGGAGGAAAAGAAACCAACAGGGATTGCCCTAGTAACGGCGAGT  60   Neocatenulostroma germanicum CBS:539.88

Query  2287  GAAGCGGCAACAGCTCAAATTTGAAATCTGGCGCAAGCCCGAGTTGTAATTTGTAGAGGA  2346
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61    GAAGCGGCAACAGCTCAAATTTGAAATCTGGCGCAAGCCCGAGTTGTAATTTGTAGAGGA  120

Query  2347  TGCTTCTGGGCAGCGGCCGGTCTAAGTTCCTTGGAACAGGACGTCACAGAGGGTGAGAAT  2406
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   TGCTTCTGGGCAGCGGCCGGTCTAAGTTCCTTGGAACAGGACGTCACAGAGGGTGAGAAT  180

Query  2407  CCCGTATGTGATCGGTTGGCACCCGCTACGTAGCTCCTTCGACGAGTCGAGTTGTTTGGG  2466
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   CCCGTATGTGATCGGTTGGCACCCGCTACGTAGCTCCTTCGACGAGTCGAGTTGTTTGGG  240

Query  2467  AATGCAGCTCTAAATGGGAGGTAAATGCCTTCTAAAGCTAAATACCGGCCAGAGACCGAT  2526
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241   AATGCAGCTCTAAATGGGAGGTAAATGCCTTCTAAAGCTAAATACCGGCCAGAGACCGAT  300

Query  2527  AGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGGAAAGAGAGTTAAAAAGCAC  2586
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AGCGCACAAGTAGAGTGATCGAAAGATGAAAAGCACTTTGGAAAGAGAGTTAAAAAGCAC  360

Query  2587  GTGAAATTGTTGAAAGGGAAGCGCATGCAACCAGACTTGTCCGCGGTGTTCCGCCGGTCT  2646
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GTGAAATTGTTGAAAGGGAAGCGCATGCAACCAGACTTGTCCGCGGTGTTCCGCCGGTCT  420

Query  2647  TCTGACCGGTCTACTCGCCGCGGGCAGGCCAGCATCATCTGGGAGCGCCGGATAAAGGTA  2706
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421   TCTGACCGGTCTACTCGCCGCGGGCAGGCCAGCATCATCTGGGAGCGCCGGATAAAGGTA  480

Query  2707  GCGGGAATGTGGCCCCTCGGGGTGTTATAGCTCGCTACACAATACGGCGCCTCCCGGGTG  2766
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481   GCGGGAATGTGGCCCCTCGGGGTGTTATAGCTCGCTACACAATACGGCGCCTCCCGGGTG  540

Query  2767  AGGTCCGCGCTTCGGCTAGGATGCTGGCGTAATGGTTGTATGCGGCCCGTCTTGAAACAC  2826
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  541   AGGTCCGCGCTTCGGCTAGGATGCTGGCGTAATGGTTGTATGCGGCCCGTCTTGAAACAC  600

Query  2827  GGACCAAGGAGTCTACCATCTATGCGAGTGTTCGGGTGTCAAACCCCTACGCGCAATGAA  2886
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   GGACCAAGGAGTCTACCATCTATGCGAGTGTTCGGGTGTCAAACCCCTACGCGCAATGAA  660

Query  2887  AGTGAACGGAGGTGGGAACCGCAAGGTGCACCATCGACCGATCCTGATGTCTTCGGATGG  2946
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661   AGTGAACGGAGGTGGGAACCGCAAGGTGCACCATCGACCGATCCTGATGTCTTCGGATGG  720

Query  2947  ATTTGAGTAAGAGCATAGCTGGTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGT  3006
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  721   ATTTGAGTAAGAGCATAGCTGGTGGGACCCGAAAGATGGTGAACTATGCCTGAATAGGGT  780

Query  3007  GAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCA  3066
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781   GAAGCCAGAGGAAACTCTGGTGGAGGCTCGCAGCGGTTCTGACGTGCAAATCGATCGTCA  840

Query  3067  AATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCC  3117
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  841   AATTTGGGTATAGGGGCGAAAGACTAATCGAACCATCTAGTAGCTGGTTCC  891
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MLST scheme used: rpb2

Score:1351 bits(731), Expect:0.0, Identities:813/854(95%), Gaps:0/854(0%)

```
Query  1    ACGCCTCCACACTCTCGCATTTGCGGCGAACCAACACGCCAATAGGCAGAGATGGCAAGA  60  Neocatenulostroma huberii NRRL B-64422 (FJI-L3-BK-P2)
            |||| ||||| ||||| ||||| |||||||| |||||||| |||||||||||| |||||||
Sbjct  1    ACGCTTCCACGCTCTCCCATTTACGGCGAACGAACACGCCTATAGGCAGAGACGGCAAGA  60  Neocatenulostroma spinulosum FMR 18793

Query  61   TCGCGAAGCCCGCGCCAACTGCACAACACCCACTGGGGCTTGGTATGCCCTGCCGAGACGC  120
            ||||||| ||||||||||||| |||||||||||||||||||||||||| |||||||| |
Sbjct  61   TCGCGAAACCGCGCCAACTGCATAACACCCACTGGGGCTTGGTATGCCCGGCCGAGACTC  120

Query  121  CTGAAGGACAGGCTTGTGGTTTGGTGAAGAATCTGGCGCTGATGTGCTACGTCTCCGTCG  180
            | ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCGAAGGGCAGGCTTGTGGGTTGGTGAAGAATCTGGCGCTGATGTGCTACGTCTCCGTCG  180

Query  181  GCACACCGGGCACGCCACTCATCGAGTACATGCGCCACAGAGGCATGGAGCTGCTCGAGG  240
            ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  181  GCACACCGGGCACGCCACTTATCGAGTACATGCGCCACAGAGGCATGGAGCTGCTCGAGG  240

Query  241  AGTACGATGCGATCATGAACCCGAACGCTACGAAAGTATTCCTGAACGGCACATGGGTGG  300
            |||||||||| |||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  241  AGTACGATGCCATCATGAACCCGAACGCTACGAAAGTCTTCCTGAACGGCACATGGGTGG  300

Query  301  GCGTGCACACGAACGGCAAAGCGCTGACTGACGCTATTCGCGACCTGCGGCGGAAGCAGG  360
            |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  301  GCGTGCACACGAACGGCAAAGCGCTGACTGACGCCATTCGCGACCTGCGGCGGAAGCAGG  360

Query  361  TCATTGGGTTCGAGATTACAATCATCCGTGACGTCCGCGAGCGGGAGGTCAAGGTCTTCA  420
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCATTGGCTTCGAGATTACAATCATCCGTGACGTCCGCGAGCGGGAGGTCAAGGTCTTCA  420

Query  421  CCGACGCTGGAAGAGTGATGCGGCCGCTGTTTGTAGTGAACACGGATAAGCGGTCTCCGG  480
            | || |||||||||||||||||||||||||| ||||| |||||||||||||||||||||||
Sbjct  421  CGGATGCTGGAAGAGTGATGCGGCCGCTTTTGTGGTGAACACGGATAAGCGGTCTCCGG  480

Query  481  ACTTCGGCAGTCTGGCGTTGAAACAGGAGCATGTGGCTAGGCTGCAGCAAGATCAGGAGA  540
            |||||||||||||||||||||| |||||||||||||||||||||||||||| |||||||
Sbjct  481  ACTTCGGCAGTCTGGCGTTGAAGCAGGAGCATGTGGCTAGGCTGCAGCAAGACCAGGAGA  540

Query  541  TCTTGGCTGGTATGCAAGGACAAGCCATCAGTGAAGATGAGAAAGCGGATGCTACTTTCG  600
            |||||||||| ||||| || || ||||||||||||||| ||||||||||||||||||||||
Sbjct  541  TCTTGGCTGGCATGCAGGGGCAGGCCATCAGTGAAGACGAGAAAGCGGATGCTACTTTCG  600

Query  601  GCTGGAAGGGCCTCATTAAGAACGGTGTCGTTGAGTTCCTCGATGCTGAAGAGGAAGAGA  660
            |||||||||| ||||| |||||||||||||||||||||||||||||||||| |||||||
Sbjct  601  GCTGGAAGGGTCTCATCAAGAACGGTGTCGTTGAGTTCCTCGATGCTGAAGAAGAAGAGA  660

Query  661  CCGCCATGATCATCATGACGCCCGACGACCTCGAAGACTACAAGTCTGTCAAGTCTGGCA  720
            | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  661  CGGCCATGATCATCATGACGCCCGACGACCTCGAAGACTACAAGTCTGTCAAGTCTGGCA  720

Query  721  TACCCTGGGTTGAGTCGAAAGACGACCCACACCGTCGTATCAAATCCAAGCCGAATACCC  780
            |||||||||| ||||| |||||||||||| ||||| ||||||||||||||||||||||||
Sbjct  721  TACCCTGGGTGGAGTCCAAAGACGACCCGCACCGCCGTATCAAATCCAAGCCGAATACCC  780

Query  781  AGGTGGCGCAGTGGACGCATTGCGAGATCCATCCCGCCATGATTCTCGGTATCTGCGCCT  840
            | |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  781  AAGTGGCGCAATGGACGCATTGCGAGATCCATCCCGCCATGATTCTCGGTATCTGCGCCT  840

Query  841  CCATCATCCCGTTC  854
            ||||||| ||||||
Sbjct  841  CCATCATTCCGTTC  854
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MLST scheme used: tub2

Score:353 bits(191), Expect:1e-101, Identities:234/255(92%), Gaps:1/255(0%)

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Query  17   GGTAACCAAATCGGTGCCGCCTTCTGGCAGACCATCTCCGGCGAGCACGGTCTCGATGGC  76  Neocatenulostroma huberii NRRL B-64422 (FJI-L3-BK-P2)
            |||||||||||||||||||||||||||||||||||||||||||||||||| || ||||||
Sbjct  1    GGTAACCAAATCGGTGCCGCCTTCTGGCAGACCATCTCCGGCGAGCACGGCCTGGATGGC  60  Neocatenulostroma microsporum CBS:101951

Query  77   TCTGGCGTGTATGTGGACGCGAATTGAAACGAGAAGAAGATGAACGCTGATTCAGAACA  136
            |||||||||||||  ||  | | ||| | || | ||| |||| || |||||  || |||
Sbjct  61   TCTGGCGTGTATGTTAACAAGCA-TGAGATGATATAGATGATGGACACTGATGAAGGACA  119

Query  137  GGTACAATGGCACGTCCGATCTCCAGCTGGAGCGCATGAACGTCTACTTCAACGAGGTAG  196
            | |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  120  GATACAATGGCACGTCCGACCTCCAGCTGGAGCGCATGAACGTCTACTTCAACGAGGTAG  179

Query  197  GAGTCCTGAGAGTGTGGATACAAGGCACGCCAAGACTCGGTGCTAACACGCGTTCTAGGC  256
            |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Sbjct  180  GAGTCCTGAGAGTGTGGATACAAGGCACGCCAAGACTCGGTGCTAACACGCCTTCTAGGC  239

Query  257  CTCTGGCAACAAGTA  271
            |||||||||||||||
Sbjct  240  CTCTGGCAACAAGTA  254
```

MLST scheme used: tef1-α

Score:1378 bits(746), Expect:0.0, Identities:786/806(98%), Gaps:0/806(0%)

```
Query  198   GACTGCGCCATCCTCATCATTGCCGCCGGTACTGGTGAGTTCGAGGCCGGTATCTCCAAG  257  Neocatenulostroma huberii NRRL B-64422 (FJI-L3-BK-P2)
             |||||||||| ||||||||||||| ||||||||||||||||||||||||||||||||||
Sbjct  1     GACTGCGCCATTCTCATCATTGCCGCTGGTACTGGTGAGTTCGAGGCCGGTATCTCCAAG  60  Neocatenulostroma spinulosum FMR 18793

Query  258   GATGGCCAGACTCGTGAGCACGCCCTGCTCGCTTACACCCTCGGTGTCAAGCAGCTCATC  317
             |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  61    GATGGCCAGACTCGTGAGCACGCCCTGCTCGCTTACACCCTCGGTGTGAAGCAGCTCATC  120

Query  318   GTCGCCATCAACAAGATGGACACCACCAAGTGGTCCGAGGACCGCTACAACGAGATCATC  377
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  121   GTCGCCATCAACAAGATGGACACCACCAAGTGGTCCGAGGACCGCTACAACGAGATCATC  180

Query  378   AAGGAGACGTCCAACTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTCCCCTTCGTC  437
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181   AAGGAGACGTCCAACTTCATCAAGAAGGTCGGCTACAACCCCAAGACCGTCCCCTTCGTC  240

Query  438   CCGATCTCTGGCTTCAATGGCGACAACATGATCGATGCCTCCCCCAACTGCCCATGGTAC  497
             |||||||| |||||||| || ||||||||||||||| ||||||||||||||||||||||||
Sbjct  241   CCGATCTCCGGCTTCAACGGTGACAACATGATCGACGCCTCCCCCAACTGCCCATGGTAC  300

Query  498   AAGGGCTGGGAGAAGGAGACTAAGACCAAGTCGACCGGCAAGACCCTCCTCGAGGCCATT  557
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  301   AAGGGCTGGGAGAAGGAGACCAAGACCAAGTCGACCGGCAAGACCCTCCTCGAGGCCATT  360

Query  558   GACGCCATCGACCCGCCGTCGCGCCCGACCGACAAGGCTCTCCGTCTTCCCCTTCAGGAT  617
             |||||||||||||| |||  ||||||||||||||||||||||||||||||||||||||||
Sbjct  361   GACGCCATCGACCCACCGCAGCGCCCGACCGACAAGGCTCTCCGTCTTCCCCTTCAGGAC  420

Query  618   GTCTACAAGATTGGTGGCATTGGGACAGTTCCTGTCGGCCGTGTCGAGACCGGTGTCATC  677
             || ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct  421   GTTTACAAGATTGGTGGCATTGGGACAGTTCCTGTCGGCCGTGTCGAGACAGGTGTCATC  480

Query  678   AAGGCCGGCATGGTCGTTACTTTCGCCCCAGCTGGTGTCACCACTGAGGTGAAGTCCGTC  737
             |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Sbjct  481   AAGGCCGGCATGGTCGTTACCTTCGCCCCAGCTGGTGTCACCACTGAGGTGAAGTCCGTC  540

Query  738   GAGATGCACCACGAGCAGCTTACCGAGGGTCTTCCGGGTGACAACGTCGGCTTCAACGTC  797
             |||||||||||||||||||||||||||||||| |||||||||||| ||||||||||||||||
Sbjct  541   GAGATGCACCACGAGCAGCTTACCGAGGGTCTCCCGGGTGACAATGTCGGCTTCAACGTC  600

Query  798   AAGAACGTCTCTGTCAAGGAGATCCGTCGTGGCAACGTCGCCGGTGACTCCAAGAACGAC  857
             |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  601   AAGAACGTCTCCGTCAAGGAGATCCGTCGTGGCAACGTCGCCGGTGACTCCAAGAACGAC  660

Query  858   CCGCCAAAGGGCTGCGACTCCTTCAACGCCCAGGTCATCGTCCTCAACCACCCGGGTCAG  917
             |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  661   CCGCCAAAGGGCTGCGACTCCTTCAACGCCCAGGTCATCGTCCTCAACCACCCTGGTCAG  720

Query  918   GTCGGTGCCGGTTACGCTCCAGTGCTCGACTGCCACACTGCCCACATTGCCTGCAAGTTC  977
             |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Sbjct  721   GTCGGTGCCGGTTACGCTCCAGTGCTCGACTGCCACACCGCCCACATTGCCTGCAAGTTC  780

Query  978   GCCGAGCTCCTCGAGAAGATCGACCG  1003
             |||||||||||||||||||||||||
Sbjct  781   GCCGAGCTCCTCGAGAAGATCGACCG  806
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>Cladosporium prattiae_FJI-L7-BK-DG1_TUB2
ATTAACATCCGCAAAGGGCAATCAAATTGGTGCTGCATTCTGGCAGACCATCTCCGGCGAGCATGGCCTCGAC
GGCGCCGGCGTGTATGTACAC
AATGCATCAGGGCACGCGAAAACCACCAGCTGACACCGCATAGGTACAACGGCACGTCTGACCTCCAGCTCGA
GCGCATGAACGTGTACTTCAA
CGAGGTATGATCCACCGAGGCACCCGCATATGCACGCTCCAAGGCCACGCACTGACCCTATACCATTGTAGGC
CTCTGGCAACAAATACGTTCC
CCGTGCCGTCCTCGTCGACTTGGAGCCCGGCACCATGGACGCTGTTCGCGCCGGTCCCTTCGGCCAGCTCTTC
CGTCCCGACAACTTCGTCTTC
GGCCAGTCCGGCGCCGGCAACAACTGGGCCAAGGGTCACTACACTGAGGGTGCCGAGCTCGTCGACCAGGTCC
TCGACGTCGTCCGTCGCGAGG
CCGAGGGCTGCGACTGCCTCCAGGGTTTCCAAATCACCCACTCCCTCGGTGGTGGTACTGGTGCCGGTATGGG
TACGCTTCTCATCAGCAAGAT
CCGCGAGGAGTTCCCCGACCGCATGATGGCCACCTTCTCCGTCATGCCCTCTCCTAAGGTCTCCGACACCGTT
GTCGAGCCCTACAACGCCACC
CTCTCCGTCCACCAGCTTGTCGAGAACTCCGACGAGACCTTCTGTATCGACAACGAGGCCCTCTACGACATCT
GCATGCGCACCCTCAAGCTCA
GCAACCCCAGCTACGGTGACCTCAACCACCTCGTCTCTGCCGTCATGTCCGGTGTGACCACCTGCCTCCGTTT
CCCCGGTCAGCTCAACAGCGA
TCTCCGCAAGCTCGCCGTCAACATGGTTCCCTTCCCGCGTCTCCACTTCTTCATGATCGGTTTCGCTCCTCTC
ACCTCCCGTGGTGCCCACAGC
TTCCGCGCCGTCTCCGTGCCGGAGCTCACCCAGCAGATCTTCGACCCCAAGAACATGATGGCCGCCGCTGACT
TCCGCAACGGTCGCTACCTCA
CCTGCTCCGCCATCTACCGCGGTAAGGTCTCCATGAAGGAGGTCGAGGACCAGATCCGCAACGTCCAGAACAA
GAACACCGCCTACTTCGTCGA
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CCAACTGCACAACACCCACTG
GGGCTTGGTATGCCCTGCCGAGACGCCTGAAGGACAGGCTTGTGGTTTGGTGAAGAATCTGGCGCTGATGTGC
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GGCACGCCACTCATCGAGTACATGCGCCACAGAGGCATGGAGCTGCTCGAGGAGTACGATGCGATCATGAACC
CGAACGCTACGAAAGTATTCC
TGAACGGCACATGGGTGGGCGTGCACACGAACGGCAAAGCGCTGACTGACGCTATTCGCGACCTGCGGCGGAA
GCAGGTCATTGGGTTCGAGAT
TACAATCATCCGTGACGTCCGCGAGCGGGAGGTCAAGGTCTTCACCGACGCTGGAAGAGTGATGCGGCCGCTG
TTTGTAGTGAACACGGATAAG
CGGTCTCCGGACTTCGGCAGTCTGGCGTTGAAACAGGAGCATGTGGCTAGGCTGCAGCAAGATCAGGAGATCT
TGGCTGGTATGCAAGGACAAG
CCATCAGTGAAGATGAGAAAGCGGATGCTACTTTCGGCTGGAAGGGCCTCATTAAGAACGGTGTCGTTGAGTT
CCTCGATGCTGAAGAGGAAGA
GACCGCCATGATCATCATGACGCCCGACGACCTCGAAGACTACAAGTCTGTCAAGTCTGGCATACCCTGGGTT
GAGTCGAAAGACGACCCACAC
CGTCGTATCAAATCCAAGCCGAATACCCAGGTGGCGCAGTGGACGCATTGCGAGATCCATCCCGCCATGATTC
TCGGTATCTGCGCCTCCATCA
TCCCGTTC

>Neocatenulostroma huberii_FJI-L3-BK-P2_TUB2
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CCGAT
CTCCAGCTGGAGCGCATGAACGTCTACTTCAACGAGGTAGGAGTCCTGAGAGTGTGGATACAAGGCACGCCAA
GACTC
GGTGCTAACACGCGTTCTAGGCCTCTGGCAACAAGTATGTCCCGCGTGCCGTCCTCGTCGACCTGGAGCCAGG
TACCA
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CGGCA
ACAACTGGGCAAAGGGTCATTACACCGAGGGTGCTGAGCTCGTCGACCAGGTCCTCGATGTCGTGCGTCGCGA
GGCTG
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TCTTC
TTATCAGCAAGATCCGCGAGGAGTTCCCCGACCGCATGATGGCGACCTTCTCCGTTATGCCGTCCCCCAAGGT
CTCCG
ACACCGTCGTCGAGCCCTACAACGCCACTCTCTCCGTCCACCAGCTGGTCGAGAACTCCGACGAGACCTTCTG
CATTG
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CCTCG

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CGCCG
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CAGCT
TCCGCGCCGTCACCGTTCCGGAGCTCACCCAGCAGATCTTCGACCCGAAGAACATGATGGCCGCCTCCGACTT
CCGCA
ACGGCCGCTACCTCACCTGCTCCGCCATCTACCGCGGTAAAGTCAGCATGAAGGAGGTCGAGGACCAGATCCG
CAACG
TCCAGAACAAGAACACTGCTTACTTCGTCGAGTGGATCCCGAACAATGTCCAGACCGCTCTCTGCTCCATCCC
GCCTC
GTGGCCTCAAGATGAGCTCTACCTTCGTGGGTAACAGCACCGCGATCCAGGAGCTCTTCAAGCGCGTGGGCGA
CCAGT
TCACGGCTATGTTCAGGCGTAAGGCTTTCTTGCATTGGTACACGGGTGAGGGTATGGATGAGATGGAGTTCAC
GGAGG
CTGAGTCGAACATGAACGATTTGGTGTCTGAGTACCAGCAGTACCAGGAGGCGAGCGTGTCTGAGGGCGAGGA
GGAGT
ACGATGAGGAGGCGCCGCTTGAGGGCGAGGAGTAG

Supplemental Table ST1. Genomes used to construct WGS phylogenetic tree

GenBank Accession #	*Strain name*	Taxonomic lineage
GCA_000146045.2	*Saccharomyces cerevisiae S288C*	Fungi;Ascomycota;Saccharomycetes;Saccharomycetales;Saccharomycetaceae;Saccharomyces;Saccharomyces cerevisiae
GCA_000504385.2	*Exutisphaerella laricina CBS 326.52*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Mycosphaerellaceae;Exutisphaerella;Exutisphaerella laricina
GCA_001599755.1	*Gliomastix tumulicola JCM 17184*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Gliomastix;Gliomastix tumulicola
GCA_002077065.1	*Cryoendolithus antarcticus CCFEE 5527*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cryoendolithus;Cryoendolithus antarcticus
GCA_002116395.1	*Ramularia endophylla CBS 113265*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Mycosphaerellaceae;Ramularia;Ramularia endophylla
GCA_003614995.1	*Cladosporium phlei ATCC 36193*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium phlei
GCA_003788595.2	*Choiromyces venosus 120613-1*	Fungi;Ascomycota;Pezizomycetes;Pezizales;Tuberaceae;Choiromyces;Choiromyces venosus
GCA_005059845.1	*Cryomyces minteri CCFEE 5187*	Fungi;Ascomycota;Dothideomycetes;Dothideomycetes;Dothideomycetes;Cryomyces;Cryomyces minteri
GCA_005059885.1	*Salinomyces thailandicus CCFEE 6315*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Teratosphaeriaceae;Salinomyces;Salinomyces thailandicus
GCA_010367425.1	*Teratosphaeria destructans CMW45982*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Teratosphaeriaceae;Teratosphaeria;Teratosphaeria destructans
GCA_016165855.1	*Pseudocercospora ulei GCL012*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Mycosphaerellaceae;Pseudocercospora;Pseudocercospora ulei
GCA_019670975.1	*Acidiella bohemica*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Teratosphaeriaceae;Acidiella;Acidiella bohemica
GCA_021030915.1	*Astrothelium macrocarpum*	Fungi;Ascomycota;Dothideomycetes;Trypetheliales;Trypetheliaceae;Astrothelium;Astrothelium macrocarpum
GCA_021030925.1	*Trypethelium eluteriae*	Fungi;Ascomycota;Dothideomycetes;Trypetheliales;Trypetheliaceae;Trypethelium;Trypethelium eluteriae
GCA_021401465.1	*Teratosphaeria epicoccoides CMW31933*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Teratosphaeriaceae;Teratosphaeria;Teratosphaeria epicoccoides
GCA_022457075.1	*Cladosporium cladosporioides SYC63*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium cladosporioides
GCA_022560015.1	*Diplodia mutila CBS 112553*	Fungi;Ascomycota;Dothideomycetes;Botryosphaeriales;Botryosphaeriaceae;Diplodia;Diplodia mutila
GCA_022828445.1	*Graphiopsis chlorocephala*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Graphiopsis;Graphiopsis chlorocephala
GCA_023512815.1	*Cercospora zeae-maydis LN*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Mycosphaerellaceae;Cercospora;Cercospora zeae-maydis
GCA_023621355.1	*Cladosporium sphaerospermum R2409*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium sphaerospermum
GCA_023634325.1	*Cladosporium cucumerinum C1*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium cucumerinum
GCA_023653515.1	*Trichoderma orchidacearum COAD 3006*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Hypocreaceae;Trichoderma;Trichoderma orchidacearum
GCA_024604135.1	*Cladosporium velox C4*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium velox
GCA_026023875.1	*Bathelium mastoideum*	Fungi;Ascomycota;Dothideomycetes;Trypetheliales;Trypetheliaceae;Bathelium;Bathelium mastoideum
GCA_026122715.1	*Cladosporium colombiae 601*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium colombiae
GCA_026725115.1	*Cercospora janseana RL44*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Mycosphaerellaceae;Cercospora;Cercospora janseana
GCA_027569275.1	*Emericellopsis terricola NRRL 54109*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Emericellopsis;Emericellopsis terricola
GCA_029490675.1	*Cercospora nicotianae 1110*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Mycosphaerellaceae;Cercospora;Cercospora nicotianae
GCA_030411845.1	*Friedmanniomyces endolithicus CCFEE 5001*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Teratosphaeriaceae;Friedmanniomyces;Friedmanniomyces endolithicus
GCA_030566895.1	*Phaffomyces coquimbonensis CBS 12348*	Fungi;Ascomycota;Saccharomycetes;Phaffomycetales;Phaffomycetaceae;Phaffomyces;[Candida] coquimbonensis
GCA_030581455.1	*Wickerhamiella allomyrinae CBS 13167*	Fungi;Ascomycota;Dipodascomycetes;Dipodascales;Trichomonascaceae;Wickerhamiella;Wickerhamiella allomyrinae
GCA_033119265.1	*Coniosporium uncinatum CCFEE 5737*	Fungi;Ascomycota;Dothideomycetes;Dothideomycetes;Dothideomycetes;Coniosporium;Coniosporium uncinatum
GCA_033816765.1	*Nothopassalora personata LLS_Mitchell_2*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Mycosphaerellaceae;Nothopassalora;Nothopassalora personata
GCA_035135055.1	*Oleoguttula mirabilis CCFEE 5522*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Teratosphaeriaceae;Oleoguttula;Oleoguttula mirabilis
GCA_035771495.1	*Cladosporium oxysporum AAAS_A1*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium oxysporum
GCA_035926095.1	*Elasticomyces elasticus CCFEE 5806*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Teratosphaeriaceae;Elasticomyces;Elasticomyces elasticus
GCA_035927975.1	*Rachicladosporium monterosium CCFEE 5386*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Rachicladosporium;Rachicladosporium monterosium
GCA_036872655.1	*Meristemomyces frigidus CCFEE 5501*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Teratosphaeriaceae;Meristemomyces;Meristemomyces frigidus
GCA_037044255.1	*Cladosporium endophyticum LH_A213*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium endophyticum
GCA_037367355.1	*Neoscytalidium dimidiatum ND8*	Fungi;Ascomycota;Dothideomycetes;Botryosphaeriales;Botryosphaeriaceae;Neoscytalidium;Neoscytalidium dimidiatum
GCA_037952775.1	*Clonostachys chloroleuca Co878*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Clonostachys;Clonostachys chloroleuca
GCA_041721165.1	*Cladosporium subtilissimum*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium subtilissimum

GenBank Accession #	*Strain name*	Taxonomic lineage
GCA_044120895.1	*Clonostachys rhizophaga CGMCC3.3657*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Clonostachys;Clonostachys rhizophaga
GCA_046128805.1	*Cladosporium rectoides A179*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium rectoides
GCA_046128905.1	*Cladosporium tenuissimum ACCC 37043*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium tenuissimum
GCA_046718245.1	*Catenulostroma hermanusense GZ55-1*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Teratosphaeriaceae;Catenulostroma;Catenulostroma hermanusense
GCA_047667015.1	*Macrophomina euphorbiicola ARM498*	Fungi;Ascomycota;Dothideomycetes;Botryosphaeriales;Botryosphaeriaceae;Macrophomina;Macrophomina euphorbiicola
GCA_048593495.1	*Aureobasidium zeae 15JLMHKDK516*	Fungi;Ascomycota;Dothideomycetes;Dothideales;Saccotheciaceae;Aureobasidium;Aureobasidium zeae
GCA_051201255.1	*Hapsidospora chrysogena CGMCC3.3795*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Hapsidospora;Hapsidospora chrysogena
GCA_051227325.1	*Rhizina undulata CMW412*	Fungi;Ascomycota;Pezizomycetes;Pezizales;Rhizinaceae;Rhizina;Rhizina undulata
GCA_051820575.1	*Trichoderma chlorosporum CBS 114231*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Hypocreaceae;Trichoderma;Trichoderma chlorosporum
GCA_052323965.1	*Cladosporium dominicanum ZJUC76*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium dominicanum
GCA_052323985.1	*Cladosporium lebrasiae ZJUC516*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium lebrasiae
GCA_052324005.1	*Cladosporium ramotenellum ZJUC95*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium ramotenellum
GCA_052324025.1	*Cladosporium asperulatum ZJUC90*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium asperulatum
GCA_052324045.1	*Cladosporium xanthochromaticum ZJUC393*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium xanthochromaticum
GCA_052324085.1	*Cladosporium subuliforme ZJUC123*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium subuliforme
GCA_052324185.1	*Cladosporium anthropophilum ZJUC72*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium anthropophilum
GCA_052576325.1	*Cladosporium allicinum IBT 42152*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium allicinum
GCA_052576345.1	*Cladosporium fusiforme IBT 42164*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium fusiforme
GCA_052576375.1	*Cladosporium inversicolor IBT 42153*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium inversicolor
GCA_054135185.1	*Aureobasidium castaneae ZX033*	Fungi;Ascomycota;Dothideomycetes;Dothideales;Saccotheciaceae;Aureobasidium;Aureobasidium castaneae
GCA_054490815.1	*Waltergamsia polychromum NFCCI 6138*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Hypocreales;Waltergamsia;Waltergamsia polychromum
GCA_054828895.1	*Clonostachys rosea NF-06*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Clonostachys;Clonostachys rosea
GCA_055863025.1	*Morchella disparilis PhC 293*	Fungi;Ascomycota;Pezizomycetes;Pezizales;Morchellaceae;Morchella;Morchella disparilis
GCA_058716005.1	*Clonostachys chuyangsinensis YFCC 8591*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Clonostachys;Clonostachys chuyangsinensis
GCA_058716125.1	*Clonostachys rogersoniana YFCC 895*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Clonostachys;Clonostachys rogersoniana
GCA_058716145.1	*Clonostachys compactiuscula YFCC 8592*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Clonostachys;Clonostachys compactiuscula
GCA_059054135.1	*Cladosporium pseudocladosporioides F105*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium pseudocladosporioides
GCA_059054235.1	*Cladosporium xylophilum F42*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium xylophilum
GCA_059054255.1	*Cladosporium europaeum F32*	Fungi;Ascomycota;Dothideomycetes;Cladosporiales;Cladosporiaceae;Cladosporium;Cladosporium europaeum
GCA_060355315.1	*Septoria astericola*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Mycosphaerellaceae;Septoria;Septoria astericola
GCA_900188565.1	*Geosmithia flava*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Geosmithia;Geosmithia flava
GCA_900188575.1	*Geosmithia putterillii*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Geosmithia;Geosmithia putterillii
GCA_902006505.2	*Clonostachys byssicola*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Clonostachys;Clonostachys byssicola
GCA_902141235.2	*Clonostachys solani*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Bionectriaceae;Clonostachys;Clonostachys solani
GCA_903853725.1	*Aureobasidium uvarum*	Fungi;Ascomycota;Dothideomycetes;Dothideales;Saccotheciaceae;Aureobasidium;Aureobasidium uvarum
GCA_964256705.1	*Bathelium carolinianum*	Fungi;Ascomycota;Dothideomycetes;Trypetheliales;Trypetheliaceae;Bathelium;Bathelium carolinianum
GCA_976913895.1	*Ramularia vizellae*	Fungi;Ascomycota;Dothideomycetes;Mycosphaerellales;Mycosphaerellaceae;Ramularia;Ramularia vizellae
GCA_977013665.2	*Lasiodiplodia brasiliensis LaRA1*	Fungi;Ascomycota;Dothideomycetes;Botryosphaeriales;Botryosphaeriaceae;Lasiodiplodia;Lasiodiplodia brasiliensis
GCA_982375315.1	*Trichoderma afroharzianum*	Fungi;Ascomycota;Sordariomycetes;Hypocreales;Hypocreaceae;Trichoderma;Trichoderma afroharzianum

Supplemental table ST2. The sequence similarities of *tef1, act,* and ITS of the *C. perangustum* CBS 125996T vs various other closely related strains forming various groups.

		Percent similarities of *tef1* sequence of type			Percent similarities of *act* sequence of type			Percent similarities of ITS sequence of type		
Strain # as shown in Fig 4	Grouping in this study	*tef1* accession # of related strains	Percent similarity with type strain	*tef1* sequence length (bp)	*tef1* accession # of related strains	Percent similarity with type strain	*act* sequence length (bp)	ITS accession # of related strains	Percent similarity with type strain	ITS sequence length (bp)
SFC20230103-M	I	OQ185122.1	89.00	200	OQ185161.1	98.05	205	OQ186113.1	100.00	557
JZB390056	I	OR980970.1	89.45	199	OR964128.1	97.33	187	OR958627.1	100.00	491
SFC20230103-M	I	OQ185121.1	89.11	202	OQ185160.1	98.13	214	OQ186112.1	100.00	557
SFC20230103-M	I	OQ185123.1	89.11	202	OQ185162.1	98.14	215	OQ186114.1	100.00	557
SFC20230103-M	I	OQ185124.1	89.11	202	OQ185163.1	98.14	215	OQ186115.1	100.00	557
CPC 22331	I	MF473598.1	90.89	373	MF474023.1	97.69	216	MF473176.1	100.00	541
CPC 22297	I	MF473595.1	90.89	373	MF474020.1	95.58	226	MF473172.1	100.00	640
JZB390057	I	OR980971.1	89.45	199	OR964129.1	97.86	187	OR958628.1	100.00	491
GUCC 401.6	I	OL581726.1	87.45	247	OL519779.1	96.92	227	OL579742.1	100.00	543
CPC 22328	I	MF473596.1	90.89	373	MF474021.1	97.79	226	MF473174.1	100.00	541
CPC 22329	I	MF473597.1	90.89	373	MF474022.1	97.66	214	MF473175.1	100.00	541
FKII-L3-CM-PAE	I	JC-1062 (WGS)	91.19	386	JC-1062 (WGS)	97.79	226	JC-1062 (WGS)	100.00	462
FJII-L10-SW-DF	I	JC-1028 (WGS)	91.19	386	JC-1028 (WGS)	97.79	226	JC-1028 (WGS)	100.00	462
DTO 127-E2	I	MF473601.1	92.66	259	MF474026.1	94.25	226	MF473179.1	100.00	586
SM1	I	LC573984.1	88.46	182	LC573982.1	97.87	188	LC573980.1	99.81	515
SM4	I	LC573985.1	88.46	182	LC573983.1	97.87	188	LC573981.1	99.81	515
DTO 323-E8	I	MF473603.1	90.86	372	MF474028.1	98.03	203	MF473181.1	100.00	637
DTO 324-D1	I	MF473607.1	90.89	373	MF474033.1	97.66	214	MF473185.1	100.00	640
DTO 324-A6	I	MF473606.1	90.89	373	MF474031.1	98.03	203	MF473185.1	100.00	640
DTO 324-A2	I	MF473605.1	90.89	373	MF474030.1	98.03	203	MF473184.1	100.00	640
CMG 46	I	MN066646.1	91.19	386	MN066641.1	96.72	183	MF473183.1	100.00	640
DTO 323-E9	I	MF473604.1	90.86	372	MF474029.1	98.03	203	MN053020.1	99.81	515
CPC 14247	I	HM148389.1	90.93	375	HM148634.1	98.23	226	MF473182.1	100.00	639
CPC 12216	I	HM148379.1	91.01	378	HM148624.1	98.22	225	HM148145.1	100.00	639
GP20-28	I	OQ053167.1	91.78	231	OQ053141.1	97.47	158	HM148135.1	100.00	507
GP20-29	I	OQ053168.1	90.48	231	OQ053142.1	97.30	148	-	-	-
DTO 323-E4		MF473602.1	95.98	373	MF474027.1	97.58	165	-	-	-
SFC20230103-M	II	OQ185130.1	93.13	233	OQ185169.1	95.85	217	MF473180.1	100.00	639
SFC20190416-M	II	OQ185129.1	92.34	222	OQ185168.1	95.83	216	OQ186121.1	100.00	551
SFC20230103-M	II	OQ185131.1	92.41	224	OQ185170.1	96.02	226	OQ186120.1	100.00	554
KUC1767		JN033523.1	95.24	210	JN033495.1	98.05	205	OQ186122.1	100.00	557
KUC1462	III	JN033536.1	99.08	217	JN033508.1	100.00	205	JN033481.1	99.81	524
CPC 13870	III	HM148386.1	98.94	378	HM148631.1	100.00	227	OR958628.1	100.00	491

Strain # as shown in Fig 4	Grouping in this study	Percent similarities of *tef1* sequence of type			Percent similarities of *act* sequence of type			Percent similarities of ITS sequence of type		
		tef1 accession # of related strains	Percent similarity with type strain	*tef1* sequence length (bp)	*tef1* accession # of related strains	Percent similarity with type strain	*act* sequence length (bp)	ITS accession # of related strains	Percent similarity with type strain	ITS sequence length (bp)
CPC 22375		MF473599.1	94.10	373	MF474024.1	97.78	225	HM148142.1	100.00	632
CPC 11819	IV	HM148375.1	91.07	336	HM148620.1	94.69	226	MF473177.1	100.00	640
CPC 11831	IV	HM148377.1	91.10	337	HM148622.1	94.69	226	HM148131.1	100.00	500
CPC 11821	IV	HM148376.1	91.07	336	HM148621.1	94.69	226	HM148133.1	100.00	500
CPC 11663	IV	HM148372.1	91.35	347	HM148617.1	94.69	226	HM148132.1	100.00	500
CPC 11815	IV	HM148374.1	91.10	337	HM148619.1	94.67	225	HM148128.1	100.00	498
CBS 12635	IV	HM148367.1	91.07	336	HM148612.1	94.25	226	HM148130.1	100.00	500
CPC 22378	IV	MF473600.1	91.02	334	MF474025.1	96.02	226	HM148123.1	100.00	500
DTO 127-E1		KP701811.1	94.19	258	KP702056.1	91.52	165	MF473178.1	100.00	640
CPC 13730	V	HM148384.1	94.03	385	HM148629.1	93.78	225	KP701934.1	100.00	613
CPC 13774	V	HM148385.1	93.85	374	HM148630.1	93.40	212	HM148140.1	100.00	625
CPC 13727	V	HM148383.1	94.03	385	HM148628.1	93.81	226	HM148141.1	100.00	639
CPC 15192	V	HM148393.1	94.03	385	HM148638.1	93.81	226	HM148139.1	100.00	625
CMG 44		MN066643.1	92.22	334	MN066638.1	92.35	183	-	-	-

Supplemental Table ST3 Overview of the functional characteristics of the seven isolates described in this study

	Novel fungal strain:	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramaniani (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)
	Bases masked (bp)	1,364,576	2,104,219	2,125,997	522,689	404,495	572,120	873,547
	Bases masked (%)	4.64	6.78	6.70	1.51	1.28	2.23	1.40
	SINEs	53	88	89	85	0	0	0
	Penelope	0	0	0	0	0	0	0
	LINEs:	0	0	0	0	0	68	0
	CRE/SLACS	0	0	0	0	0	0	0
	R1/LOA/Jockey	0	0	0	0	0	0	0
	R2/R4/NeSL	0	0	0	0	0	0	0
	RTE/Bov-B	0	0	0	0	0	0	0
	L1/CIN4	0	0	0	0	0	0	0
Retroelements	**LTR elements:**	82	127	133	85	47	14	0
	BEL/Pao	31	48	49	0	0	0	0
	Ty1/Copia	0	0	0	0	0	0	0
	Gypsy/DIRS1	38	3	7	85	0	14	0
	Retroviral	13	76	77	0	0	0	0
	hobo-Activator	0	0	0	0	0	0	0
	Tc1-IS630-Pogo	178	134	128	0	0	243	0
	En-Spm	0	0	0	0	0	0	0
	MULE-MuDR	0	0	0	0	0	0	0
	PiggyBac	0	0	0	0	0	32	0
	Tourist/Harbinger	0	0	0	0	0	0	0
	DNA/Holobok-H	18	17	17	0	0	0	0
	Other	0	0	0	0	0	0	0
	Rolling-circles	0	0	0	0	0	0	0
	Unclassified	1,019	1,785	1,850	294	375	856	2,760
	Total interspersed repeats (bp)	1,000,757	1,618,750	1,642,673	177,811	168,654	0	0
	Small RNAs	283	416	335,860	0	0	0	24
	Satellites	0	0	0	0	0	0	0
	Simple repeats	3,377	3,089	3,094	305,884	4,878	4,399	7,150
	Low-complexity	306	293	333	812	538	978	969

Supplemental Table ST4. Overview of the COG characteristics of the seven isolates described in this study

COG functions	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)
(S) Function unknown	2736	2880	2906	2889	3567	2195	5802
(E) Amino acid transport and metabolism	597	618	613	644	716	419	1405
(I) Lipid transport and metabolism	380	408	405	408	506	357	1377
(J) Translation, ribosomal structure and biogenesis	402	403	407	417	456	417	1327
(T) Signal transduction mechanisms	392	421	425	403	451	408	1202
(G) Carbohydrate transport and metabolism	797	801	813	763	883	479	1054
(P) Inorganic ion transport and metabolism	352	342	343	345	364	279	839
(C) Energy production and conversion	377	406	406	435	489	319	826
(O) Posttranslational modification, protein turnover, chaperones	609	626	630	665	757	608	817
(Q) Secondary metabolites biosynthesis, transport and catabolism	539	545	552	639	778	478	808
(A) RNA processing and modification	318	324	331	320	373	366	725
(D) Cell cycle control, cell division, chromosome partitioning	182	190	186	181	209	194	690
(H) Coenzyme transport and metabolism	212	244	244	266	285	198	596
(K) Transcription	381	394	401	472	400	370	545
(L) Replication, recombination and repair	253	267	273	282	345	300	485
(U) Intracellular trafficking, secretion, and vesicular transport	491	485	491	515	543	521	381
(Z) Cytoskeleton	129	139	149	143	152	163	376
(B) Chromatin structure and dynamics	158	158	158	170	217	141	293
(V) Defense mechanisms	51	52	53	53	74	42	270
(M) Cell wall/membrane/envelope biogenesis	107	112	119	142	120	100	208
(F) Nucleotide transport and metabolism	125	139	140	135	152	113	134
(W) Extracellular structures	6	5	5	7	11	4	61
(Y) Nuclear structure	27	25	25	27	30	34	11
(N) Cell motility	6	5	5	5	6	9	11

Supplemental Table ST5. Overview of the BGC characteristics of the seven isolates described in this study

Species	Strain	Contig	Cluster #	Start	End	Length (bp)	Product	Closest similarity (cumulative BLAST score)
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_1	1	51,348	83,253	31,905	terpene	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_1	2	537,452	568,577	31,125	terpene-precursor	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_1	3	1,211,243	1,243,679	32,436	terpene	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_1	4	2,137,685	2,169,152	31,467	terpene-precursor	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_3	1	63,236	94,298	31,062	terpene	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_3	2	1,450,924	1,512,206	61,282	T3PKS	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_5	1	569,880	600,730	30,850	terpene	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_5	2	1,049,395	1,098,223	48,828	fungal-RiPP	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_5	3	1,301,988	1,365,243	63,255	NRPS-like	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_6	1	353,652	416,620	62,968	NRPS-like	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_6	2	1,181,642	1,248,249	66,607	T1PKS	BGC0002161.2 scytalone/T3HN (2187.0)
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_7	1	237,449	268,864	31,415	terpene	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_9	1	0	39,437	39,437	NRPS	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_10	1	1,057,666	1,121,221	63,555	NRPS	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_13	1	120,783	256,359	135,576	NRPS-like; NRP-metallophore; NRPS	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_13	2	727,255	790,969	63,714	NRPS	BGC0002198.3 nanangelenin B/terreazepine (1581.0); nanangelenin
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_17	1	328,732	392,460	63,728	NRPS-like	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_19	1	529,104	560,673	31,569	terpene	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_21	1	178,650	241,421	62,771	NRPS-like	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_23	1	251,920	315,169	63,249	NRPS-like	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_24	1	57,715	122,974	65,259	NRPS-like	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_26	1	145,558	176,687	31,129	terpene	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_30	1	195,390	228,045	32,655	terpene	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_33	1	186,091	220,587	34,496	NAPAA	
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_34	1	146,308	207,173	60,865	NRPS	BGC0002710.2 metachelin C/metachelin A/metachelin A-CE/metachelin
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_35	1	0	115,663	115,663	NRPS-like; isocyanide-nrp	BGC0002276.2 choline (1807.0)
Cladosporium pratiae	FJI-L7-BK-DG1	NODE_38	1	0	28,910	28,910	betalactone	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_1	1	1,476,741	1,507,794	31,053	terpene	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_1	2	2,319,198	2,385,103	65,905	terpene; T3PKS	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_2	1	814,610	878,165	63,555	NRPS	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_2	2	1,159,309	1,223,048	63,739	NRPS-like	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_5	1	1,565,293	1,628,812	63,519	NRPS	BGC0001277.4 15-acetyldeoxynivalenol/3-decalonectrin (831.0)
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_8	1	208,770	275,742	66,972	NRPS	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_8	2	362,737	393,850	31,113	terpene-precursor	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_8	3	502,610	551,473	48,863	fungal-RiPP	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_8	4	929,973	996,259	66,286	NRPS	BGC0002710.2 metachelin C/metachelin A/metachelin A-CE/metachelin
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_8	5	1,007,652	1,070,907	63,255	NRPS-like	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_9	1	172,602	235,513	62,911	NRPS-like	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_9	2	533,446	597,342	63,896	NRPS-like	AN5318.2 choline (1787.0)
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_9	3	612,249	643,353	31,104	terpene-precursor	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_9	4	867,477	899,973	32,496	terpene	ACF70484.1 clavaric acid (657.0)
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_12	1	869,555	937,841	68,286	T1PKS	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_13	1	115,607	178,822	63,215	T1PKS	BGC0001988.3 neosartorin (2999.0)
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_13	2	316,043	379,541	63,498	NRPS	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_14	1	54,733	117,973	63,240	NRPS-like	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_15	1	653,218	721,020	67,802	T1PKS	BGC0000027.4 ankaflavin/monascin/rubropunctatine/monascorubrin
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_15	2	783,587	846,888	63,301	NRPS-like	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_15	3	864,136	947,020	82,884	NRP-metallophore; NRPS	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_16	1	405,521	454,793	49,272	NAPAA	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_17	1	330,478	361,591	31,113	terpene	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_19	1	411,217	442,708	31,491	terpene-precursor	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_20	1	566,995	597,308	30,313	terpene	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_21	1	428,804	460,702	31,898	terpene	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_22	1	364,350	429,615	65,265	NRPS-like	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_23	1	287,702	354,292	66,590	T1PKS	BGC0002161.2 scytalone/T3HN (2176.0)
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_25	1	361,925	393,269	31,344	indole	

Species	Strain	Contig	Cluster #	Start	End	Length (bp)	Product	Closest similarity (cumulative BLAST score)
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_75	1	0	3,869	3,869	T1PKS	
Cladosporium cranfordii	FJII-L10-SW-DR1	NODE_107	1	0	1,776	1,776	terpene	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_2	1	1,477,572	1,508,625	31,053	terpene	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_3	1	779,569	843,308	63,739	NRPS-like	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_3	2	1,129,443	1,192,998	63,555	NRPS	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_6	1	82,458	150,720	68,262	T1PKS	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_6	2	1,168,409	1,233,674	65,265	NRPS-like	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_7	1	420,128	469,400	49,272	NAPAA	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_8	1	16,459	77,806	61,347	NRPS-like	BGC0001277.4 15-acetyldeoxynivalenol/3-decalonectrin (828.0)
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_9	1	403,982	435,473	31,491	terpene-precursor	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_9	2	739,043	821,927	82,884	NRP-metallophore; NRPS	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_9	3	839,074	902,375	63,301	NRPS-like	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_9	4	965,255	1,033,056	67,801	T1PKS	BGC0000027.4 ankaflavin/monascin/rubropunctatine/monascorubrin
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_10	1	418,807	450,705	31,898	terpene	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_10	2	630,725	693,965	63,240	NRPS-like	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_12	1	1,034,198	1,097,702	63,504	NRPS	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_12	2	1,235,994	1,301,455	65,461	T1PKS	BGC0001886.2 Secalonic acid B/Secalonic acid A/Secalonic acid
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_13	1	343,548	374,661	31,113	terpene	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_13	2	1,036,533	1,103,118	66,585	T1PKS	BGC0002161.2 scytalone/T3HN (2181.0)
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_14	1	207,676	275,732	68,056	NRPS	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_14	2	362,508	393,621	31,113	terpene-precursor	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_14	3	502,570	551,433	48,863	fungal-RiPP	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_14	4	929,932	996,218	66,286	NRPS	BGC0002710.2 metachelin C/metachelin A/metachelin A-CE/metachelin
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_14	5	1,007,611	1,070,866	63,255	NRPS-like	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_15	1	170,169	233,080	62,911	NRPS-like	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_15	2	523,508	587,404	63,896	NRPS-like	AN5318.2 choline (1787.0)
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_15	3	602,299	633,403	31,104	terpene-precursor	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_15	4	857,523	890,019	32,496	terpene	ACF70484.1 clavaric acid (657.0)
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_22	1	0	49,833	49,833	T3PKS; terpene	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_24	1	0	30,307	30,307	terpene	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_41	1	0	19,966	19,966	NRPS-like	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_54	1	0	9,514	9,514	terpene	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_79	1	0	5,779	5,779	T1PKS	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_101	1	0	3,869	3,869	T1PKS	
Cladosporium cranfordii	FKII-L3-CM-PAB1	NODE_141	1	0	1,776	1,776	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_1	1	864,208	948,607	84,399	NRPS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_1	2	1,286,003	1,351,259	65,256	NRPS	BGC0002710.2 coprogen/dimerumic-acid siderophore (9080.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_1	3	1,640,111	1,701,960	61,849	NRPS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_2	1	542,407	580,350	37,943	terpene	BGC0000688.4 copalyl diphosphate (1690.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_3	1	334,380	398,423	64,043	NRPS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_3	2	444,998	513,290	68,292	T1PKS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_3	3	1,012,058	1,071,664	59,606	NRPS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_4	1	858,595	890,186	31,591	terpene	BGC0001839.3 squalestatin S1 (931.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_5	1	901,042	948,225	47,183	NRPS-like	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_7	1	425,041	488,163	63,122	NRPS-like	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_7	2	659,585	722,492	62,907	NRPS-like	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_9	1	539,737	607,167	67,430	T1PKS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_11	1	169,509	201,037	31,528	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_11	2	350,120	381,581	31,461	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_11	3	598,495	644,577	46,082	T1PKS	BGC0002227.3 AKML B/AKML D/AKML A/AKML C (3581.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_12	1	437,242	505,365	68,123	T1PKS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_13	1	304,983	373,026	68,043	T1PKS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_14	1	545,782	578,128	32,346	terpene	ACF70484.1 clavaric acid (662.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_16	1	32,579	64,442	31,863	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_17	1	319,085	384,251	65,166	NRPS-like	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_21	1	0	28,328	28,328	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_21	2	113,728	148,644	34,916	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_22	1	166,917	198,234	31,317	terpene-precursor	

Species	Strain	Contig	Cluster #	Start	End	Length (bp)	Product	Closest similarity (cumulative BLAST score)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_22	2	430,708	489,336	58,628	NRPS; T1PKS	BGC0000992.4 fusaridione A NRPS+PKS (7437.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_26	1	172,240	255,235	82,995	NRPS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_26	2	389,922	421,036	31,114	terpene-precursor	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_30	1	42,686	105,846	63,160	NRPS-like	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_34	1	130,886	194,663	63,777	NRPS-like	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_38	1	54,170	122,777	68,607	T1PKS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_38	2	206,646	270,528	63,882	NRPS-like	AN5318.2 choline (1617.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_38	3	286,816	337,694	50,878	NRPS; T1PKS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_39	1	188,174	219,637	31,463	NRPS; T1PKS	BGC0000992.4 fusaridione A NRPS+PKS (7437.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_40	1	206,221	238,524	32,303	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_41	1	209,025	277,651	68,626	T1PKS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_42	1	0	76,195	76,195	NRP-metallophore; NRPS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_42	2	85,636	203,404	117,768	NRPS-like; T1PKS; T3PKS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_46	1	33,636	65,043	31,407	indole	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_46	2	75,046	166,724	91,678	NRPS	ACJ04424.1 Aureobasidin A biosynthesis complex AbT1 (8980.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_46	3	188,301	259,072	70,771	NRPS; T1PKS	BGC0002186.2 fusaristatin A (8023.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_49	1	87,030	195,367	108,337	NRPS-like; T1PKS; indole	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_51	1	0	39,529	39,529	T1PKS; indole	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_52	1	0	59,752	59,752	isocyanide	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_55	1	0	19,041	19,041	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_63	1	0	34,818	34,818	NRPS-like	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_71	1	118,324	149,618	31,294	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_73	1	78,219	152,561	74,342	NRPS-like; T1PKS	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_75	1	28,454	96,252	67,798	T1PKS	BGC0002234.3 flavoglaucin (5175.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_76	1	407	69,746	69,339	T1PKS	BGC0001954.2 wortmanamide A/wortmanamide B (6283.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_78	1	72,232	103,225	30,993	terpene	BGC0000686.3 helvolic acid (3573.0)
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_79	1	14,086	45,317	31,231	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_99	1	21,280	52,943	31,663	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_102	1	22,807	55,015	32,208	terpene	
Waltergamsia balasubramanianii	FKII-L8-BK-P5	NODE_106	1	7,343	48,481	41,138	T3PKS	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000001.1	1	659,066	724,245	65,179	NRPS-like	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000001.1	2	2,528,060	2,580,460	52,400	NAPAA	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000001.1	3	2,749,705	2,799,813	50,108	NRPS	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000002.1	1	1,242,180	1,273,833	31,653	terpene-precursor	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000002.1	2	1,364,534	1,456,047	91,513	NRPS; T1PKS	BGC0000307.4 AbT1 (2133.0)
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000002.1	3	2,212,511	2,282,797	70,286	NRPS	BGC0002501.3 penigainamide A/penigainamide B/penigainamide
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000002.1	4	2,463,134	2,531,894	68,760	T1PKS	BGC0002185.2 gregatin A (4179.0)
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000004.1	1	1,869,694	1,936,414	66,720	T1PKS	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000005.1	1	420,153	451,757	31,604	terpene	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000005.1	2	1,725,669	1,756,602	30,933	terpene	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000006.1	1	1,027,055	1,062,433	35,378	terpene	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000006.1	2	1,266,609	1,329,980	63,371	NRPS-like	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000006.1	3	1,813,265	1,880,669	67,404	T1PKS	BGC0001541.3 cercosporin (7478.0)
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000007.1	1	710	65,545	64,835	NRPS-like; terpene	BGC0000011.3 Sterigmatocystin/Aflatoxin B1/Aflatoxin B2 (488.0)
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000007.1	2	126,356	195,002	68,646	T1PKS	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000007.1	3	1,527,751	1,595,469	67,718	T1PKS	BGC0002483.2 usnic acid (5153.0)
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000008.1	1	873,042	905,542	32,500	terpene	ACF70484.1 clavaric acid (714.0)
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000008.1	2	1,131,521	1,199,392	67,871	T1PKS	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000009.1	1	105,348	239,713	134,365	NRPS-like; NRPS	BGC0002710.2 metachelin C/metachelin A/metachelin A-CE/metachelin
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000009.1	2	502,546	569,101	66,555	T1PKS	BGC0002161.2 scytalone/T3HN (2143.0)
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000010.1	1	348,194	438,096	89,902	NRPS; NRPS-like	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000011.1	1	187,036	268,827	81,791	NRPS	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000011.1	2	329,094	391,145	62,051	isocyanide	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000011.1	3	396,026	459,323	63,297	NRPS-like	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000012.1	1	795,044	862,002	66,958	T1PKS	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000013.1	1	316,540	399,784	83,244	NRP-metallophore; NRPS	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000013.1	2	922,604	989,372	66,768	T1PKS	BGC0002215.3 HEx-pks23 polyketide (4275.0)
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000015.1	1	172,588	203,697	31,109	terpene-precursor	

Species	Strain	Contig	Cluster #	Start	End	Length (bp)	Product	Closest similarity (cumulative BLAST score)
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000015.1	2	420,278	492,684	72,406	NRPS; T1PKS	BGC0001124.4 pyranonigrin E (3051.0); pyranonigrin E
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000015.1	3	748,221	811,773	63,552	NRPS	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000019.1	1	92,864	157,892	65,028	NRPS	BGC0002501.3 penigainamide A/penigainamide B/penigainamide
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000019.1	2	285,334	316,453	31,119	terpene	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000020.1	1	156,827	188,748	31,921	terpene	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000020.1	2	257,712	338,265	80,553	T1PKS	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000026.1	1	17,931	86,225	68,294	T1PKS	
Phaeophleospora burdickii	FKII-L3-CM-PAB3	AKLNG010000029.1	1	0	53,842	53,842	NRPS-like	
Spissiomyces californiae	FJII-L1-SW-P2	NODE_65	1	0	33,598	33,598	betalactone	
Spissiomyces californiae	FJII-L1-SW-P2	NODE_100	1	3,377	31,374	27,997	terpene	ACF70484.1 clavaric acid (728.0)
Spissiomyces californiae	FJII-L1-SW-P2	NODE_174	1	0	25,497	25,497	T1PKS	MGG_07219 conidial yellow pigment biosynthesis polyketide synthase (2004.0)
Spissiomyces californiae	FJII-L1-SW-P2	NODE_279	1	0	20,462	20,462	terpene	
Spissiomyces californiae	FJII-L1-SW-P2	NODE_324	1	0	18,898	18,898	terpene-precursor	
Spissiomyces californiae	FJII-L1-SW-P2	NODE_907	1	0	8,508	8,508	NRPS-like	
Spissiomyces californiae	FJII-L1-SW-P2	NODE_1066	1	0	7,221	7,221	T1PKS	
Spissiomyces californiae	FJII-L1-SW-P2	NODE_1631	1	0	3,860	3,860	isocyanide	
Spissiomyces californiae	FJII-L1-SW-P2	NODE_2337	1	0	2,222	2,222	NRPS	
Spissiomyces californiae	FJII-L1-SW-P2	NODE_3159	1	0	1,414	1,414	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_12_length_94	1	0	94,530	94,530	T1PKS	BGC0000027.4 ankaflavin/monascin/rubropunctatine/monascorubrin
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_14_length_92	1	28,621	60,091	31,470	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_18_length_87	1	16,852	87,892	71,040	T1PKS	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_21_length_86	1	20,065	86,427	66,362	T1PKS	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_36_length_76	1	0	40,352	40,352	T1PKS	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_38_length_75	1	39,714	75,372	35,658	NRPS-like	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_44_length_71	1	0	19,874	19,874	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_73_length_63	1	16,714	63,166	46,452	NRPS-like	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_140_length_5	1	0	46,122	46,122	NRPS-like	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_162_length_5	1	0	25,068	25,068	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_173_length_4	1	30,135	49,616	19,481	terpene-precursor	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_196_length_4	1	0	41,442	41,442	NRPS-like	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_236_length_4	1	27,875	44,732	16,857	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_272_length_4	1	0	42,492	42,492	T1PKS	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_342_length_3	1	19,262	38,785	19,523	terpene-precursor	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_382_length_3	1	19,488	36,345	16,857	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_392_length_3	1	0	28,058	28,058	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_402_length_3	1	0	35,321	35,321	T1PKS	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_432_length_3	1	1,847	34,054	32,207	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_519_length_3	1	11,784	31,087	19,303	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_566_length_2	1	1,429	29,586	28,157	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_605_length_2	1	0	28,496	28,496	NRPS-like	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_781_length_2	1	7,378	24,036	16,658	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_799_length_2	1	0	23,641	23,641	NRPS-like	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_840_length_2	1	0	22,939	22,939	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_906_length_2	1	0	18,966	18,966	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_966_length_2	1	0	20,635	20,635	NRPS	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_1080_length_	1	0	19,148	19,148	NRPS	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_1093_length_	1	0	18,951	18,951	terpene-precursor	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_1157_length_	1	0	18,058	18,058	NRPS-like	BGC0002276.2 choline (1841.0)
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_1466_length_	1	0	14,744	14,744	terpene-precursor	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_1758_length_	1	0	11,970	11,970	terpene	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_1838_length_	1	0	11,301	11,301	NRPS	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_2411_length_	1	0	7,399	7,399	NRPS-like	BGC0002276.2 choline (1550.0)
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_2580_length_	1	0	6,496	6,496	NRPS-like	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_2626_length_	1	0	6,309	6,309	NRPS-like	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_2709_length_	1	0	5,936	5,936	NRPS-like	
Neocatenulostroma huberi	FJI-L3-BK-P2	ODE_2792_length_	1	0	5,623	5,623	NRPS-like	

Supplemental Table ST6. Overview of the Pfam characteristics of the seven isolates described in this study

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF01753	18	19	19	6	19	1	46	MYND finger
PF24324	1	1	1	0	0	0	4	ZMYND11/ZMYD8, MYND zinc finger
PF13826	1	1	1	1	1	2	6	Monooxygenase af470-like
PF00933	25	27	28	14	26	11	34	Glycosyl hydrolase family 3 N terminal domain
PF01915	21	26	27	13	23	10	31	Glycosyl hydrolase family 3 C-terminal domain
PF14310	18	22	23	13	22	8	28	Fibronectin type III-like domain
PF00083	148	139	135	162	128	66	192	Sugar (and other) transporter
PF07690	442	443	441	456	473	199	652	Major Facilitator Superfamily
PF01328	13	13	13	2	44	1	35	Peroxidase, family 2
PF00465	3	4	4	4	3	5	9	Iron-containing alcohol dehydrogenase
PF25137	3	4	4	3	3	5	12	Fe-containing alcohol dehydrogenase family, C-terminal
PF12224	2	1	1	2	3	3	7	Putative amidoligase enzyme
PF05577	2	2	2	2	4	0	7	Serine carboxypeptidase S28
PF00026	14	17	19	19	24	16	38	Eukaryotic aspartyl protease
PF01494	28	48	47	34	72	21	117	FAD binding domain
PF03188	2	2	2	3	5	1	7	Eukaryotic cytochrome b561
PF10348	3	3	3	2	7	3	3	Domain of unknown function (DUF2427)
PF16010	4	5	5	6	6	5	7	Cytochrome domain of cellobiose dehydrogenase
PF00023	60	66	76	67	74	24	98	Ankyrin repeat
PF05729	17	27	30	13	5	5	13	NACHT domain
PF12796	52	63	72	65	67	22	95	Ankyrin repeats (3 copies)
PF13606	29	36	42	44	50	16	57	Ankyrin repeat
PF13637	43	45	53	52	52	18	65	Ankyrin repeats (many copies)
PF13857	18	17	21	28	29	13	30	Ankyrin repeats (many copies)
PF24883	47	57	63	37	17	8	37	Nephrocystin 3, N-terminal
PF13911	2	2	2	3	3	2	6	AhpC/TSA antioxidant enzyme
PF00106	168	162	163	209	238	119	369	short chain dehydrogenase
PF08659	119	112	115	162	159	91	256	KR domain
PF13561	159	144	146	176	217	114	351	Enoyl-(Acyl carrier protein) reductase
PF09414	1	1	1	1	2	1	3	RNA ligase
PF00097	31	38	33	28	53	29	85	Zinc finger, C3HC4 type (RING finger)
PF12678	5	5	5	8	7	6	16	RING-H2 zinc finger domain
PF13445	19	23	20	20	35	14	54	RING-type zinc-finger
PF13639	30	34	31	26	45	28	77	Ring finger domain
PF13923	18	24	21	17	31	14	54	Zinc finger, C3HC4 type (RING finger)
PF17123	6	7	6	7	9	8	19	RING-like zinc finger
PF01699	10	8	7	6	12	13	16	Sodium/calcium exchanger protein
PF15341	1	1	1	1	2	1	1	Ribosome biogenesis protein SLX9
PF00999	8	6	8	7	8	6	15	Sodium/hydrogen exchanger, transmembrane
PF04724	2	1	1	0	1	1	2	Glycosyltransferase family 17
PF03178	3	4	3	3	3	5	6	CPSF A subunit region
PF10433	4	4	4	4	4	4	8	RSE1/DDB1/CPSF1 first beta-propeller
PF23726	3	3	4	4	3	4	8	RSE1/DDB1/CPSF1 second beta-propeller
PF10685	1	1	1	1	0	2	4	Stress-induced bacterial acidophilic repeat motif
PF00118	9	9	9	9	12	9	13	TCP-1/cpn60 chaperonin family
PF01008	4	4	4	3	4	4	8	Initiation factor 2 subunit family
PF00018	21	20	21	19	23	21	42	SH3 domain
PF00096	31	30	30	41	45	19	44	Zinc finger, C2H2 type
PF07653	19	19	20	17	20	19	37	Variant SH3 domain
PF13894	5	4	4	6	5	5	11	C2H2-type zinc finger
PF01083	9	12	13	6	15	0	18	Cutinase
PF03357	7	7	7	6	8	8	14	Snf7
PF25880	1	1	1	0	1	2	2	CHMP7 N-terminal winged helix domain
PF25484	3	3	3	2	5	3	9	Domain of unknown function (DUF7907)
PF00076	65	67	67	61	77	72	112	RNA recognition motif
PF13893	3	3	3	4	3	4	5	RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)
PF00394	20	19	20	3	23	10	26	Multicopper oxidase
PF07731	21	21	21	3	29	18	32	Multicopper oxidase
PF07732	22	21	21	3	24	15	30	Multicopper oxidase
PF03198	7	8	8	5	8	4	16	Glucanosyltransferase
PF00171	22	19	19	47	30	16	50	Aldehyde dehydrogenase family
PF00036	7	8	8	7	8	10	10	EF hand domain
PF00070	17	18	18	18	19	9	23	Pyridine nucleotide-disulphide oxidoreductase
PF07992	39	43	42	44	50	25	80	Pyridine nucleotide-disulphide oxidoreductase
PF13405	7	6	6	6	7	8	13	EF-hand domain
PF22366	4	4	4	2	6	2	7	NDH2 C-terminal domain
PF02475	1	1	1	2	2	0	3	TRM5/TYW2 methyltransferase domain
PF05686	7	4	4	2	5	1	10	Glycosyl transferase family 90
PF27577	1	1	1	1	1	1	2	Pre-rRNA-processing protein ESF2 C-terminal domain
PF27909	1	1	1	1	1	1	2	C613.03 C-terminal domain
PF00610	4	4	4	4	4	4	7	Domain found in Dishevelled, Egl-10, and Pleckstrin (DEP)
PF12257	1	1	1	1	1	0	2	Vacuolar membrane-associated protein Iml1, N-terminal domain
PF19418	0	0	0	1	0	0	2	DEPDC5 protein C-terminal region
PF00107	71	69	72	84	95	53	141	Zinc-binding dehydrogenase
PF08240	76	72	74	87	100	62	142	Alcohol dehydrogenase GroES-like domain
PF02353	6	6	6	6	6	2	12	Mycolic acid cyclopropane synthetase
PF08241	47	53	54	80	111	43	119	Methyltransferase domain
PF08242	31	35	35	62	91	28	88	Methyltransferase domain
PF08498	2	2	2	2	1	1	6	Sterol methyltransferase C-terminal
PF13489	35	36	37	73	94	33	94	Methyltransferase domain
PF13649	44	52	53	76	110	41	115	Methyltransferase domain
PF13847	28	36	38	50	70	23	75	Methyltransferase domain
PF03061	11	11	11	6	15	3	17	Thioesterase superfamily
PF13279	3	3	3	3	3	3	8	Thioesterase-like superfamily
PF00400	103	113	116	109	122	108	190	WD domain, G-beta repeat
PF03029	3	3	3	3	3	3	6	Conserved hypothetical ATP binding protein
PF13924	2	1	1	1	4	2	5	Lipocalin-like domain
PF13862	1	1	1	1	1	1	2	BCCIP
PF00940	1	1	2	1	1	1	2	DNA-dependent RNA polymerase
PF14700	1	1	2	1	1	0	2	DNA-directed RNA polymerase N-terminal
PF26713	1	1	2	1	1	0	2	RPO41-like, TPR repeats
PF20179	1	1	1	1	2	1	4	MSS51 C-terminal domain
PF03009	4	5	5	3	5	4	8	Glycerophosphoryl diester phosphodiesterase family
PF25329	2	3	3	2	2	1	4	GDE1-like C2 domain
PF20150	11	14	14	12	35	3	171	2EXR family
PF01138	6	5	5	6	6	6	10	3' exoribonuclease family, domain 1

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF01679	6	5	5	2	6	4	7	Proteolipid membrane potential modulator
PF12799	3	2	2	3	2	5	5	Leucine Rich repeats (2 copies)
PF14580	1	1	1	1	1	1	3	Leucine-rich repeat
PF02966	1	1	1	1	2	0	2	Mitosis protein DIM1
PF01171	2	3	3	2	3	2	4	PP-loop domain
PF00069	105	120	128	106	148	106	192	Protein kinase domain
PF07714	104	109	113	98	129	104	174	Protein tyrosine and serine/threonine kinase
PF00583	33	38	40	34	54	23	74	Acetyltransferase (GNAT) family
PF00651	36	57	62	12	71	22	196	BTB/POZ domain
PF03850	1	1	1	1	1	1	2	Transcription factor Tfb4
PF01301	2	5	4	1	7	3	8	Glycosyl hydrolases family 35
PF10435	3	5	4	0	6	3	8	Beta-galactosidase, domain 2
PF13363	3	5	5	0	6	3	8	Beta-galactosidase, domain 3
PF13364	3	6	6	1	7	3	8	Beta-galactosidase second all-beta domain
PF05185	1	1	1	1	1	2	2	PRMT5 arginine-N-methyltransferase
PF17285	1	1	1	1	1	2	2	PRMT5 TIM barrel domain
PF17286	1	1	1	1	1	2	2	PRMT5 oligomerisation domain
PF01112	2	2	2	3	2	2	3	Asparaginase
PF00022	8	7	8	10	9	6	16	Actin
PF04082	132	140	143	243	144	49	133	Fungal specific transcription factor domain
PF00270	57	62	62	56	72	65	91	DEAD/DEAH box helicase
PF00271	79	82	84	77	94	82	130	Helicase conserved C-terminal domain
PF04408	5	6	6	8	11	8	19	Helicase associated domain (HA2), winged-helix
PF07717	7	7	7	9	9	9	19	Oligonucleotide/oligosaccharide-binding (OB)-fold
PF21010	7	8	8	9	11	9	19	Helicase associated domain (HA2), ratchet-like
PF11905	3	4	3	10	5	8	3	Domain of unknown function (DUF3425)
PF13450	42	51	52	66	80	39	147	NAD(P)-binding Rossmann-like domain
PF06609	8	14	12	7	26	12	33	Fungal trichothecene efflux pump (TRI12)
PF05721	12	13	12	12	13	5	28	Phytanoyl-CoA dioxygenase (PhyH)
PF03028	1	1	1	1	2	0	2	Dynein heavy chain region D6 P-loop domain
PF12781	1	1	1	1	2	0	1	ATP-binding dynein motor region
PF18198	1	1	1	1	2	1	2	Dynein heavy chain AAA lid domain
PF00814	1	1	1	2	3	1	2	tRNA N6-adenosine threonylcarbamoyltransferase
PF00899	9	9	8	8	7	10	18	ThiF family
PF10230	1	1	1	1	1	1	2	Lipid-droplet associated hydrolase
PF12697	67	72	73	60	74	47	117	Alpha/beta hydrolase family
PF07814	1	1	1	1	1	1	2	Wings apart-like protein regulation of heterochromatin
PF14681	4	5	5	4	3	2	9	Uracil phosphoribosyltransferase
PF14040	0	1	1	1	3	1	5	Deoxyribonuclease NucA/NucB
PF00172	211	215	210	325	165	52	180	Fungal Zn(2)-Cys(6) binuclear cluster domain
PF03959	3	9	11	4	13	6	10	Serine hydrolase (FSH1)
PF06682	1	1	1	1	2	1	2	SOCE-associated regulatory factor of calcium homoeostasis
PF04055	7	5	5	6	9	5	13	Radical SAM superfamily
PF16199	1	1	1	1	1	1	2	Radical_SAM C-terminal domain
PF23613	1	1	1	1	1	1	2	ELP3 N-terminal domain
PF04179	2	2	2	1	1	2	4	Rit1 DUSP-like domain
PF17184	1	1	1	1	1	2	2	Rit1 N-terminal domain
PF06058	1	1	1	1	1	1	2	Dcp1-like decapping family
PF21310	1	1	1	1	1	0	2	Inositol polyphosphate 5-phosphatase OCRL-like, ASH domain
PF22669	5	4	4	5	5	4	8	Endonuclease/Exonuclease/phosphatase family 2
PF27604	1	1	1	1	1	0	2	PB2B2.08-like
PF00646	41	49	51	28	70	23	198	F-box domain
PF00134	9	8	8	7	7	7	12	Cyclin, N-terminal domain
PF16899	1	1	1	1	1	1	2	Cyclin C-terminal domain
PF00389	12	15	15	19	15	6	23	D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain
PF02826	17	18	18	23	17	8	26	D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain
PF20253	3	0	2	0	8	2	42	Family of unknown function (DUF6604)
PF20684	76	83	86	77	97	17	107	Fungal rhodopsin domain
PF00891	5	6	7	16	34	3	30	O-methyltransferase domain
PF08100	3	1	1	5	7	2	12	O-methyltransferase dimerisation domain
PF16131	1	1	1	1	1	1	3	Torus domain
PF17389	5	5	5	5	5	2	8	Bacterial alpha-L-rhamnosidase 6 hairpin glycosidase domain
PF17390	5	5	5	4	6	1	5	Bacterial alpha-L-rhamnosidase C-terminal domain
PF01613	3	3	4	3	5	3	6	Flavin reductase like domain
PF00004	50	47	47	53	65	53	107	ATPase family associated with various cellular activities (AAA)
PF03215	3	3	3	1	3	2	4	Rad17 P-loop domain
PF07728	17	18	18	17	24	22	42	AAA domain (dynein-related subfamily)
PF08542	3	3	3	3	4	4	5	Replication factor C C-terminal domain
PF13177	2	2	2	3	4	3	6	DNA polymerase III, delta subunit
PF13604	6	6	7	7	13	5	14	AAA domain
PF04062	1	1	1	1	1	2	2	ARP2/3 complex ARPC3 (21 kDa) subunit
PF07173	2	1	1	1	2	1	2	Glycine-rich domain-containing protein-like
PF01680	1	1	1	1	1	1	2	SOR/SNZ family
PF07910	1	1	1	1	3	1	4	Peptidase family C78
PF00328	13	17	17	8	11	8	21	Histidine phosphatase superfamily (branch 2)
PF10256	1	1	1	1	1	1	2	Golgin subfamily A member 7/ERF4 family
PF05131	1	1	1	1	1	1	2	Pep3/Vps18/deep orange beta-propeller domain
PF26148	1	1	1	1	1	1	2	VPS18 RING C-terminal domain
PF00067	82	81	85	117	148	53	154	Cytochrome P450
PF09346	1	1	1	1	2	1	2	SMI1 / KNR4 family (SUKH-1)
PF00149	23	24	24	24	38	18	52	Calcineurin-like phosphoesterase
PF13191	7	10	11	4	8	6	15	AAA ATPase domain
PF14630	1	1	1	1	1	1	2	Origin recognition complex (ORC) subunit 5 C-terminus
PF21639	1	1	1	1	1	1	2	ORC5, lid domain
PF05316	1	1	1	0	1	0	2	Mitochondrial ribosomal protein (VAR1)
PF02936	1	1	2	1	1	1	3	Cytochrome c oxidase subunit IV
PF01522	5	8	8	11	9	3	22	Polysaccharide deacetylase
PF01425	19	24	25	22	24	12	46	Amidase
PF13391	0	0	0	1	0	4	2	HNH endonuclease
PF20345	1	1	1	0	2	0	4	Family of unknown function (DUF6640)
PF00850	4	4	4	5	5	5	10	Histone deacetylase domain
PF09757	1	1	1	1	1	1	2	Arb2-like domain
PF00289	5	6	6	4	6	5	9	Biotin carboxylase, N-terminal domain
PF00364	9	10	10	14	11	8	19	Biotin-requiring enzyme
PF02626	1	2	2	0	2	1	2	Carboxyltransferase domain, subdomain A and B
PF02682	1	2	2	1	2	1	2	Carboxyltransferase domain, subdomain C and D
PF02785	5	6	6	4	6	5	8	Biotin carboxylase C-terminal domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF02786	8	8	7	6	9	8	12	Carbamoyl-phosphate synthase L chain, ATP binding domain
PF07478	7	5	5	6	8	7	13	D-ala D-ala ligase C-terminus
PF03746	1	1	1	1	1	1	3	LamB/YcsF family
PF24106	1	1	1	1	1	1	2	EDC4-like protein pdc1 beta-propeller
PF00472	3	3	3	3	5	3	7	RF-1 domain
PF11779	2	2	2	1	3	1	3	Small subunit of serine palmitoyltransferase-like
PF00043	19	17	17	23	22	15	37	Glutathione S-transferase, C-terminal domain
PF02798	18	16	16	21	17	15	34	Glutathione S-transferase, N-terminal domain
PF13409	28	23	24	24	33	22	52	Glutathione S-transferase, N-terminal domain
PF13410	14	13	13	16	12	14	19	Glutathione S-transferase, C-terminal domain
PF13417	21	18	18	19	29	21	45	Glutathione S-transferase, N-terminal domain
PF14497	13	13	13	22	18	9	30	Glutathione S-transferase, C-terminal domain
PF08613	6	6	6	8	7	6	9	Cyclin
PF00474	4	4	4	1	5	1	8	Sodium:solute symporter family
PF02366	3	3	3	3	3	3	6	Dolichyl-phosphate-mannose-protein mannosyltransferase
PF02815	3	3	3	3	3	4	4	MIR domain
PF16192	3	3	3	3	3	3	4	C-terminal four TMM region of protein-O-mannosyltransferase
PF00300	13	16	16	11	14	12	28	Histidine phosphatase superfamily (branch 1)
PF24864	18	11	13	1	18	6	58	Domain of unknown function (DUF7730)
PF00441	14	13	13	16	24	11	35	Acyl-CoA dehydrogenase, C-terminal domain
PF02770	15	14	14	16	21	11	30	Acyl-CoA dehydrogenase, middle domain
PF08028	12	12	12	12	16	8	22	Acyl-CoA dehydrogenase, C-terminal domain
PF01370	71	65	65	82	70	44	110	NAD dependent epimerase/dehydratase family
PF13460	47	42	41	53	37	21	81	NAD(P)H-binding
PF00251	5	4	4	3	4	3	6	Glycosyl hydrolases family 32 N-terminal domain
PF08244	4	4	4	1	5	3	6	Glycosyl hydrolases family 32 C terminal
PF00248	32	38	35	42	50	28	77	Aldo/keto reductase family
PF07798	2	2	3	2	2	1	4	Coiled-coil domain-containing protein 90-like
PF07110	3	6	6	4	4	1	10	EthD domain
PF06102	1	1	1	1	1	1	2	rRNA biogenesis protein RRP36
PF04588	3	3	3	2	2	2	4	Hypoxia induced protein conserved region
PF02985	8	7	8	6	7	10	14	HEAT repeat
PF20210	1	1	1	1	2	1	2	Laa1/Sip1/HEATR5 HEAT repeat region
PF25808	1	1	1	1	2	1	2	LAA1-like, C-terminal TPR repeats
PF01709	1	1	1	2	1	1	2	TACO1/YebC second and third domain
PF20772	1	1	1	1	1	1	2	TACO1/YebC protein N-terminal domain
PF00970	9	8	8	7	9	6	14	Oxidoreductase FAD-binding domain
PF00704	6	9	10	11	23	3	21	Glycosyl hydrolases family 18
PF00732	30	31	30	29	43	12	53	GMC oxidoreductase
PF00013	7	7	7	8	12	6	15	KH domain
PF26657	1	1	1	1	2	1	2	KH-domain
PF01553	5	8	6	6	6	4	11	Acyltransferase
PF16076	3	6	4	2	4	2	6	Acyltransferase C-terminus
PF11951	33	32	31	49	27	7	26	Fungal specific transcription factor domain
PF01738	10	12	13	10	15	5	22	Dienelactone hydrolase family
PF26286	1	1	1	1	1	1	2	UBA-like domain
PF01546	13	16	15	16	15	9	24	Peptidase family M20/M25/M40
PF07687	8	12	11	9	9	8	16	Peptidase dimerisation domain
PF01641	1	1	1	2	1	2	2	SelR domain
PF07976	1	5	4	3	5	3	10	Phenol hydroxylase, C-terminal dimerisation domain
PF00924	3	4	5	3	3	4	4	Mechanosensitive ion channel, beta-domain
PF25886	3	4	5	3	3	4	5	Mechanosensitive ion channel protein Msy1-like, transmembrane domain
PF00009	21	24	24	23	25	21	39	Elongation factor Tu GTP binding domain
PF03143	5	4	4	4	3	4	7	Elongation factor Tu C-terminal domain
PF22594	2	2	2	3	2	3	3	GTP-eEF1A C-terminal domain-like
PF05508	1	1	1	1	1	2	2	RanGTP-binding protein
PF16944	1	1	1	1	1	1	2	Fungal potassium channel
PF26118	3	3	3	8	6	4	11	Family of unknown function (DUF8035)
PF00550	18	24	26	39	53	9	36	Phosphopantetheine attachment site
PF14498	2	1	1	2	2	0	2	Glycosyl hydrolase family 65, N-terminal domain
PF21307	1	1	1	2	0	0	2	Glycoside hydrolase family 95, C-terminal domain
PF22124	2	1	1	2	2	0	2	Glycosyl hydrolase family 95 catalytic domain
PF05254	0	0	0	1	1	0	2	Uncharacterised protein family (UPF0203)
PF14832	2	3	3	1	4	1	6	Putative oxalocrotonate tautomerase enzyme
PF00205	5	8	9	8	11	6	13	Thiamine pyrophosphate enzyme, central domain
PF02775	5	8	9	10	12	6	17	Thiamine pyrophosphate enzyme, C-terminal TPP binding domain
PF02776	5	8	9	11	12	6	15	Thiamine pyrophosphate enzyme, N-terminal TPP binding domain
PF04115	1	1	2	1	1	1	2	Ureidoglycolate lyase
PF13878	1	1	1	1	2	1	2	zinc-finger of acetyl-transferase ESCO
PF13174	3	2	4	5	4	5	10	Tetratricopeptide repeat
PF13176	6	7	15	7	7	10	10	Tetratricopeptide repeat
PF13181	18	17	26	21	25	22	37	Tetratricopeptide repeat
PF13432	14	14	18	16	17	18	29	Tetratricopeptide repeat
PF14559	9	10	10	10	7	10	27	Tetratricopeptide repeat
PF18833	1	1	1	1	1	1	2	Tetratricopeptide repeat
PF25563	1	1	1	2	1	1	2	E3 ubiquitin-protein ligase synoviolin-like, TPR repeats
PF01779	0	0	0	0	1	0	1	Ribosomal L29e protein family
PF00330	6	5	6	7	6	4	8	Aconitase family (aconitate hydratase)
PF00694	6	5	6	7	6	4	8	Aconitase C-terminal domain
PF12171	6	4	4	7	9	5	16	Zinc-finger double-stranded RNA-binding
PF07989	3	3	3	5	2	3	5	Centrosomin N-terminal motif 1
PF12808	1	1	1	1	1	2	2	Micro-tubular organiser Mto1 C-term Mto2-binding region
PF09337	1	1	1	1	2	0	2	H2C2 zinc finger
PF17921	1	1	1	1	4	0	3	Integrase zinc binding domain
PF04136	1	1	1	1	1	1	2	Conserved oligomeric Golgi complex subunit 3, N-terminal
PF20671	1	1	1	1	1	1	2	Conserved oligomeric Golgi complex subunit 3, C-terminal
PF10252	1	1	1	1	1	1	2	Casein kinase substrate phosphoprotein PP28
PF07470	5	4	3	4	8	1	6	Glycosyl Hydrolase Family 88
PF14683	1	0	0	1	2	2	2	Polysaccharide lyase family 4, domain III
PF14686	1	0	0	1	2	2	2	Polysaccharide lyase family 4, domain II
PF28395	1	0	0	0	2	1	2	Probable rhamnogalacturonate lyase B C-terminal domain
PF20180	1	1	1	1	1	1	2	Complex III assembly factor UQCC2/CBP6
PF01926	30	41	44	30	34	34	65	50S ribosome-binding GTPase
PF11987	2	4	4	2	2	2	4	Translation-initiation factor 2
PF22042	5	7	7	5	7	4	9	Elongation factor G domain 2
PF00570	0	1	1	1	2	3	2	HRDC domain
PF01612	2	4	4	4	7	3	6	3'-5' exonuclease

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF08066	0	1	1	1	2	1	2	PMC2NT (NUC016) domain
PF00072	29	32	33	15	28	22	60	Response regulator receiver domain
PF00512	23	26	27	10	19	16	42	His Kinase A (phospho-acceptor) domain
PF01590	5	4	4	4	4	2	14	GAF domain
PF02518	31	33	34	17	30	23	59	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
PF00324	67	75	75	47	71	21	112	Amino acid permease
PF13520	69	76	74	45	74	22	120	Amino acid permease
PF05368	29	28	30	39	20	15	52	NmrA-like family
PF01399	12	13	13	14	17	13	25	PCI domain
PF09440	1	1	1	1	2	1	2	eIF3 subunit 6 N terminal domain
PF21357	1	1	1	1	2	1	2	Eukaryotic translation initiation factor 3 subunit E, C-terminal
PF00642	13	11	11	9	12	9	19	Zinc finger C-x8-C-x5-C-x3-H type (and similar)
PF18044	2	2	2	2	5	2	7	CCCH-type zinc finger
PF27634	1	1	1	1	1	1	2	Amo1 N-terminal domain
PF05024	1	2	2	1	2	1	2	N-acetylglucosaminyl transferase component (Gpi1)
PF11176	1	1	1	1	2	1	2	Translation machinery-associated protein 16
PF00752	4	4	4	5	5	5	9	XPG N-terminal domain
PF00867	7	7	7	4	8	4	11	XPG I-region
PF04515	2	2	2	2	2	2	4	Plasma-membrane choline transporter
PF05602	1	1	1	1	1	1	2	Cleft lip and palate transmembrane protein 1 (CLPTM1)
PF00806	4	4	4	4	5	5	6	Pumilio-family RNA binding repeat
PF05879	1	1	1	1	1	1	4	Root hair defective 3 GTP-binding protein (RHD3) GTPase domain
PF20428	1	1	1	1	1	1	4	Sey1 three-helix bundle domain
PF00326	5	6	7	13	14	3	20	Prolyl oligopeptidase family
PF03151	6	6	6	5	11	3	9	Triose-phosphate Transporter family
PF00153	43	42	42	45	42	32	76	Mitochondrial carrier protein
PF09441	1	1	1	1	1	1	2	ARS binding protein 2
PF17733	1	1	1	1	2	0	2	PEX14-like KPWE domain
PF25871	1	1	1	1	2	0	2	Helix-turn-helix domain
PF09532	1	1	1	1	1	2	2	FDF domain
PF12701	1	1	1	1	1	1	2	Scd6-like Sm domain
PF00085	10	12	13	13	17	10	22	Thioredoxin
PF04982	1	2	2	1	1	1	2	HPP, transmembrane region
PF13602	28	23	22	37	38	25	51	Zinc-binding dehydrogenase
PF00245	3	3	3	4	2	2	4	Alkaline phosphatase
PF26732	1	1	1	1	1	1	2	PhoA-like N-terminal domain
PF21924	0	0	0	1	1	0	1	XRCC4 coiled-coil
PF02696	1	1	1	1	1	2	2	Protein adenylyltransferase SelO
PF04818	3	4	4	6	4	5	10	CID domain
PF21380	1	1	1	2	1	1	2	Nrd1/Seb1, domain 2
PF09724	1	1	1	0	1	2	2	Sister chromatid cohesion protein Dcc1
PF01814	5	2	4	5	1	2	4	Hemerythrin HHE cation binding domain
PF00566	13	14	13	11	15	11	21	Rab-GTPase-TBC domain
PF23436	11	13	12	9	13	10	18	RabGAP TBC domain
PF12832	3	2	2	1	2	1	4	MFS_1 like family
PF04548	0	0	0	0	0	0	1	AIG1 family
PF03370	1	1	1	1	2	1	5	Carbohydrate/starch-binding module (family 21)
PF00011	3	4	4	3	4	2	4	Hsp20/alpha crystallin family
PF00010	11	11	11	11	18	8	21	Helix-loop-helix DNA-binding domain
PF03807	11	8	8	11	7	6	17	NADP oxidoreductase coenzyme F420-dependent
PF00493	6	6	6	6	6	8	15	MCM P-loop domain
PF14551	6	6	6	6	6	8	15	MCM N-terminal domain
PF17207	6	6	6	6	6	8	15	MCM OB domain
PF17855	6	6	6	6	6	8	15	MCM AAA-lid domain
PF18263	1	1	1	1	1	1	4	MCM6 C-terminal winged-helix domain
PF00293	13	16	15	13	14	11	24	NUDIX domain
PF00168	15	11	11	9	17	14	16	C2 domain
PF17047	1	1	1	0	0	0	2	Synaptotagmin-like mitochondrial-lipid-binding domain
PF01979	15	18	20	12	20	7	39	Amidohydrolase family
PF01602	8	8	8	10	9	7	17	Adaptin N terminal region
PF12717	6	7	7	6	6	5	12	non-SMC mitotic condensation complex subunit 1
PF03800	1	2	2	2	1	1	1	Nuf2 family
PF18595	1	2	2	2	1	1	1	Nuf2, DHR10-like domain
PF08450	5	8	8	6	6	1	9	SMP-30/Gluconolactonase/LRE-like region
PF01485	18	17	18	8	15	5	54	IBR domain, a half RING-finger domain
PF22605	3	2	3	3	1	1	15	IBR domain
PF05693	1	1	1	1	1	1	2	Glycogen synthase
PF15508	1	0	0	1	1	0	2	beta subunit of N-acylethanolamine-hydrolyzing acid amidase
PF00753	13	12	10	6	14	6	24	Metallo-beta-lactamase superfamily
PF00109	3	8	9	19	22	4	16	Beta-ketoacyl synthase, N-terminal domain
PF00698	2	7	9	19	22	4	14	Acyl transferase domain
PF02801	3	7	10	19	22	4	15	Beta-ketoacyl synthase, C-terminal domain
PF14765	0	2	4	16	15	2	8	Polyketide synthase dehydratase N-terminal domain
PF16197	0	2	5	12	12	1	3	Ketoacyl-synthetase C-terminal extension
PF21089	0	2	3	15	15	1	6	Polyketide synthase dehydratase domain
PF23114	0	1	1	9	4	1	4	HRPKS sdrA-like, NAD(P)-binding Rossmann-fold domain
PF02458	9	9	8	10	4	1	7	Transferase family
PF22664	6	6	6	6	4	1	6	Trichothecene 3-O-acetyltransferase-like N-terminal domain
PF01565	31	34	34	51	42	11	56	FAD binding domain
PF08031	15	14	14	14	18	2	21	Berberine and berberine like
PF05199	32	31	31	30	42	12	50	GMC oxidoreductase
PF16884	2	2	2	3	4	2	5	N-terminal domain of oxidoreductase
PF01073	19	20	20	19	10	13	36	3-beta hydroxysteroid dehydrogenase/isomerase family
PF07993	13	14	17	20	21	9	30	Male sterility protein
PF18558	0	1	1	1	3	0	3	Methyltransferase, Helix-turn-helix domain
PF04820	0	0	0	0	0	0	1	Tryptophan halogenase
PF01205	2	2	2	2	2	2	4	Impact N-terminal domain
PF05773	5	5	5	5	7	5	8	RWD domain
PF02731	1	1	1	1	1	1	2	SKIP/SNW domain
PF18129	1	1	1	1	1	1	2	Xrn1 SH3-like domain
PF18332	1	1	1	1	1	1	2	Exoribonuclease Xrn1 D1 domain
PF18334	1	1	1	1	1	1	2	Exoribonuclease Xrn1 D2/D3 domain
PF08518	1	1	1	1	2	1	3	Spa2 homology domain (SHD) of GIT
PF23742	1	1	1	1	2	1	2	C3G9 VBS-like domain
PF12239	2	3	3	2	3	2	4	Protein of unknown function (DUF3605)
PF01965	6	6	7	13	2	7	7	DJ-1/PfpI family
PF00773	4	4	4	5	3	3	5	RNB domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF23214	1	1	1	2	1	1	2	Mitochondrial protein cyt-4 SH3 domain
PF23216	1	1	1	2	1	1	2	Mitochondrial protein cyt-4, winged helix
PF00108	7	7	7	6	8	8	17	Thiolase, N-terminal domain
PF02803	7	7	7	6	8	8	14	Thiolase, C-terminal domain
PF22691	2	3	2	1	2	2	4	Thiolase C-terminal domain-like
PF06985	50	65	65	40	117	3	308	Heterokaryon incompatibility protein (HET)
PF00561	38	35	37	47	52	29	66	alpha/beta hydrolase fold
PF12146	14	21	21	19	16	16	37	Serine aminopeptidase, S33
PF01090	1	1	1	2	1	1	2	Ribosomal protein S19e
PF00920	5	6	6	5	7	2	7	Dihydroxy-acid/6-phosphogluconate dehydratase N-terminal
PF24877	5	6	6	5	7	2	6	Dihydroxy-acid/6-phosphogluconate dehydratase C-terminal
PF00810	2	2	3	2	2	2	6	ER lumen protein retaining receptor
PF00291	11	12	12	15	15	10	21	Pyridoxal-phosphate dependent enzyme
PF01055	11	11	11	8	16	6	23	Glycosyl hydrolases family 31 TIM-barrel domain
PF13802	7	7	6	6	9	3	9	Glycosyl hydrolase 31 N-terminal galactose mutarotase-like domain
PF21365	11	11	11	8	16	6	23	Glycosyl hydrolase family 31 C-terminal domain
PF01593	12	13	13	18	21	12	22	Flavin containing amine oxidoreductase
PF07156	1	1	1	1	2	1	7	Prenylcysteine lyase
PF03452	5	5	5	3	5	4	8	Anp1
PF03936	0	0	0	1	0	0	1	Terpene synthase family, metal binding domain
PF19086	4	1	2	5	3	0	7	Terpene synthase family 2, C-terminal metal binding
PF03095	2	2	2	2	2	2	4	Phosphotyrosyl phosphate activator (PTPA) protein
PF00175	17	16	16	21	16	12	26	Oxidoreductase NAD-binding domain
PF00667	8	8	8	11	6	6	12	FAD binding domain
PF01558	1	1	1	1	1	0	2	Pyruvate ferredoxin/flavodoxin oxidoreductase
PF17147	0	0	0	0	1	0	2	Pyruvate:ferredoxin oxidoreductase core domain II
PF11789	1	2	2	2	3	1	4	Zinc-finger of the MIZ type in Nse subunit
PF15454	2	2	2	1	1	1	1	Late endosomal/lysosomal adaptor and MAPK and MTOR activator
PF22244	0	0	0	1	0	0	2	Glucuronyl esterase, fungi
PF00975	3	3	3	3	3	0	3	Thioesterase domain
PF01119	3	3	3	2	4	2	6	DNA mismatch repair protein, C-terminal domain
PF13589	4	5	5	5	6	5	8	Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase
PF13462	1	0	0	1	2	0	4	Thioredoxin
PF09335	1	1	1	1	1	1	2	VTT domain
PF10287	1	1	1	0	1	1	2	Cell wall protein YJL171C/Tos1, C-terminal
PF10290	1	1	1	0	1	1	2	Cell wall protein YJL171C/Tos1, N-terminal
PF05127	1	1	1	1	1	2	2	RNA cytidine acetyltransferase NAT10/TcmA, helicase domain
PF08351	1	1	1	1	1	2	2	tRNA(Met) cytidine acetyltransferase TmcA, N-terminal
PF13718	1	1	1	1	1	2	2	GNAT acetyltransferase 2
PF13725	1	1	1	1	1	2	2	Possible tRNA binding domain
PF00135	23	32	33	24	41	15	39	Carboxylesterase family
PF00856	24	20	20	12	37	16	66	SET domain
PF01384	6	5	5	5	3	0	4	Phosphate transporter family
PF05186	1	1	1	1	1	1	2	Dpy-30 motif
PF04088	1	1	1	1	2	1	4	Peroxin 13, N-terminal region
PF12223	3	2	2	4	6	3	8	Protein of unknown function (DUF3602)
PF02535	10	8	8	6	12	7	10	ZIP Zinc transporter
PF00249	12	11	11	12	13	7	24	Myb-like DNA-binding domain
PF26082	3	1	2	3	1	0	4	Oxidoreductase acuF-like, C2H2 type zinc-finger
PF24476	3	4	5	7	2	2	6	Domain of unknown function (DUF7580)
PF00488	7	8	8	7	8	5	7	MutS domain V
PF01624	4	5	5	5	5	4	5	MutS domain I
PF05188	4	7	7	4	5	3	3	MutS domain II
PF05192	7	8	8	7	8	5	7	MutS domain III
PF01208	2	2	2	1	1	0	2	Uroporphyrinogen decarboxylase (URO-D)
PF00383	6	9	9	7	9	6	13	Cytidine and deoxycytidylate deaminase zinc-binding region
PF14437	3	5	5	1	5	3	7	MafB19-like deaminase
PF02671	3	1	1	1	1	3	5	Paired amphipathic helix repeat
PF08295	2	1	1	1	1	1	2	Sin3 family co-repressor
PF16879	2	1	1	1	1	1	2	C-terminal domain of Sin3a protein
PF06964	1	2	2	4	2	0	6	Alpha-L-arabinofuranosidase C-terminal domain
PF22848	1	2	2	4	2	0	4	Alpha-L-arabinofuranosidase 1 domain
PF00181	2	2	2	2	2	2	5	Ribosomal Proteins L2, RNA binding N-terminal domain
PF15612	1	1	1	2	2	3	2	WSTF, HB1, Itc1p, MBD9 motif 1
PF10296	2	2	2	2	5	2	2	Maintenance of mitochondrial morphology protein 1
PF05175	4	4	4	5	9	4	12	Methyltransferase small domain
PF04048	1	1	1	1	2	0	2	Exocyst complex component Sec8 N-terminal
PF20651	2	2	2	2	1	1	4	Exocyst complex component EXOC6/Sec15, N-terminal
PF20652	1	1	1	1	2	0	2	Exocyst complex component Sec8 C-terminal
PF09435	1	1	1	1	1	1	2	Fungal protein of unknown function (DUF2015)
PF01778	2	2	2	2	2	2	4	Ribosomal L28e protein family
PF08038	1	1	1	1	1	0	2	TOM7 family
PF04091	1	1	1	1	1	0	2	Exocyst complex subunit Sec15 C-terminal
PF04059	2	1	1	1	2	1	2	RNA recognition motif 2
PF19316	1	1	1	3	2	1	2	GPI ethanolamine phosphate transferase membrane region
PF20945	1	1	1	1	2	1	2	Ribonuclease MRP protein subunit RMP1
PF00775	7	10	10	5	7	6	8	Dioxygenase
PF04444	4	7	7	4	4	5	7	Catechol dioxygenase N terminus
PF24809	4	6	6	3	3	1	7	Domain of unknown function (DUF7708)
PF22942	7	4	4	5	10	3	13	Domain of unknown function (DUF7025)
PF23232	3	2	2	3	4	2	12	Fungal AAA+ ATPase lid domain
PF01135	3	3	3	3	3	3	6	Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PCMT)
PF01209	8	9	9	12	31	8	18	ubiE/COQ5 methyltransferase family
PF04190	1	1	1	1	2	2	2	Golgi to ER traffic protein 4
PF01490	24	26	26	21	25	8	35	Transmembrane amino acid transporter protein
PF02953	5	4	4	4	5	4	6	Tim10/DDP family zinc finger
PF00276	1	1	1	2	1	2	2	Ribosomal protein L23
PF03939	1	1	1	1	1	0	2	Ribosomal protein L23, N-terminal domain
PF00027	4	4	4	4	5	3	8	Cyclic nucleotide-binding domain
PF16643	1	1	1	1	1	1	2	Unstructured region on cNMP-binding protein
PF00916	6	5	5	7	3	3	8	Sulfate permease family
PF08238	6	6	6	6	9	8	12	Sel1 repeat
PF00581	10	12	9	11	13	7	15	Rhodanese-like domain
PF03328	5	5	6	11	7	1	8	HpcH/HpaI aldolase/citrate lyase
PF05832	1	1	1	1	1	2	2	Eukaryotic protein of unknown function (DUF846)
PF12874	15	10	10	14	15	9	25	Zinc-finger of C2H2 type
PF13912	6	4	4	6	3	3	12	C2H2-type zinc finger

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF02018	0	0	0	0	1	0	1	Carbohydrate binding domain
PF00596	8	8	8	13	10	4	19	Class II Aldolase and Adducin N-terminal domain
PF00503	3	3	3	5	5	4	4	G-protein alpha subunit
PF02668	16	23	22	15	20	3	41	Taurine catabolism dioxygenase TauD, TfdA family
PF06155	2	1	1	2	4	1	4	Gamma-butyrobetaine hydroxylase-like, N-terminal
PF11935	1	1	1	1	1	1	2	Symplekin/PTA1 N-terminal
PF09813	1	1	1	1	1	1	2	Cytochrome c oxidase assembly factor 3
PF23297	0	1	2	9	10	1	4	Highly reducing polyketide synthase sdgA, C-terminal ACP domain
PF16073	2	4	5	3	7	2	8	Starter unit:ACP transacylase in aflatoxin biosynthesis
PF22621	1	2	3	7	11	1	3	CurL-like, PKS C-terminal
PF00179	22	22	22	20	28	23	54	Ubiquitin-conjugating enzyme
PF04099	2	2	2	2	2	1	4	Sybindin-like family
PF26639	1	1	0	2	0	1	6	Het-6 beta-barrel domain
PF00082	6	11	10	28	20	4	28	Subtilase family
PF07393	1	1	1	2	2	2	4	Exocyst complex component Sec10-like, alpha-helical bundle
PF20667	1	1	1	1	1	1	2	Exocyst complex component Sec10, N-terminal
PF04909	13	15	15	10	14	6	22	Amidohydrolase
PF02628	1	1	1	1	1	2	2	Cytochrome oxidase assembly protein
PF01866	2	2	3	2	2	2	4	Putative diphthamide synthesis protein
PF03171	14	18	18	15	17	9	43	2OG-Fe(II) oxygenase superfamily
PF00355	9	10	10	9	7	3	12	Rieske [2Fe-2S] domain
PF02921	1	1	1	1	1	1	2	Ubiquinol cytochrome reductase transmembrane region
PF01661	2	2	2	1	3	2	4	Macro domain
PF00117	8	8	8	10	12	8	15	Glutamine amidotransferase class-I
PF00958	1	1	1	1	1	1	2	GMP synthase C terminal domain
PF23394	1	1	1	1	1	1	2	Domain of unknown function (DUF7102)
PF23395	1	1	1	1	1	1	2	SAM-like domain
PF02714	6	6	8	6	6	6	8	Calcium-dependent channel, 7TM region, putative phosphate
PF12621	4	4	4	4	4	4	3	Extracellular tail, of 10TM putative phosphate transporter
PF13967	5	6	7	6	6	4	7	Late exocytosis, associated with Golgi transport
PF14703	6	6	7	5	5	5	9	Cytosolic domain of 10TM putative phosphate transporter
PF00994	3	3	3	2	3	3	4	Probable molybdopterin binding domain
PF24102	0	2	2	1	1	1	2	FAD synthase, middle domain
PF00176	28	26	27	27	30	22	48	SNF2-related domain
PF00628	19	17	16	13	17	16	33	PHD-finger
PF04851	47	48	48	42	60	48	79	Type III restriction enzyme, res subunit
PF10383	2	2	2	1	2	2	4	Transcription-silencing protein Clr2
PF16761	2	2	2	1	7	2	4	Transcription-silencing protein, cryptic loci regulator Clr2
PF00756	4	7	7	3	5	2	5	Putative esterase
PF05383	3	3	3	2	4	3	6	La domain
PF09692	1	1	1	3	1	1	2	Argonaute siRNA chaperone (ARC) complex subunit Arb1
PF03770	3	2	2	2	3	2	4	Inositol polyphosphate kinase
PF02515	7	9	9	7	11	2	15	CoA-transferase family III
PF06807	1	1	1	1	2	1	2	Pre-mRNA cleavage complex II protein Clp1
PF16573	1	1	1	1	2	1	2	N-terminal beta-sandwich domain of polyadenylation factor
PF16575	2	2	2	2	3	1	4	mRNA cleavage and polyadenylation factor CLP1 P-loop
PF08700	4	4	4	3	3	3	9	Vps51/EXO84/COG1 N-terminal
PF16528	1	1	1	1	1	1	2	Exocyst component 84 C-terminal
PF25345	1	1	1	1	1	1	2	PH domain found in exocyst complex component Exo84
PF02064	1	1	1	1	1	1	2	MAS20 protein import receptor
PF00501	48	52	52	57	88	32	85	AMP-binding enzyme
PF13193	27	31	30	23	46	25	54	AMP-binding enzyme C-terminal domain
PF02771	13	12	12	13	17	12	25	Acyl-CoA dehydrogenase, N-terminal domain
PF08159	2	2	2	2	2	2	4	NUC153 domain
PF25121	1	1	1	1	1	1	2	ESF1 RRM domain
PF01900	1	1	1	1	1	1	2	Rpp14/Pop5 family
PF14632	1	1	1	1	1	1	2	Acidic N-terminal SPT6
PF14635	1	1	1	1	1	1	1	Helix-hairpin-helix motif
PF14639	1	1	1	1	1	1	1	Holliday-junction resolvase-like of SPT6
PF14641	1	1	1	1	1	1	2	Helix-turn-helix DNA-binding domain of SPT6
PF22706	1	1	1	1	1	1	2	Tex central region-like
PF13714	2	2	2	4	6	2	6	Phosphoenolpyruvate phosphomutase
PF14604	17	15	16	16	18	16	28	Variant SH3 domain
PF00763	3	2	2	2	2	2	3	Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain
PF01268	2	1	1	1	1	1	2	Formate--tetrahydrofolate ligase
PF02882	2	1	1	1	1	1	2	Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain
PF24805	1	1	1	1	1	1	2	EIF3I
PF00668	4	4	2	11	21	3	4	Condensation domain
PF14226	14	18	18	12	17	8	42	non-haem dioxygenase in morphine synthesis N-terminal
PF22336	1	0	2	4	5	1	1	RhiE-like, KS-MAT linker domain
PF28402	0	1	2	0	0	1	1	Pneumocandin biosynthesis cluster protein B C-terminal domain
PF07859	27	34	36	32	45	17	61	alpha/beta hydrolase fold
PF13577	5	6	6	4	13	2	15	SnoaL-like domain
PF06220	2	2	2	2	2	2	4	U1 zinc finger
PF00481	7	6	7	5	7	5	9	Protein phosphatase 2C
PF01535	5	8	10	5	6	7	12	PPR repeat
PF16124	3	2	2	3	4	2	4	RecQ zinc-binding
PF24840	1	1	1	1	1	1	3	SigF NTF2-like domain
PF00625	1	2	2	4	1	1	2	Guanylate kinase
PF10375	1	1	1	1	1	1	2	GRAB domain
PF00890	5	6	6	8	8	5	17	FAD binding domain
PF01266	25	25	23	43	37	15	44	FAD dependent oxidoreductase
PF16901	1	1	1	2	1	1	2	C-terminal domain of alpha-glycerophosphate oxidase
PF02133	7	22	22	3	18	3	32	Permease for cytosine/purines, uracil, thiamine, allantoin
PF09159	1	1	1	0	2	1	2	Mitochondrial resolvase Ydc2 / RNA splicing MRS1
PF06741	1	1	1	1	1	1	2	LsmAD domain
PF14438	1	1	1	1	1	2	2	Ataxin 2 SM domain
PF03915	1	1	1	1	1	1	2	Actin interacting protein 3
PF23153	1	1	1	1	1	1	2	Aip3p/Bud6 N-terminal domain
PF00892	2	1	1	6	5	4	4	EamA-like transporter family
PF00208	2	2	2	2	4	1	4	Glutamate/Leucine/Phenylalanine/Valine dehydrogenase
PF02812	1	1	1	1	1	1	2	Glu/Leu/Phe/Val dehydrogenase, dimerisation domain
PF13516	6	7	7	8	3	4	10	Leucine Rich repeat
PF01243	5	6	5	3	3	4	8	Pyridoxamine 5'-phosphate oxidase
PF10590	1	2	2	1	2	1	2	Pyridoxine 5'-phosphate oxidase C-terminal dimerisation region
PF01868	1	1	1	1	2	1	2	Ribonuclease P/MRP, subunit p29
PF02656	5	7	8	6	8	6	13	Domain of unknown function (DUF202)

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF02127	2	3	3	2	2	2	4	Aminopeptidase I zinc metalloprotease (M18)
PF12396	2	2	2	2	2	1	3	Protein of unknown function (DUF3659)
PF04042	4	3	3	3	3	3	6	DNA polymerase alpha/epsilon subunit B
PF18018	1	1	1	1	1	1	2	DNA polymerase delta subunit OB-fold domain
PF26176	3	2	2	3	3	0	6	C2H2-domain containing protein second zinc finger domain
PF26177	3	2	2	3	2	1	5	C2H2-domain containing protein first zinc finger domain
PF22766	1	1	1	1	1	1	2	ZW10 C-terminal helical domain
PF04106	1	1	1	1	2	1	2	Autophagy protein ATG5, UblB domain
PF20637	1	1	1	1	2	1	3	Autophagy protein ATG5, alpha-helical bundle region
PF20638	1	1	1	1	2	1	3	Autophagy protein ATG5, UblA domain
PF00730	4	4	4	6	9	5	7	HhH-GPD superfamily base excision DNA repair protein
PF08625	1	1	1	1	1	1	2	Utp13 specific WD40 associated domain
PF00227	10	11	11	15	15	14	27	Proteasome subunit
PF10584	6	6	6	7	8	7	13	Proteasome subunit A N-terminal signature
PF00789	6	5	5	5	5	6	10	UBX domain
PF13098	3	4	4	5	4	4	7	Thioredoxin-like domain
PF13899	2	2	2	1	2	3	4	Thioredoxin-like
PF14555	4	5	5	6	7	6	12	UBA-like domain
PF17784	11	9	9	13	28	3	21	Sulfotransferase domain
PF24920	1	1	1	1	1	2	2	Tricalbin-1-like, C2 domain
PF25669	3	3	3	2	4	3	4	MUG190-like SMP domain
PF00368	1	1	1	1	3	2	5	Hydroxymethylglutaryl-coenzyme A reductase
PF12349	3	3	3	3	4	2	7	Sterol-sensing domain of SREBP cleavage-activation
PF13323	1	1	1	1	1	0	4	N-terminal domain with HPIH motif
PF00295	11	10	9	2	18	1	18	Glycosyl hydrolases family 28
PF00225	12	12	12	13	16	11	16	Kinesin motor domain
PF16796	12	12	12	12	13	12	17	Microtubule binding
PF00710	2	2	2	3	2	0	4	Asparaginase, N-terminal
PF17763	2	2	2	3	2	0	2	Glutaminase/Asparaginase C-terminal domain
PF01215	1	1	1	1	1	1	2	Cytochrome c oxidase subunit Vb
PF08617	1	1	1	1	1	1	2	Kinase binding protein CGI-121
PF00857	6	11	12	8	12	5	30	Isochorismatase domain
PF00238	2	2	2	2	3	2	5	Ribosomal protein L14p/L23e
PF01417	3	3	3	3	2	2	3	ENTH domain
PF01207	2	2	3	4	4	3	8	Dihydrouridine synthase (Dus)
PF27522	2	7	7	2	20	2	18	YDMC
PF08643	2	1	1	1	1	2	4	Fungal family of unknown function (DUF1776)
PF00692	1	1	1	1	1	1	3	dUTPase
PF22769	1	1	1	1	0	1	3	dCTP deaminase-like
PF04003	2	2	2	3	3	3	6	Dip2/Utp12 Family
PF25172	1	1	1	1	1	1	2	WDR3 second beta-propeller domain
PF25173	1	1	1	1	1	1	2	WDR3 first beta-propeller domain
PF04045	1	1	1	1	1	1	2	Arp2/3 complex, 34 kD subunit p34-Arc
PF12768	1	1	1	1	1	1	2	Rax2 C-terminal beta propeller domain
PF20842	1	1	1	1	1	1	2	Rax2 second domain
PF20843	1	1	1	1	1	1	2	Rax2 third domain
PF01137	2	2	2	2	2	2	4	RNA 3'-terminal phosphate cyclase
PF05189	1	1	1	1	1	1	2	RNA 3'-terminal phosphate cyclase (RTC), insert domain
PF00312	2	2	2	2	2	2	4	Ribosomal protein S15
PF08069	1	1	1	1	1	1	2	Ribosomal S13/S15 N-terminal domain
PF04791	1	1	1	2	2	1	4	LMBR1-like membrane protein
PF04147	1	1	1	1	1	1	2	Nop14-like family
PF06052	1	1	1	1	3	2	2	3-hydroxyanthranilic acid dioxygenase
PF01619	2	3	3	7	7	1	2	Proline dehydrogenase
PF09494	1	1	1	1	1	1	2	Slx4 endonuclease
PF05158	1	1	1	1	1	1	2	RNA polymerase Rpc34 subunit
PF14618	1	1	1	1	1	1	1	Domain of unknown function (DUF4452)
PF03367	0	0	0	1	1	1	2	ZPR1 zinc-finger domain
PF22794	0	0	0	1	1	1	2	ZPR1 jelly-roll domain
PF12937	30	37	39	32	42	24	120	F-box-like
PF13202	8	6	6	8	8	9	10	EF hand
PF13499	9	7	7	10	8	12	12	EF-hand domain pair
PF00258	8	9	9	11	7	7	13	Flavodoxin
PF01077	2	2	2	2	2	2	4	Nitrite and sulphite reductase 4Fe-4S domain
PF03460	2	2	2	2	2	2	4	Nitrite/Sulfite reductase ferredoxin-like half domain
PF04193	10	11	10	8	11	7	19	PQ loop repeat
PF11701	1	1	1	1	1	1	2	Myosin-binding striated muscle assembly central
PF13668	4	4	4	5	6	4	9	Ferritin-like domain
PF00805	0	2	2	0	1	0	2	Pentapeptide repeats (8 copies)
PF00333	2	2	2	2	2	3	4	Ribosomal protein S5, N-terminal domain
PF03719	2	2	2	2	2	3	4	Ribosomal protein S5, C-terminal domain
PF14821	1	1	1	1	1	1	2	Threonine synthase N terminus
PF24857	1	1	1	1	1	1	2	Threonine synthase, C-terminal
PF03167	2	2	2	3	3	2	4	Uracil DNA glycosylase superfamily
PF10906	0	0	0	1	3	1	2	MIOREX complex component 7
PF00445	2	2	2	1	2	2	10	Ribonuclease T2 family
PF25488	1	1	1	0	1	2	6	RNase T2-like C-terminal domain
PF00378	14	15	16	16	27	12	33	Enoyl-CoA hydratase/isomerase
PF16113	12	14	14	12	21	9	27	Enoyl-CoA hydratase/isomerase
PF08881	2	3	2	1	1	0	7	CVNH domain
PF13233	7	6	8	8	9	7	10	Complex1_LYR-like
PF14543	3	4	5	7	4	4	4	Xylanase inhibitor N-terminal
PF07986	2	2	2	2	1	1	2	Tubulin binding cofactor C
PF16752	2	2	2	2	1	1	2	Tubulin-specific chaperone C N-terminal domain
PF28358	2	2	2	1	2	1	2	NADH-ubiquinone oxidoreductase 21.3 kDa subunit C-terminal domain
PF09801	1	1	1	1	1	1	3	Integral membrane protein S linking to the trans Golgi network
PF09336	2	2	2	5	2	3	4	Vps4 C terminal oligomerisation domain
PF17862	16	17	17	16	21	16	34	AAA+ lid domain
PF00152	8	10	10	10	8	7	13	tRNA synthetases class II (D, K and N)
PF01336	6	8	8	8	7	4	14	OB-fold nucleic acid binding domain
PF01532	8	8	10	12	13	10	14	Glycosyl hydrolase family 47
PF22917	3	5	5	3	6	6	12	PRISE-like Rossmann-fold domain
PF00443	20	19	21	16	24	19	39	Ubiquitin carboxyl-terminal hydrolase
PF13446	1	1	1	1	2	1	3	A repeated domain in UCH-protein
PF07519	11	12	12	3	16	6	18	Tannase and feruloyl esterase
PF28471	0	0	0	0	0	0	1	Domain of unknown function (DUF8411)
PF02057	1	0	0	0	0	0	4	Glycosyl hydrolase family 59

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF17189	3	2	2	0	3	0	6	Glycosyl hydrolase family 30 beta sandwich domain
PF04900	2	2	2	3	2	2	4	Fcf1
PF24779	1	1	1	2	1	1	2	UTP23 sensor motif
PF05277	3	2	2	3	2	1	6	Protein of unknown function (DUF726)
PF07970	2	2	2	2	2	1	6	Endoplasmic reticulum vesicle transporter
PF13850	2	2	2	2	2	2	6	Endoplasmic Reticulum-Golgi Intermediate Compartment (ERGIC)
PF08774	1	1	1	1	1	1	3	VRR-NUC domain
PF21170	0	1	1	1	0	1	3	Fanconi-associated nuclease 1, TPR domain
PF21315	1	1	1	1	1	1	3	FAN1, HTH domain
PF22485	1	1	1	1	1	1	1	Domain of unknown function (DUF6987)
PF01702	2	2	2	3	3	3	4	Queuine tRNA-ribosyltransferase
PF09768	1	1	1	1	1	1	2	Peptidase M76 family
PF08294	1	1	1	2	1	0	2	TIM21
PF02910	1	1	1	1	3	2	4	Fumarate reductase flavoprotein C-term
PF12539	1	1	1	1	1	1	2	Chromosome segregation protein Csm1/Pcs1
PF02836	7	4	4	7	2	0	5	Glycosyl hydrolases family 2, TIM barrel domain
PF02837	5	3	3	5	2	0	4	Glycosyl hydrolases family 2, sugar binding domain
PF00627	8	8	8	7	9	8	9	UBA/TS-N domain
PF09668	1	1	1	2	2	1	2	Aspartyl protease
PF16891	2	1	1	2	3	2	4	Serine-threonine protein phosphatase N-terminal domain
PF02823	1	1	1	1	1	1	2	ATP synthase, Delta/Epsilon chain, beta-sandwich domain
PF21334	1	1	1	1	1	1	2	Fungal epsilon subunit of F1F0-ATP synthase C-terminal domain
PF01997	3	2	3	2	3	3	5	Translin family
PF13738	17	19	19	23	26	8	34	Pyridine nucleotide-disulphide oxidoreductase
PF00133	5	7	6	6	5	3	8	tRNA synthetases class I (I, L, M and V)
PF08264	5	6	5	5	3	3	8	Anticodon-binding domain of tRNA ligase
PF10568	2	4	4	3	3	2	4	Outer mitochondrial membrane transport complex protein
PF17171	2	4	4	2	3	2	4	Glutathione S-transferase, C-terminal domain
PF00226	29	26	27	24	35	26	66	DnaJ domain
PF14308	1	1	1	1	1	1	2	X-domain of DnaJ-containing
PF00580	4	2	2	2	2	1	3	UvrD/REP helicase N-terminal domain
PF13245	13	11	12	13	23	7	24	AAA domain
PF13361	2	1	1	1	1	0	2	UvrD-like helicase C-terminal domain
PF13538	2	1	1	1	1	0	2	UvrD-like helicase C-terminal domain
PF00254	6	4	4	4	4	4	9	FKBP-type peptidyl-prolyl cis-trans isomerase
PF12632	1	1	1	1	1	1	3	Mysoin-binding motif of peroxisomes
PF07019	1	1	1	1	1	1	2	EMC6
PF00705	1	1	1	1	1	1	2	Proliferating cell nuclear antigen, N-terminal domain
PF02747	1	1	1	1	1	1	2	Proliferating cell nuclear antigen, C-terminal domain
PF04139	2	2	2	2	3	2	4	Rad9
PF00173	26	28	28	28	30	21	48	Cytochrome b5-like Heme/Steroid binding domain
PF00787	13	12	13	12	13	10	23	PX domain
PF24808	1	1	1	2	3	2	4	Domain of unknown function (DUF7707)
PF04828	17	15	15	13	23	12	36	Glutathione-dependent formaldehyde-activating enzyme
PF00063	4	4	5	4	4	5	8	Myosin head (motor domain)
PF06017	1	0	0	1	1	1	2	Unconventional myosin tail, actin- and lipid-binding
PF03129	5	5	5	8	6	6	12	Anticodon binding domain
PF13393	3	2	2	3	3	3	5	Histidyl-tRNA synthetase
PF00350	9	11	13	11	11	8	19	Dynamin family
PF12955	1	1	1	1	1	1	2	Vacuolar sorting protein Vps3844, C-terminal domain
PF21656	1	0	0	0	0	1	2	Domain of unknown function (DUF6859)
PF04752	1	1	1	1	2	1	2	ChaC-like protein
PF10250	1	2	2	0	4	0	4	GDP-fucose protein O-fucosyltransferase
PF08447	4	4	4	6	7	5	11	PAS fold
PF08448	5	3	3	3	6	5	10	PAS fold
PF13426	11	8	8	9	15	10	14	PAS domain
PF08325	3	3	3	3	3	2	6	WLM domain
PF08003	0	0	0	0	0	0	2	Protein of unknown function (DUF1698)
PF00439	5	6	6	8	9	10	15	Bromodomain
PF22994	1	1	1	1	1	1	2	RSC4 Ig-like domain
PF01111	2	0	0	1	1	1	2	Cyclin-dependent kinase regulatory subunit
PF10294	8	9	9	8	10	5	15	Lysine methyltransferase
PF00156	6	6	6	6	6	6	13	Phosphoribosyl transferase domain
PF15463	1	1	1	1	1	2	2	Extracellular mutant protein 11
PF05336	1	1	1	1	2	0	2	L-rhamnose mutarotase
PF02733	5	3	3	5	4	1	6	Dak1 domain
PF00860	1	2	2	1	4	1	6	Permease family
PF01124	5	5	6	2	9	3	12	MAPEG family
PF05241	3	4	4	3	3	2	7	EXPERA (EXPanded EBP superfamily)
PF00808	9	10	10	11	11	8	15	Histone-like transcription factor (CBF/NF-Y) and archaeal histone
PF00535	8	7	6	5	8	5	13	Glycosyl transferase family 2
PF11927	3	4	3	4	5	5	8	Haem-dependent oxidative N-demethylase, alpha subunit-like
PF00385	7	4	5	8	9	4	17	Chromo (CHRomatin Organisation MOdifier) domain
PF06884	1	1	1	0	1	3	4	Protein of unknown function (DUF1264)
PF00025	32	32	32	33	41	29	54	ADP-ribosylation factor family
PF00071	33	36	37	34	43	31	62	Ras family
PF08477	31	34	34	31	38	27	52	Ras of Complex, Roc, domain of DAPkinase
PF01656	4	3	3	4	5	3	10	CobQ/CobB/MinD/ParA nucleotide binding domain
PF10609	4	2	2	3	5	2	6	NUBPL iron-transfer P-loop NTPase
PF20434	20	17	19	14	36	10	33	BD-FAE
PF20254	0	0	0	2	0	0	3	N,N-dimethylformamidase beta subunit-like, C-terminal
PF20399	2	2	2	2	2	2	4	PH domain
PF20400	2	2	2	2	2	2	4	BAR-like domain
PF04185	1	2	2	0	6	0	6	Phosphoesterase family
PF03194	1	1	1	1	1	1	2	LUC7 N_terminus
PF04113	1	1	1	1	1	1	2	Gpi16 subunit, GPI transamidase component
PF09286	2	4	4	5	17	1	22	Pro-kumamolisin, activation domain
PF06172	1	1	1	1	1	1	2	Cupin superfamily (DUF985)
PF08320	1	1	1	1	1	1	2	PIG-X / PBN1
PF00549	4	4	4	7	5	4	7	CoA-ligase
PF02629	3	3	3	4	5	3	5	CoA binding domain
PF13380	1	2	2	1	4	3	4	CoA binding domain
PF13607	2	2	2	3	1	2	4	Succinyl-CoA ligase like flavodoxin domain
PF04930	0	1	1	0	1	1	1	FUN14 family
PF05544	3	0	0	5	3	1	2	Proline racemase
PF23257	2	3	3	1	2	1	9	Domain of unknown function (DUF7071)
PF03630	0	1	1	2	2	2	2	Fumble

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF04641	1	1	1	1	1	1	2	Rtf2 RING-finger
PF05730	10	10	10	13	23	5	14	CFEM domain
PF01169	1	1	1	1	1	1	2	Divalent cation/proton antiporter GDT1
PF27641	1	1	1	1	2	1	2	SIP5 protein N-terminal domain
PF22514	1	1	1	0	1	0	2	EXPB1-like domain 1
PF25875	1	1	1	0	1	1	2	Rad26/CSB winged helix DNA-binding domain
PF12906	3	4	4	2	2	2	5	RING-variant domain
PF00352	0	0	0	1	1	1	2	Transcription factor TFIID (or TATA-binding protein, TBP)
PF22607	1	1	1	0	5	2	6	FAD binding domain-like
PF11913	2	6	5	1	16	3	13	Protein of unknown function (DUF3431)
PF08574	1	1	1	1	1	1	2	Transcription factor Iwr1
PF00241	4	5	5	6	5	4	6	Cofilin/tropomyosin-type actin-binding protein
PF10282	4	4	4	4	5	3	6	Lactonase, 7-bladed beta-propeller
PF04857	1	1	1	0	1	1	2	CAF1 family ribonuclease
PF04968	1	1	1	1	1	1	3	CHORD
PF18826	1	1	1	1	1	1	2	Bacteroidetes VLRF1 release factor
PF08740	5	4	4	4	5	2	10	BCS1 N terminal
PF25426	5	4	4	4	5	3	7	Mitochondrial chaperone BCS1-like, ATPase lid domain
PF03911	1	1	1	1	2	1	3	Sec61beta family
PF24494	4	1	1	0	13	0	17	Domain of unknown function (DUF7587)
PF00122	15	18	17	26	22	14	18	P-type ATPase actuator domain
PF13246	15	15	15	18	16	12	16	P-type ATPase, cytoplasmic domain N
PF16209	4	4	4	5	7	2	10	Phospholipid-translocating ATPase N-terminal
PF16212	4	4	4	5	7	5	10	Phospholipid-translocating P-type ATPase C-terminal
PF13508	26	27	28	29	34	14	47	Acetyltransferase (GNAT) domain
PF13920	19	20	19	16	20	12	39	Zinc finger, C3HC4 type (RING finger)
PF00132	6	4	4	8	6	3	10	Bacterial transferase hexapeptide (six repeats)
PF00483	3	3	3	3	3	3	6	Nucleotidyl transferase
PF12804	2	2	2	2	3	3	4	MobA-like NTP transferase domain
PF25087	4	4	4	5	5	4	6	GMPPB C-terminal domain
PF02212	2	3	3	3	3	2	6	Dynamin GTPase effector domain
PF14295	8	3	5	0	13	5	12	PAN domain
PF02055	2	1	1	0	4	0	4	Glycosyl hydrolase family 30 TIM-barrel domain
PF00160	13	12	12	11	18	11	15	Cyclophilin type peptidyl-prolyl cis-trans isomerase/CLD
PF01480	3	3	3	3	4	4	11	PWI domain
PF00155	20	21	21	27	26	14	32	Aminotransferase class I and II
PF00494	3	3	3	3	3	4	6	Squalene/phytoene synthase
PF02225	9	9	9	12	6	6	10	PA domain
PF04389	11	13	13	18	12	7	17	Peptidase family M28
PF00144	8	12	11	19	12	4	21	Beta-lactamase
PF11954	1	2	2	1	3	0	4	Domain of unknown function (DUF3471)
PF04095	1	1	1	1	1	0	2	Nicotinate phosphoribosyltransferase (NAPRTase) family
PF17767	1	1	1	1	1	1	2	Nicotinate phosphoribosyltransferase (NAPRTase) N-terminal domain
PF04117	6	6	6	8	7	6	12	Mpv17 / PMP22 family
PF21730	1	1	1	1	1	1	2	Vma22/CCDC115
PF03364	1	1	1	1	2	1	4	Polyketide cyclase / dehydrase and lipid transport
PF07885	2	2	2	1	3	1	7	Ion channel
PF23187	1	0	0	2	1	3	2	UBX7 N-terminal domain
PF17907	2	2	2	2	2	2	4	AWS domain
PF01529	9	6	6	8	6	6	11	DHHC palmitoyltransferase
PF00012	9	7	7	9	7	7	18	Hsp70 protein
PF15985	1	1	1	1	1	1	4	KH domain
PF18311	1	1	1	1	1	1	2	Exosome complex exonuclease Rrp40 N-terminal domain
PF21262	1	1	1	1	1	1	2	Exosome complex component RRP40, S1 domain
PF12311	6	9	11	3	4	2	16	Protein of unknown function (DUF3632)
PF09139	1	1	1	1	1	1	2	Phosphatidate cytidylyltransferase, mitochondrial
PF00653	1	1	1	1	2	1	2	Inhibitor of Apoptosis domain
PF12234	1	1	1	1	2	1	2	RAVE protein 1 C terminal
PF09994	6	6	7	4	7	5	11	T6SS, Phospholipase effector Tle1-like, catalytic domain
PF00180	8	9	8	10	7	8	16	Isocitrate/isopropylmalate dehydrogenase
PF07745	2	2	2	1	1	3	2	Glycosyl hydrolase family 53
PF03159	2	2	2	3	2	2	3	XRN 5'-3' exonuclease N-terminus
PF04869	1	1	1	1	1	0	2	Uso1 / p115 like vesicle tethering protein, head region
PF04871	1	1	1	1	0	1	2	Uso1 / p115 like vesicle tethering protein, C terminal region
PF19302	1	1	1	1	1	1	2	Domain of unknown function (DUF5915)
PF03022	3	4	4	0	7	2	8	Major royal jelly protein
PF00296	6	7	6	0	11	0	19	Luciferase-like monooxygenase
PF11711	1	1	1	1	1	1	2	Inner membrane protein import complex subunit Tim54
PF07718	1	1	1	1	1	1	2	Coatomer beta C-terminal region
PF14806	1	1	1	1	1	1	2	Coatomer beta subunit appendage platform
PF02792	1	1	1	1	1	1	2	Mago nashi protein
PF00091	2	2	2	4	4	4	6	Tubulin/FtsZ family, GTPase domain
PF03953	2	2	2	4	4	4	6	Tubulin C-terminal domain
PF01585	7	8	8	7	7	5	12	G-patch domain
PF07713	1	1	1	1	1	1	2	Protein of unknown function (DUF1604)
PF26093	1	1	1	1	1	1	2	TGH-like, helix-turn-helix domain
PF02149	1	1	1	2	1	1	2	Kinase associated domain 1
PF08449	6	6	6	3	7	4	8	UAA transporter family
PF06441	7	8	8	12	11	6	16	Epoxide hydrolase N terminus
PF08609	1	1	1	1	1	1	2	Nucleotide exchange factor Fes1
PF08236	1	1	1	1	1	1	2	SRI (Set2 Rpb1 interacting) domain
PF08711	3	3	3	3	4	3	6	TFIIS helical bundle-like domain
PF20976	0	0	0	1	0	1	2	Ribonucleases P/MRP protein subunit Pop8
PF00188	2	4	4	3	4	2	7	Cysteine-rich secretory protein family
PF03190	1	1	1	1	2	2	2	Protein of unknown function, DUF255
PF03031	5	5	5	5	5	4	9	NLI interacting factor-like phosphatase
PF01408	14	16	16	26	15	15	27	Oxidoreductase family, NAD-binding Rossmann fold
PF22725	9	12	13	21	11	10	18	GFO/IDH/MocA C-terminal domain
PF09430	1	1	1	2	1	1	2	ER membrane protein complex subunit 7, beta-sandwich domain
PF11326	1	0	0	1	1	1	2	Synaptic plasticity regulator PANTS-like
PF09428	1	1	1	1	2	1	2	Fungal protein of unknown function (DUF2011)
PF00457	9	8	8	3	2	0	5	Glycosyl hydrolases family 11
PF13874	1	1	1	1	1	1	2	Nucleoporin complex subunit 54
PF18570	1	1	1	1	1	1	2	NUP57/Nup54 C-terminal domain
PF03372	6	6	5	8	12	7	10	Endonuclease/Exonuclease/phosphatase family
PF00755	4	4	4	2	2	2	4	Choline/Carnitine o-acyltransferase
PF01663	5	7	7	7	8	4	4	Type I phosphodiesterase / nucleotide pyrophosphatase

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF04987	1	1	1	1	1	1	2	Phosphatidylinositolglycan class N (PIG-N)
PF10332	1	1	1	1	1	1	2	Protein of unknown function (DUF2418)
PF14587	1	0	0	0	0	0	2	O-Glycosyl hydrolase family 30
PF02219	2	2	2	2	2	2	4	Methylenetetrahydrofolate reductase
PF21895	2	2	2	2	2	1	4	MTHFR, SAM-binding regulatory domain
PF21897	1	1	1	0	1	0	2	Domain of unknown function (DUF6919)
PF00121	2	2	2	2	2	2	4	Triosephosphate isomerase
PF05390	2	1	1	0	1	2	2	Yeast cell wall synthesis protein KRE9/KNH1 C-terminal
PF10342	5	5	5	1	8	5	6	Kre9/KNH-like N-terminal Ig-like domain
PF00557	11	10	10	12	13	9	19	Metallopeptidase family M24
PF05195	3	3	3	3	4	3	6	Aminopeptidase P, N-terminal domain
PF23441	22	21	21	24	27	18	28	SDR-like rossmann domain
PF10602	1	1	1	2	1	2	4	26S proteasome subunit RPN7
PF13434	3	3	3	2	5	3	4	L-lysine 6-monooxygenase/L-ornithine 5-monooxygenase
PF00150	18	17	17	11	13	6	24	Cellulase (glycosyl hydrolase family 5)
PF00903	5	9	8	8	8	5	9	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily
PF13669	2	1	1	1	4	2	4	Glyoxalase/Bleomycin resistance protein/Dioxygenase superfamily
PF01467	5	4	4	4	3	3	8	Cytidylyltransferase-like
PF08914	1	1	1	1	2	1	2	Rap1 Myb domain
PF11626	1	1	1	1	2	1	2	TRF2-interacting telomeric protein/Rap1 - C terminal domain
PF16589	3	3	3	6	7	5	10	BRCT domain
PF00686	7	7	8	0	4	3	8	Starch binding domain
PF22936	0	0	0	2	3	0	10	Pol polyprotein, beta-barrel domain
PF00382	0	1	1	2	3	3	4	Transcription factor TFIIB repeat
PF24086	1	1	1	0	2	1	3	Domain of unknown function (DUF7371)
PF13634	3	3	3	3	3	5	5	Nucleoporin FG repeat region
PF03659	1	1	2	4	2	2	8	Glycosyl hydrolase family 71
PF01873	2	2	2	2	2	2	4	Domain found in IF2B/IF5
PF19117	1	1	1	1	1	1	2	Mitochondrial import 2
PF03462	1	1	1	1	2	1	2	PCRF domain
PF01794	18	15	15	14	17	8	20	Ferric reductase like transmembrane component
PF08022	15	13	12	12	14	8	17	FAD-binding domain
PF08030	17	13	13	13	16	9	19	Ferric reductase NAD binding domain
PF01451	1	1	1	1	1	1	2	Low molecular weight phosphotyrosine protein phosphatase
PF22041	3	5	5	1	4	2	12	Glutathione S-transferase, C-terminal domain
PF00266	11	9	10	7	9	9	14	Aminotransferase class-V
PF00588	2	2	2	1	3	2	4	SpoU rRNA Methylase family
PF08032	1	1	1	1	1	1	2	RNA 2'-O ribose methyltransferase substrate binding
PF11496	4	5	6	5	5	5	8	Class II histone deacetylase complex subunits 2 and 3
PF15446	1	1	1	1	1	0	2	PHD/FYVE-zinc-finger like domain
PF18585	1	1	1	0	1	1	4	Chromatin remodeling factor Mit1 C-terminal Zn finger 2
PF23615	1	1	1	1	1	0	2	MIT1 Chromo domain
PF01237	7	6	6	6	8	5	10	Oxysterol-binding protein
PF04054	1	1	1	1	1	1	2	CCR4-Not complex component, Not1
PF12842	1	1	1	1	1	1	2	CCR4-Not complex, Not1 subunit, domain of unknown function DUF3819
PF16415	1	1	1	1	1	1	2	CCR4-NOT transcription complex subunit 1 CAF1-binding domain
PF16417	1	1	1	1	1	1	2	CCR4-NOT transcription complex subunit 1 TTP binding domain
PF16418	1	1	1	1	1	1	2	CCR4-NOT transcription complex subunit 1 HEAT repeat
PF24625	1	1	1	0	1	0	2	Domain of unknown function (DUF7626)
PF22191	7	6	7	2	9	3	29	IBR domain
PF04097	0	0	0	1	1	1	3	Nup93/Nic96
PF02204	4	4	4	5	3	3	6	Vacuolar sorting protein 9 (VPS9) domain
PF25581	1	0	0	0	0	0	4	AsqO-like, C-terminal domain
PF01179	6	7	8	6	7	4	7	Copper amine oxidase, enzyme domain
PF02728	5	4	5	1	3	2	5	Copper amine oxidase, N3 domain
PF02205	2	2	2	3	3	3	8	WH2 motif
PF08226	1	2	2	3	2	2	2	Domain of unknown function (DUF1720)
PF12763	3	4	3	5	5	3	5	EH domain
PF28338	1	1	1	0	3	1	2	AclK C-terminal domain
PF07818	1	0	0	1	2	1	2	HCNGP-like protein
PF08597	1	0	0	1	1	0	2	Translation initiation factor eIF3 subunit
PF00637	1	1	1	5	3	4	4	Region in Clathrin and VPS
PF01394	0	0	0	2	1	1	2	Clathrin propeller repeat
PF13838	0	0	0	2	1	1	2	Clathrin-H-link
PF08154	1	1	1	1	1	2	2	NLE (NUC135) domain
PF07281	1	1	1	1	2	1	2	Insulin-induced protein (INSIG)
PF01808	1	1	1	1	1	1	2	AICARFT/IMPCHase bienzyme
PF02142	2	2	2	2	2	2	3	MGS-like domain
PF00743	2	3	3	7	2	1	8	Flavin-binding monooxygenase-like
PF21052	0	1	1	1	0	1	2	EFR3, armadillo repeat
PF02883	3	3	3	3	3	3	6	Adaptin C-terminal domain
PF01885	1	1	1	1	1	1	2	RNA 2'-phosphotransferase, Tpt1 / KptA family
PF28394	1	1	1	0	1	1	2	Glucan 1,3-beta-glucosidase 3 C-terminal domain
PF01131	1	1	1	1	2	1	2	DNA topoisomerase
PF01751	2	2	2	2	4	2	4	Toprim domain
PF16035	0	1	1	1	2	1	2	Chalcone isomerase like
PF02746	3	2	2	9	3	2	3	Mandelate racemase / muconate lactonizing enzyme, N-terminal domain
PF13378	5	3	3	12	4	3	5	Enolase C-terminal domain-like
PF00564	2	4	4	4	4	3	6	PB1 domain
PF00621	6	6	6	6	6	5	11	RhoGEF domain
PF06395	2	2	2	1	1	1	2	CDC24 Calponin
PF15411	3	3	3	2	2	3	4	Pleckstrin homology domain
PF22697	2	2	2	1	1	1	2	SOS1/NGEF-like PH domain
PF20174	1	2	1	3	16	0	5	Family of unknown function (DUF6540)
PF00081	2	2	2	2	2	1	3	Iron/manganese superoxide dismutases, alpha-hairpin domain
PF02777	2	2	2	2	3	1	3	Iron/manganese superoxide dismutases, C-terminal domain
PF02320	1	1	1	1	2	1	2	Ubiquinol-cytochrome C reductase hinge protein
PF06371	1	1	1	2	2	2	5	Diaphanous GTPase-binding Domain
PF03067	1	2	2	3	1	0	2	Lytic polysaccharide mono-oxygenase, cellulose-degrading
PF11578	4	7	6	2	2	1	6	Protein of unknown function (DUF3237)
PF03639	1	1	1	3	1	2	2	Glycosyl hydrolase family 81 N-terminal domain
PF17652	1	1	1	3	1	3	2	Glycosyl hydrolase family 81 C-terminal domain
PF02170	2	2	2	2	3	5	5	PAZ domain
PF02171	4	3	3	2	11	6	12	Piwi domain
PF08699	4	2	3	2	7	3	9	Argonaute linker 1 domain
PF16486	3	2	2	2	3	4	7	N-terminal domain of argonaute
PF03969	1	2	2	1	3	1	6	AFG1-like ATPase

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF03737	4	2	2	5	1	2	2	Aldolase/RraA
PF01496	2	1	1	1	1	1	1	V-type ATPase 116kDa subunit family
PF00560	3	2	2	5	8	5	4	Leucine Rich Repeat
PF13855	3	4	4	6	8	8	7	Leucine rich repeat
PF12430	1	1	1	1	1	1	2	Abscisic acid G-protein coupled receptor
PF12537	1	1	1	1	1	1	2	The Golgi pH Regulator (GPHR) Family N-terminal
PF00582	2	2	2	2	1	2	4	Universal stress protein family
PF01544	10	10	9	7	8	7	12	CorA-like Mg2+ transporter protein
PF16717	1	1	1	1	1	1	4	Ribosome-associated complex head domain
PF21884	1	1	1	3	2	2	4	Zuotin-like, zuotin homology domain
PF26185	1	1	1	1	1	1	2	Zuotin N-terminal domain
PF00650	5	5	5	7	6	6	10	CRAL/TRIO domain
PF03765	4	4	4	5	4	5	10	CRAL/TRIO, N-terminal domain
PF01103	1	1	1	1	1	1	2	Omp85 superfamily domain
PF16815	1	1	1	2	1	0	2	Protein HRI1
PF00909	3	4	4	5	3	3	9	Ammonium Transporter Family
PF00722	10	9	10	17	10	8	17	Glycosyl hydrolases family 16
PF01249	1	1	1	1	1	1	2	Ribosomal protein S21e
PF03810	12	10	10	9	12	11	15	Importin-beta N-terminal domain
PF25758	1	1	1	1	3	1	2	Importin-11-like, TPR repeats
PF00250	6	6	7	6	7	4	8	Forkhead domain
PF09732	1	1	1	1	1	1	2	Cactus-binding C-terminus of cactin protein
PF10312	1	1	1	1	1	1	2	Conserved mid region of cactin
PF09302	1	1	1	1	1	0	2	XLF N-terminal domain
PF21928	1	1	1	1	1	0	2	XLF protein coiled-coil region
PF04199	5	7	7	7	4	5	16	Putative cyclase
PF00240	13	14	14	12	27	13	31	Ubiquitin family
PF14560	4	3	3	3	5	3	9	Ubiquitin-like domain
PF04418	1	1	1	1	1	1	2	Domain of unknown function (DUF543)
PF10441	1	1	1	1	1	1	2	Urb2/Npa2 family
PF02666	2	3	2	2	6	2	6	Phosphatidylserine decarboxylase
PF12588	0	1	0	1	3	1	2	Phophatidylserine decarboxylase
PF03663	9	8	9	11	13	4	11	Glycosyl hydrolase family 76
PF00046	7	7	6	5	10	4	7	Homeodomain
PF28401	1	1	1	0	1	1	2	MAP-homologous protein 1 C-terminal domain
PF25316	1	1	1	1	1	0	2	TAF2 Ig-like domain
PF25577	1	1	1	1	1	1	2	TAF2-like, TPR repeats
PF08825	2	1	1	1	1	1	2	E2 binding domain
PF10193	1	1	1	2	1	2	2	Telomere length regulation protein
PF06331	1	1	1	1	2	0	7	Transcription factor TFIIH complex subunit Tfb5
PF01855	0	0	0	0	0	0	1	Pyruvate flavodoxin/ferredoxin oxidoreductase, thiamine diP-bdg
PF08216	1	1	1	1	1	1	2	Catenin-beta-like, Arm-motif containing nuclear
PF02176	1	2	1	1	1	0	2	TRAF-type zinc finger
PF05739	7	7	6	7	5	5	11	SNARE domain
PF09753	1	0	0	0	0	0	2	Membrane fusion protein Use1
PF11816	1	1	1	2	1	1	2	Domain of unknown function (DUF3337)
PF13673	16	12	13	14	19	10	31	Acetyltransferase (GNAT) domain
PF02301	3	3	3	2	4	1	6	HORMA domain
PF25018	1	1	1	2	1	1	2	Importin-9 central HEAT repeats
PF06824	2	2	2	3	5	3	4	Metal-independent alpha-mannosidase (GH125)
PF01793	3	3	3	4	3	3	9	Glycolipid 2-alpha-mannosyltransferase
PF08649	1	1	1	1	1	1	2	DASH complex subunit Dad1
PF04757	3	3	3	3	4	3	6	Pex2 / Pex12 amino terminal region
PF26534	3	3	3	0	15	1	12	NTF2-like domain
PF07883	18	16	17	12	23	9	36	Cupin domain
PF13875	1	1	1	1	2	1	2	Domain of unknown function (DUF4202)
PF01545	8	7	7	11	15	10	16	Cation efflux transmembrane domain
PF16916	2	2	2	3	8	4	5	Cation efflux protein, cytoplasmic domain
PF04616	24	21	21	13	22	4	25	Glycosyl hydrolases family 43
PF00724	9	9	10	11	11	3	13	NADH:flavin oxidoreductase / NADH oxidase family
PF07287	2	2	2	7	4	3	13	Acyclic terpene utilisation family protein AtuA
PF13087	11	8	8	10	15	9	18	AAA domain
PF21369	1	1	1	1	1	1	3	STI11, N-terminal
PF01329	1	1	1	0	1	0	3	Pterin 4 alpha carbinolamine dehydratase
PF02779	7	6	6	10	7	7	10	Transketolase, pyrimidine binding domain
PF02780	6	5	5	8	5	4	6	Transketolase, C-terminal domain
PF00136	4	4	4	4	4	2	7	DNA polymerase family B
PF03104	4	4	4	4	4	3	7	DNA polymerase family B, exonuclease domain
PF08996	1	1	1	1	1	1	2	DNA Polymerase alpha zinc finger
PF12254	1	1	1	1	1	1	2	DNA polymerase alpha subunit p180 N terminal
PF01294	1	1	1	1	1	1	2	Ribosomal protein L13e
PF03992	2	2	2	3	2	1	13	Antibiotic biosynthesis monooxygenase
PF00614	2	2	2	3	4	3	4	Phospholipase D Active site motif
PF01423	16	17	18	16	21	17	31	LSM domain
PF07985	0	1	1	1	8	3	12	SRR1 domain
PF00749	3	3	3	4	3	4	5	tRNA synthetases class I (E and Q), catalytic domain
PF03950	2	2	2	3	4	3	3	tRNA synthetases class I (E and Q), anti-codon binding domain
PF16969	1	1	1	1	1	1	2	RNA-binding signal recognition particle 68
PF01687	1	1	1	2	1	1	3	Riboflavin kinase
PF01479	4	4	4	3	4	4	7	S4 domain
PF04450	1	1	1	1	2	1	2	Peptidase of plants and bacteria
PF12348	1	1	1	1	1	1	2	CLASP N terminal
PF13921	14	13	13	9	16	8	23	Myb-like DNA-binding domain
PF00735	6	7	7	4	6	7	13	Septin
PF28131	3	2	3	1	0	0	6	Domain of unknown function (DUF8372)
PF11976	11	10	10	10	17	10	26	Ubiquitin-2 like Rad60 SUMO-like
PF00187	2	1	2	2	5	3	9	Chitin recognition protein
PF01476	2	5	7	4	22	5	11	LysM domain
PF04433	5	4	4	4	4	4	12	SWIRM domain
PF23562	6	6	7	8	12	2	11	AMP-binding enzyme C-terminal domain
PF01780	1	1	2	2	2	1	2	Ribosomal L37ae protein family
PF03435	6	5	5	3	5	3	7	Saccharopine dehydrogenase NADP binding domain
PF03660	1	1	1	1	3	0	2	PHF5-like protein
PF03725	2	1	1	2	1	2	2	3' exoribonuclease family, domain 2
PF04889	1	1	1	1	1	1	2	Cwf15/Cwc15 cell cycle control protein
PF00551	3	2	2	2	6	1	6	Formyl transferase
PF01842	3	3	3	3	4	2	10	ACT domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF08386	5	3	3	11	7	2	9	TAP-like protein
PF14737	1	2	2	1	3	0	3	Domain of unknown function (DUF4470)
PF10391	1	2	2	2	2	2	4	Fingers domain of DNA polymerase lambda
PF14716	1	2	2	3	2	1	4	Helix-hairpin-helix domain
PF14791	1	2	2	2	2	2	4	DNA polymerase beta thumb
PF14792	1	2	2	2	2	2	4	DNA polymerase beta palm
PF04696	1	1	1	1	1	1	2	pinin/SDK/memA/ protein conserved region
PF02110	1	1	1	1	1	1	2	Hydroxyethylthiazole kinase family
PF02581	1	1	1	1	1	1	2	Thiamine monophosphate synthase
PF02020	1	1	1	3	3	2	3	eIF4-gamma/eIF5/eIF2-epsilon
PF00005	43	44	44	56	47	40	63	ABC transporter
PF14510	6	6	6	11	9	5	8	ABC-transporter N-terminal
PF04135	2	2	2	1	1	0	2	Nucleolar RNA-binding protein, Nop10p family
PF28115	1	1	1	1	1	1	2	Long chronological lifespan protein 2 C-terminal domain
PF08772	1	1	1	1	1	1	2	Nin one binding (NOB1) Zn-ribbon like
PF17146	1	1	1	1	1	0	2	PIN domain of ribonuclease
PF00349	5	6	6	4	4	4	9	Hexokinase
PF03727	5	6	6	4	4	4	9	Hexokinase
PF07890	1	1	1	1	1	1	2	Rrp15p
PF00448	2	2	2	2	2	2	4	SRP54-type protein, GTPase domain
PF02881	2	2	2	2	2	2	4	SRP54-type protein, helical bundle domain
PF02978	1	1	1	1	1	1	2	Signal peptide binding domain
PF01068	3	3	3	3	4	2	6	ATP dependent DNA ligase domain
PF04675	4	4	4	4	5	2	8	DNA ligase N terminus
PF03835	3	2	2	3	3	4	5	Rad4 transglutaminase-like domain
PF04716	1	1	1	1	1	1	2	ETC complex I subunit conserved region
PF00342	1	1	1	1	1	1	2	Phosphoglucose isomerase
PF00433	5	4	4	5	6	3	8	Protein kinase C terminal domain
PF00644	1	1	1	1	1	1	4	Poly(ADP-ribose) polymerase catalytic domain
PF02877	1	1	1	1	1	1	4	Poly(ADP-ribose) polymerase, regulatory domain
PF05406	1	1	1	1	1	1	4	WGR domain
PF17111	7	5	8	0	0	1	9	Pigment biosynthesis cluster protein PigI. N-terminal
PF00569	3	4	5	3	5	3	12	Zinc finger, ZZ type
PF22941	1	1	1	1	1	1	2	Transcriptional adapter 2-alpha-like domain
PF25299	1	1	1	1	1	1	2	ADA2 ZZ-type zing finger
PF01841	3	3	3	3	3	4	5	Transglutaminase-like superfamily
PF24707	1	1	1	1	2	1	2	Swc3
PF03531	1	1	1	1	1	1	2	Structure-specific recognition protein (SSRP1)
PF08512	3	3	3	3	4	3	6	Histone chaperone Rttp106-like, middle domain
PF17292	1	1	1	1	1	0	2	POB3-like N-terminal PH domain
PF21103	1	1	1	1	1	1	2	SSRP1 PH domain
PF08719	1	1	1	1	5	1	10	NADAR domain
PF12825	2	2	2	2	2	2	4	Domain of unknown function in PX-proteins (DUF3818)
PF12828	2	2	2	2	3	2	4	PX-associated
PF09631	1	1	1	1	1	1	2	Sen15 protein
PF11204	3	3	3	2	1	2	3	Protein of unknown function (DUF2985)
PF03271	1	1	1	1	1	1	2	EB1-like C-terminal motif
PF13468	1	1	1	1	1	1	2	Glyoxalase-like domain
PF11790	2	2	2	2	6	3	10	Glycosyl hydrolase catalytic core
PF01846	3	2	2	3	2	2	4	FF domain
PF01728	3	4	5	3	5	3	7	FtsJ-like methyltransferase
PF26335	4	5	4	8	3	1	5	Beta-lactamase-like ARB_00930-like, C-terminal domain
PF12756	4	2	2	2	3	1	2	C2H2 type zinc-finger (2 copies)
PF12927	1	1	1	1	1	1	2	Domain of unknown function (DUF3835)
PF13758	1	1	1	1	1	1	2	Prefoldin subunit
PF06516	1	2	2	1	3	0	2	Purine nucleoside permease (NUP)
PF02466	5	4	4	4	6	6	5	Tim17/Tim22/Tim23/Pmp24 family
PF06391	1	1	1	1	1	1	2	CDK-activating kinase assembly factor MAT1
PF17121	1	1	1	1	1	1	2	Zinc finger, C3HC4 type (RING finger)
PF01735	3	2	3	4	4	2	8	Lysophospholipase catalytic domain
PF07724	3	4	4	5	5	7	13	AAA domain (Cdc48 subfamily)
PF16483	5	6	7	2	5	2	6	Beta-1,3-glucanase
PF00615	5	5	5	4	7	5	8	Regulator of G protein signaling domain
PF00505	9	9	10	8	11	5	12	HMG (high mobility group) box
PF09011	5	5	6	5	7	1	8	HMG-box domain
PF00449	2	1	1	1	2	3	2	Urease alpha-subunit, N-terminal domain
PF00547	2	1	1	1	2	3	2	Urease, gamma subunit
PF00699	2	1	1	1	2	3	2	Urease beta subunit
PF01734	13	12	15	7	10	9	19	Patatin-like phospholipase
PF27826	1	1	1	1	1	0	2	Adenylate cyclase activation protein git1 third TPR-like domain
PF23181	0	0	0	1	2	0	2	INO4 bHLH domain
PF00092	5	5	5	5	7	7	8	von Willebrand factor type A domain
PF08487	1	1	1	1	2	2	2	Vault protein inter-alpha-trypsin domain
PF13519	4	5	5	5	5	6	9	von Willebrand factor type A domain
PF13768	2	2	2	3	3	3	4	von Willebrand factor type A domain
PF06472	2	3	3	2	2	2	4	ABC transporter transmembrane region 2
PF02036	1	1	1	1	1	1	2	SCP-2 sterol transfer family
PF01061	12	13	13	17	14	6	19	ABC-2 type transporter
PF13522	6	6	6	5	5	6	10	Glutamine amidotransferase domain
PF13869	1	1	1	1	2	1	2	Nucleotide hydrolase
PF00687	3	3	3	3	4	3	6	Ribosomal protein L1p/L10e family
PF09296	1	1	1	1	2	1	2	NADH pyrophosphatase-like rudimentary NUDIX domain
PF09297	1	1	1	1	2	1	2	NADH pyrophosphatase zinc ribbon domain
PF06148	1	0	0	1	1	1	2	COG2 N-terminal
PF04502	2	1	1	2	2	2	4	Saf4/Yju2 protein
PF12895	3	3	3	4	3	3	5	Anaphase-promoting complex, cyclosome, subunit 3
PF13424	6	9	18	8	3	8	6	Tetratricopeptide repeat
PF03366	3	3	3	2	3	3	5	YEATS family
PF02913	3	4	4	7	4	3	7	FAD linked oxidases, C-terminal domain
PF00545	1	4	2	3	1	0	6	ribonuclease
PF01912	1	1	1	1	1	1	2	eIF-6 family
PF19535	0	1	1	1	4	0	4	Family of unknown function (DUF6060)
PF03200	1	1	1	1	1	1	3	Glycosyl hydrolase family 63 C-terminal domain
PF16923	1	1	1	1	1	1	3	Glycosyl hydrolase family 63 N-terminal domain
PF22422	4	4	4	3	3	2	5	Mannosylglycerate hydrolase MGH1-like glycoside hydrolase domain
PF10159	1	1	1	1	2	1	2	Multiple myeloma tumor-associated
PF00190	10	10	10	7	9	3	18	Cupin

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF01050	0	0	0	0	0	0	1	Mannose-6-phosphate isomerase C-terminal
PF12341	1	1	1	1	1	1	2	Minichromosome loss protein, Mcl1, middle region
PF12894	12	15	16	14	14	13	23	Anaphase-promoting complex subunit 4 WD40 domain
PF20946	1	1	1	1	1	1	2	DNA polymerase alpha-binding protein Ctf4, C-terminal domain
PF24817	1	1	1	1	1	1	2	WDHD1 first WD40 domain
PF09649	1	1	1	1	1	1	4	Histone chaperone domain CHZ
PF00310	1	1	1	1	1	1	2	Glutamine amidotransferases class-II
PF01493	1	1	1	1	1	1	2	GXGXG motif
PF01645	1	1	1	1	1	1	2	Conserved region in glutamate synthase
PF04898	1	1	1	1	1	1	2	Glutamate synthase central domain
PF14691	1	1	1	1	1	1	2	Dihydroprymidine dehydrogenase domain II, 4Fe-4S cluster
PF18596	1	1	1	0	2	1	2	Sld7 C-terminal domain
PF17119	0	1	1	0	2	2	2	Mitochondrial protein up-regulated during meiosis
PF04321	11	8	9	10	9	5	15	RmlD substrate binding domain
PF16363	12	12	13	6	7	7	13	GDP-mannose 4,6 dehydratase
PF10178	1	1	1	0	2	0	2	Proteasome assembly chaperone 3
PF00332	3	3	3	1	3	2	5	Glycosyl hydrolases family 17
PF00797	2	3	3	2	2	1	8	N-acetyltransferase
PF20826	3	3	2	3	3	3	10	PhD finger domain
PF07719	6	4	5	6	9	7	22	Tetratricopeptide repeat
PF05620	1	1	1	1	1	0	2	SRP-independent targeting protein 2/TMEM208
PF19834	2	2	2	1	4	2	6	Family of unknown function (DUF6314)
PF06500	2	3	3	0	2	2	4	Esterase FrsA-like
PF04756	1	1	1	1	1	1	2	OST3 / OST6 family, transporter family
PF08925	1	1	1	2	2	0	2	Domain of Unknown Function (DUF1907)
PF02148	3	5	4	5	4	5	6	Zn-finger in ubiquitin-hydrolases and other protein
PF13423	11	10	13	11	12	4	20	Ubiquitin carboxyl-terminal hydrolase
PF17807	1	1	1	2	1	1	2	Variant UBP zinc finger
PF22562	2	2	2	3	2	4	4	UBA-like domain
PF00307	5	5	5	7	6	5	10	Calponin homology (CH) domain
PF02146	6	6	6	7	8	4	10	Sir2 family
PF27704	1	1	1	1	0	1	2	Guanidinoacetate N-methyltransferase
PF03062	5	5	5	5	7	5	8	MBOAT, membrane-bound O-acyltransferase family
PF13813	4	7	4	2	11	1	11	Membrane bound O-acyl transferase family
PF02567	2	2	2	1	1	1	2	Phenazine biosynthesis-like protein
PF08318	1	1	1	1	1	1	2	COG4 transport protein, middle alpha-helical bundle
PF20662	1	1	1	1	1	1	2	Conserved oligomeric Golgi complex subunit 4, C-terminal
PF20663	1	1	1	1	1	1	2	Conserved oligomeric Golgi complex subunit 4, N-terminal
PF05653	4	4	4	5	4	5	6	Magnesium transporter NIPA
PF00403	4	4	4	7	5	6	9	Heavy-metal-associated domain
PF21948	1	2	2	2	6	2	4	Lipoyl protein ligase A/B catalytic domain
PF08569	1	1	1	1	1	1	2	Mo25-like
PF21962	1	1	1	0	0	0	1	Domain of unknown function (DUF6924)
PF13757	1	1	1	1	2	2	1	Vault protein inter-alpha-trypsin domain
PF18314	1	1	1	1	2	1	2	Fatty acid synthase type I helical domain
PF18325	1	1	1	1	2	1	2	Fatty acid synthase subunit alpha Acyl carrier domain
PF01575	3	3	3	4	7	4	5	MaoC like domain
PF08354	1	1	1	1	2	0	2	Fatty acid synthase subunit beta/Fas1-like, helical
PF13452	1	1	1	1	1	1	2	FAS1-like, dehydratase domain region
PF17828	1	1	1	1	1	1	2	N-terminal domain in fatty acid synthase subunit beta
PF17951	1	1	1	1	2	1	2	Fatty acid synthase meander beta sheet domain
PF22235	1	1	1	1	2	2	2	Fatty acid synthase subunit beta, insertion domain
PF22622	3	2	2	4	6	3	5	MFE-2 hydratase 2 N-terminal domain
PF13324	1	1	1	1	1	1	2	Grap2 and cyclin-D-interacting, N-terminal
PF20936	0	0	0	0	1	0	2	Grap2 and cyclin-D-interacting, C-terminal
PF13041	3	4	4	3	6	5	6	PPR repeat family
PF01035	3	3	3	2	4	1	6	6-O-methylguanine DNA methyltransferase, DNA binding domain
PF09736	1	1	1	1	1	1	2	Pre-mRNA-splicing factor of RES complex
PF00677	1	1	1	1	1	1	2	Lumazine binding domain
PF00578	7	8	8	5	10	7	19	AhpC/TSA family
PF08534	6	7	7	5	9	7	17	Redoxin
PF00702	28	32	32	42	37	25	47	haloacid dehalogenase-like hydrolase
PF22061	1	1	1	1	1	1	2	CSN7 helical bundle subdomain
PF01221	1	1	1	1	1	1	2	Dynein light chain type 1
PF00638	3	2	2	2	2	3	4	RanBP1 domain
PF10544	2	1	1	1	2	1	4	T5orf172 domain
PF13455	2	1	1	1	1	1	3	Meiotically up-regulated gene 113
PF01648	1	2	1	4	2	1	4	4'-phosphopantetheinyl transferase superfamily
PF06417	1	1	1	2	1	1	1	ER membrane protein complex subunit 4
PF10558	1	1	1	1	1	1	2	Mitochondrial 18 KDa protein (MTP18)
PF11022	1	1	1	1	1	1	2	ATP synthase subunit K
PF27566	2	1	1	5	3	3	3	KpeA transcription factor
PF01937	2	3	3	4	1	1	4	Damage-control phosphatase ARMT1-like domain
PF01053	6	6	6	6	8	7	7	Cys/Met metabolism PLP-dependent enzyme
PF07721	1	0	1	0	3	6	1	Tetratricopeptide repeat
PF13374	5	6	15	6	8	7	4	Tetratricopeptide repeat
PF01412	5	6	6	5	5	6	10	Putative GTPase activating protein for Arf
PF16114	1	1	1	1	1	1	2	ATP citrate lyase citrate-binding
PF00575	4	4	4	4	4	5	8	S1 RNA binding domain
PF12451	1	1	1	1	2	1	2	Vacuolar protein sorting protein 11 C terminal
PF23266	1	1	1	1	2	1	2	VPS11-like, N-terminal beta-propeller
PF23341	1	1	1	1	2	1	2	PEP5/VPS11 N-terminal
PF23356	0	1	1	0	2	1	2	PEP5/VPS11 Clathrin repeat
PF21121	1	1	1	1	1	1	2	Nucleoporin Nup49 C-terminal helical region
PF05182	1	1	1	1	1	1	2	Fip1 motif
PF03227	1	1	1	1	1	1	2	Gamma interferon inducible lysosomal thiol reductase (GILT)
PF17104	1	1	1	1	1	1	2	YBL010C/LAA2
PF05064	1	1	1	1	1	1	2	Nsp1-like C-terminal region
PF10607	4	5	5	4	5	5	8	CTLH/CRA C-terminal to LisH motif domain
PF25995	1	1	1	1	1	1	2	STB6-like, N-terminal domain
PF28231	1	1	1	1	1	1	2	STB2 C-terminal domain
PF00795	11	15	14	7	22	8	18	Carbon-nitrogen hydrolase
PF00411	3	1	1	2	2	2	4	Ribosomal protein S11
PF03446	15	14	13	23	15	10	31	NAD binding domain of 6-phosphogluconate dehydrogenase
PF20463	0	0	0	1	1	1	2	Prephenate dehydrogenase, dimerization domain
PF27505	2	0	0	1	1	0	2	Tyr1-like, 6-phosphogluconate dehydrogenase C-terminal domain
PF06775	1	1	1	1	1	1	2	Putative adipose-regulatory protein (Seipin)

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF00929	5	4	4	5	6	4	7	Exonuclease
PF01088	4	4	5	4	5	5	6	Ubiquitin carboxyl-terminal hydrolase, family 1
PF24179	1	1	1	1	2	1	2	Neuropathy Target Esterase family P-loop like domain
PF03985	1	1	1	1	1	1	2	Paf1
PF03632	1	2	2	0	1	0	2	Glycosyl hydrolase family 65 central catalytic domain
PF03633	1	1	1	0	1	0	4	Glycosyl hydrolase family 65, C-terminal domain
PF03636	1	2	2	0	1	0	2	Glycosyl hydrolase family 65, N-terminal domain
PF01212	2	4	4	7	3	4	10	Beta-eliminating lyase
PF02347	1	1	1	1	1	3	2	Glycine cleavage system P-protein
PF21478	1	1	1	1	1	3	2	Glycine dehydrogenase, C-terminal domain
PF05191	2	2	2	2	2	2	6	Adenylate kinase, active site lid
PF13207	6	5	5	7	8	4	10	AAA domain
PF07766	1	1	1	1	2	2	2	LETM1-like, RBD
PF01074	1	1	1	1	2	2	2	Glycosyl hydrolases family 38 N-terminal domain
PF07748	1	1	1	1	2	2	2	Glycosyl hydrolases family 38 C-terminal domain
PF09261	1	1	1	1	2	2	2	Alpha mannosidase middle domain
PF17677	1	1	1	1	2	2	2	Glycosyl hydrolases family 38 C-terminal beta sandwich domain
PF22907	1	1	1	1	2	2	2	Alpha-mannosidase, jelly roll domain
PF24852	0	1	1	0	3	2	6	Domain of unknown function (DUF7726)
PF00346	1	1	1	1	1	0	2	Respiratory-chain NADH dehydrogenase, 49 Kd subunit
PF01000	2	2	2	2	2	2	4	RNA polymerase Rpb3/RpoA insert domain
PF01193	5	5	6	4	4	4	5	RNA polymerase Rpb3/Rpb11 dimerisation domain
PF20163	4	4	5	1	2	0	2	Family of unknown function (DUF6536)
PF01287	2	2	2	1	2	2	4	Eukaryotic elongation factor 5A hypusine, DNA-binding OB fold
PF21485	2	2	2	2	2	2	2	Translation initiation factor 5A-like, N-terminal
PF10637	1	1	1	1	1	1	2	Oxoglutarate and iron-dependent oxygenase degradation C-term
PF13640	6	5	5	6	5	4	18	2OG-Fe(II) oxygenase superfamily
PF13661	1	1	1	1	1	1	2	2OG-Fe(II) oxygenase superfamily
PF10017	1	2	2	3	1	1	3	Histidine-specific methyltransferase, SAM-dependent
PF12900	1	1	1	1	1	2	2	Pyridoxamine 5'-phosphate oxidase
PF02238	1	1	1	1	1	1	2	Cytochrome c oxidase subunit VII
PF00206	6	6	6	8	5	5	9	Lyase
PF10397	3	4	4	2	3	3	6	Adenylosuccinate lyase C-terminus
PF14087	2	2	2	5	2	2	6	Domain of unknown function (DUF4267)
PF07946	1	1	1	1	1	1	2	PAT complex subunit CCDC47
PF24990	3	2	2	3	2	3	6	ERT1/acuK family PAS domain
PF07500	2	2	2	2	3	2	4	Transcription factor S-II (TFIIS), central domain
PF07744	1	1	1	1	1	1	2	SPOC domain
PF08938	2	1	1	1	3	1	2	HBS1 N-terminus
PF00415	4	5	5	5	7	5	10	Regulator of chromosome condensation (RCC1) repeat
PF13540	5	5	5	7	8	4	9	Regulator of chromosome condensation (RCC1) repeat
PF13513	7	6	6	6	7	9	10	HEAT-like repeat
PF25780	2	2	2	2	2	2	4	IPO5-like, TPR repeats
PF00884	7	9	9	20	8	2	7	Sulfatase
PF04479	14	14	15	19	12	11	11	RTA1 like protein
PF13085	1	1	1	1	1	1	2	2Fe-2S iron-sulfur cluster binding domain
PF13183	1	1	1	1	1	1	2	4Fe-4S dicluster domain
PF13237	1	1	1	1	2	1	2	4Fe-4S dicluster domain
PF13534	1	1	1	1	1	1	2	4Fe-4S dicluster domain
PF02182	3	3	3	0	2	1	6	SAD/SRA domain
PF09597	1	1	1	1	1	1	2	Small ribosomal subunit protein mS41 SAM domain
PF16862	3	2	2	4	5	3	4	Glycosyl hydrolase family 79 C-terminal beta domain
PF10277	1	2	2	4	2	2	4	Frag1/DRAM/Sfk1/Cwh43P N-terminal domain
PF01158	1	1	1	1	2	1	2	Ribosomal protein L36e
PF06201	2	2	2	2	3	2	4	PITH domain
PF11470	1	1	1	1	1	1	2	TUG ubiquitin-like domain
PF16854	1	1	1	1	1	1	1	Vacuolar protein sorting-associated protein 53 C-terminus
PF08571	1	1	1	1	1	1	2	Yos1-like
PF03901	4	5	5	4	4	3	7	Alg9-like mannosyltransferase family
PF05327	1	1	1	1	1	0	4	RNA polymerase I specific transcription initiation factor RRN3
PF07726	1	1	1	1	2	0	1	ATPase family associated with various cellular activities (AAA)
PF17865	1	1	1	1	2	0	2	Midasin AAA lid domain
PF17867	1	1	1	1	2	0	3	Midasin AAA lid domain
PF21108	1	1	1	1	2	1	2	Midasin AAA+ ATPase lid domain
PF00542	1	1	1	1	1	1	3	Ribosomal protein L7/L12 C-terminal domain
PF16320	1	1	1	1	1	1	3	Ribosomal protein L7/L12 dimerisation domain
PF00657	14	14	12	13	21	6	20	GDSL-like Lipase/Acylhydrolase
PF13472	14	10	9	9	14	3	13	GDSL-like Lipase/Acylhydrolase family
PF00571	6	6	6	6	10	5	16	CBS domain
PF00654	2	3	3	3	6	5	8	Voltage gated chloride channel
PF12243	1	1	1	1	1	1	2	CTD kinase subunit gamma CTK3
PF12350	1	1	1	1	1	1	2	CTD kinase subunit gamma CTK3 C-terminus
PF11807	4	6	5	10	21	2	25	Mycotoxin biosynthesis protein UstYa
PF06246	1	1	1	1	1	1	2	Isy1-like splicing family
PF10350	1	1	1	1	2	0	2	THADA/TRM732, DUF2428
PF25150	1	1	1	1	2	0	2	Trm732, TPR repeats
PF25151	1	1	1	1	2	0	2	Trm732, C-terminal TPR repeats
PF26523	1	1	1	1	2	1	2	Trm72 ARM-like repeat region
PF01966	4	5	5	3	6	3	17	HD domain
PF04664	1	1	1	0	1	0	2	Opioid growth factor receptor (OGFr) conserved region
PF03583	2	2	2	4	7	0	4	Secretory lipase
PF08619	1	1	1	1	1	1	2	Alkali metal cation/H+ antiporter Nha1 C terminus
PF00684	4	4	4	4	6	4	8	DnaJ central domain
PF01556	5	5	5	5	7	5	12	DnaJ C terminal domain
PF03896	0	1	1	1	1	1	2	Translocon-associated protein (TRAP), alpha subunit
PF05205	1	1	1	1	2	1	2	COMPASS (Complex proteins associated with Set1p) component shg1
PF02894	9	8	9	15	9	8	11	Oxidoreductase family, C-terminal alpha/beta domain
PF01933	1	1	1	1	1	1	2	2-phospho-L-lactate transferase CofD
PF17056	0	1	1	0	0	0	1	Killer toxin-resistance protein 1
PF20237	10	9	13	3	5	3	25	Family of unknown function (DUF6594)
PF25053	7	9	8	2	2	0	6	Domain of unknown function (DUF7791)
PF00041	1	2	2	1	2	2	2	Fibronectin type III domain
PF04571	1	1	1	1	1	0	2	lipin, N-terminal conserved region
PF08235	1	1	1	1	1	1	2	LNS2 (Lipin/Ned1/Smp2)
PF24565	1	1	1	1	1	1	2	Nuclear elongation and deformation protein 1-like, middle domain
PF01968	1	5	5	12	8	1	9	Hydantoinase/oxoprolinase
PF05378	1	5	5	12	8	1	9	Hydantoinase/oxoprolinase N-terminal region

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF06032	0	2	2	1	1	0	1	S-Me-THD-like, N-terminal domain
PF20906	0	2	2	1	1	0	2	S-Me-THD-like, C-terminal domain
PF14605	1	0	0	0	0	0	2	Nup53/35/40-type RNA recognition motif
PF12709	1	1	1	1	1	1	2	Fungal Transforming acidic coiled-coil (TACC) proteins
PF00202	9	13	13	11	7	8	17	Aminotransferase class-III
PF09329	1	1	1	1	1	1	2	Primase zinc finger
PF22379	0	1	1	1	1	1	2	MCM10 OB-fold
PF09468	1	1	1	1	1	1	2	Ydr279p protein family (RNase H2 complex component) wHTH domain
PF17745	1	1	1	1	1	1	2	Ydr279p protein triple barrel domain
PF03133	1	1	1	2	1	1	2	Tubulin-tyrosine ligase family
PF26569	0	1	1	1	1	1	2	EIF3CL-like, C-terminal domain
PF00365	1	1	1	1	1	1	2	Phosphofructokinase
PF10156	1	1	1	1	1	1	2	Subunit 17 of Mediator complex
PF06437	1	1	1	2	1	1	2	IMP-specific 5'-nucleotidase
PF02441	1	3	3	3	3	2	4	Flavoprotein
PF17124	1	1	1	3	0	1	1	ThiJ/PfpI family-like
PF12296	2	2	2	2	15	0	4	Hydrophobic surface binding protein A
PF05057	3	1	2	5	1	4	3	Putative serine esterase (DUF676)
PF28365	1	1	1	1	1	1	2	RNA exonuclease 3 N-terminal domain
PF00568	1	1	1	1	1	1	2	WH1 domain
PF01176	2	2	2	2	2	2	4	Translation initiation factor 1A / IF-1
PF01031	4	6	8	6	2	2	5	Dynamin central region
PF03943	1	1	1	1	0	1	8	TAP C-terminal domain
PF08059	1	1	1	1	1	1	2	SEP domain
PF22566	2	2	2	1	3	2	2	UBA-like domain
PF08219	1	1	1	1	1	1	2	Outer membrane protein TOM13
PF02096	1	2	2	1	2	1	2	60Kd inner membrane protein
PF13257	1	1	1	0	1	1	2	Domain of unknown function (DUF4048)
PF04670	7	7	7	12	10	9	16	Gtr1/RagA G protein conserved region
PF09439	5	4	5	7	8	8	16	Signal recognition particle receptor beta subunit
PF04004	1	1	1	1	1	1	2	Leo1-like protein
PF03637	4	4	4	5	4	5	8	Mob1/phocein family
PF08696	1	1	1	1	1	1	2	DNA replication factor Dna2
PF03666	1	1	1	1	2	1	2	Nitrogen Permease regulator of amino acid transport activity 3
PF24064	1	1	1	1	2	1	2	GATOR1 complex protein NPRL3, C-terminal HTH
PF05768	1	1	1	1	0	0	2	Glutaredoxin-like domain (DUF836)
PF04969	4	4	4	4	4	4	8	CS domain
PF01149	1	1	1	1	1	1	2	Formamidopyrimidine-DNA glycosylase N-terminal domain
PF06831	1	1	1	1	1	1	2	Formamidopyrimidine-DNA glycosylase H2TH domain
PF00491	5	5	4	4	8	3	7	Arginase family
PF02190	3	3	3	4	4	3	5	ATP-dependent protease La (LON) substrate-binding domain
PF05362	2	2	2	3	2	2	2	Lon protease (S16) C-terminal proteolytic domain
PF22667	2	2	2	3	2	2	4	Lon protease AAA+ ATPase lid domain
PF17109	1	2	2	1	1	0	2	fungal STAND N-terminal Goodbye domain
PF04090	1	1	1	0	1	0	2	RNA polymerase I-specific transcription initiation factor Rrn11
PF08423	3	3	3	2	4	3	7	Rad51
PF04176	1	1	1	1	1	1	2	TIP41-like family
PF13902	1	1	1	1	1	1	1	R3H-associated N-terminal domain
PF25459	1	2	2	1	1	1	2	AIM3/BBC1 Cysteine proteinase-fold domain
PF13959	4	4	4	4	4	3	8	ATP-dependent rRNA helicase SPB4-like, C-terminal extension
PF02698	0	0	0	1	0	0	2	DUF218 domain
PF26803	1	1	1	0	1	1	2	FF domain
PF21953	1	2	2	1	2	3	4	NAD nucleotidase, C-terminal domain
PF01163	3	4	4	2	3	2	2	RIO domain
PF24896	0	0	0	0	0	0	2	AHK4/CRE1/WOL first receiver domain
PF13350	5	3	3	2	3	1	7	Tyrosine phosphatase family
PF01910	1	2	2	1	1	0	4	Thiamine-binding protein
PF26545	1	1	1	1	1	1	2	Mdm34, N-terminal domain
PF28355	1	1	1	1	1	1	2	MDM34 C-terminal domain
PF26146	5	4	5	3	5	2	5	PI-PLC X 1
PF26178	3	1	2	3	4	2	5	PI-PLC-like catalytic domain
PF05920	2	2	2	3	4	2	3	Homeobox KN domain
PF01513	2	2	2	2	2	3	3	ATP-NAD kinase N-terminal domain
PF20143	4	3	3	3	5	3	5	ATP-NAD kinase C-terminal domain
PF27593	1	2	2	1	5	1	6	Meroterpenoid methyltransferase N-terminal domain
PF03109	4	4	4	3	5	3	7	ABC1 atypical kinase-like domain
PF03972	5	4	3	2	4	1	9	MmgE/PrpD N-terminal domain
PF19305	5	4	3	2	4	1	8	MmgE/PrpD C-terminal domain
PF06699	1	1	1	1	1	1	2	GPI biosynthesis protein family Pig-F
PF17172	1	2	2	3	2	1	2	Glutathione S-transferase N-terminal domain
PF00633	1	1	1	0	1	0	2	Helix-hairpin-helix motif
PF04427	5	5	5	5	6	5	10	Brix domain
PF09416	1	1	1	1	1	1	2	RNA helicase (UPF2 interacting domain)
PF18141	1	1	1	1	1	1	2	RNA helicase UPF1, 1B domain
PF12689	1	1	1	1	2	3	1	Acid Phosphatase
PF00080	3	3	3	2	2	2	5	Copper/zinc superoxide dismutase (SODC)
PF00923	2	2	2	5	1	2	3	Transaldolase/Fructose-6-phosphate aldolase
PF02222	5	3	3	6	5	5	8	ATP-grasp domain
PF01936	1	0	0	0	0	0	2	NYN domain
PF12872	2	0	0	0	0	0	2	OST-HTH/LOTUS domain
PF03345	1	1	1	1	1	1	2	OST48, N-terminal domain
PF23358	1	1	1	1	1	1	2	OST48 middle domain
PF13242	10	11	12	6	7	7	17	HAD-hyrolase-like
PF13344	4	5	5	4	4	3	5	Haloacid dehalogenase-like hydrolase
PF07539	1	1	1	1	1	1	2	U3 small nucleolar RNA-associated protein 20, N-terminal
PF20416	1	1	1	1	1	1	2	U3 small nucleolar RNA-associated protein 20 domain
PF23099	1	1	1	0	1	1	2	Small subunit processome component 20 homolog, C-terminal
PF00294	6	5	5	7	7	3	7	pfkB family carbohydrate kinase
PF04227	2	1	1	1	1	1	2	Indigoidine synthase A like protein
PF04597	1	1	1	1	1	1	2	Ribophorin I
PF03388	3	3	3	2	2	4	4	Legume-like lectin family
PF01145	5	5	5	5	7	5	8	SPFH domain / Band 7 family
PF23658	1	2	2	3	3	0	2	CPAF-like PDZ domain
PF04810	3	3	3	4	3	3	6	Sec23/Sec24 zinc finger
PF04811	3	3	3	4	3	3	6	Sec23/Sec24 trunk domain
PF04253	3	3	3	4	2	3	3	Transferrin receptor-like dimerisation domain
PF00098	9	9	9	11	11	6	9	Zinc knuckle

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii* *(FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF18149	1	1	1	1	1	2	4	N-terminal helicase PWI domain
PF08650	1	1	1	1	1	1	2	DASH complex subunit Dad4
PF22528	3	3	4	3	1	2	2	Arginine methyltransferase oligomerization subdomain
PF01670	4	3	3	3	6	1	8	Glycosyl hydrolase family 12
PF00170	10	11	11	10	10	13	9	bZIP transcription factor
PF08442	1	1	1	3	1	2	2	ATP-grasp domain
PF13549	1	1	1	1	0	1	2	ATP-grasp domain
PF01715	1	1	1	1	1	0	2	IPP transferase
PF00137	4	4	4	5	6	3	7	ATP synthase subunit C
PF04130	5	5	5	5	6	4	10	Gamma tubulin complex component C-terminal
PF17681	5	5	4	5	7	4	5	Gamma tubulin complex component N-terminal
PF05645	1	1	1	1	1	0	2	RNA polymerase III subunit RPC82
PF22536	1	1	1	1	1	1	2	POLR3C, C-terminal winged-helix domain
PF00675	4	6	6	7	6	7	11	Insulinase (Peptidase family M16)
PF05193	3	4	5	6	6	6	12	Peptidase M16 inactive domain
PF04627	1	1	1	1	1	2	2	Mitochondrial ATP synthase epsilon chain
PF04112	1	1	1	1	1	1	2	Mak10 subunit, NatC N(alpha)-terminal acetyltransferase
PF25789	1	1	1	1	1	0	2	NAA35-like, TPR repeats
PF09803	1	1	1	1	1	1	2	Pet100
PF01070	12	15	16	15	14	6	15	FMN-dependent dehydrogenase
PF01974	2	2	2	2	2	2	4	tRNA intron endonuclease, catalytic C-terminal domain
PF26577	1	1	1	1	1	1	2	TSEN34-like, N-terminal domain
PF04177	1	1	1	1	1	1	2	TAP42-like family
PF00636	4	6	6	3	8	3	11	Ribonuclease III domain
PF03368	2	3	3	2	3	1	2	Dicer dimerisation domain
PF14622	4	6	6	3	7	3	9	Ribonuclease-III-like
PF24995	1	1	1	1	2	1	2	dsRNA binding domain
PF26744	1	1	1	1	2	1	2	Dicer-like protein 1, PAZ domain
PF04388	0	0	0	1	0	0	2	Hamartin protein
PF09320	2	1	1	1	1	1	2	Domain of unknown function (DUF1977)
PF18469	1	1	1	0	0	0	2	Pleckstrin homology domain
PF24537	1	1	1	1	2	3	4	Fungal C2H2 zinc finger
PF03417	1	2	2	1	1	1	4	Acyl-coenzyme A:6-aminopenicillanic acid acyl-transferase
PF08660	1	1	1	1	1	0	2	Oligosaccharide biosynthesis protein Alg14 like
PF09779	1	1	1	1	1	1	2	Ima1 N-terminal domain
PF01693	0	1	1	1	4	1	7	Ribonuclease H1 N-terminal domain
PF05970	3	2	3	2	8	1	8	PIF1-like helicase
PF21530	3	3	3	2	4	1	7	DNA helicase Pif1, 2B domain
PF00075	5	5	5	1	6	2	8	RNase H
PF08592	4	5	5	1	8	8	17	Anthrone oxygenase
PF05935	9	4	4	6	11	0	18	Arylsulfotransferase (ASST)
PF14269	12	11	10	6	18	1	23	Arylsulfotransferase (ASST)
PF00006	4	4	4	4	4	4	9	ATP synthase alpha/beta family, nucleotide-binding domain
PF02874	4	5	5	4	4	4	9	ATP synthase alpha/beta family, beta-barrel domain
PF16886	1	1	1	1	1	1	3	ATPsynthase alpha/beta subunit barrel-sandwich domain
PF22919	3	3	3	3	3	2	7	C-terminal domain of V and A type ATP synthase
PF09742	1	1	1	1	1	1	2	Dyggve-Melchior-Clausen syndrome protein
PF12722	1	1	1	1	1	1	2	High-temperature-induced dauer-formation protein
PF06094	1	2	2	4	4	2	9	Gamma-glutamyl cyclotransferase, AIG2-like
PF02902	3	3	3	4	4	4	8	Ulp1 protease family, C-terminal catalytic domain
PF01652	3	2	2	3	4	2	6	Eukaryotic initiation factor 4E
PF04116	5	6	5	10	11	3	12	Fatty acid hydroxylase
PF01066	6	4	4	5	6	4	10	CDP-alcohol phosphatidyltransferase
PF00464	1	2	2	3	2	4	4	Serine hydroxymethyltransferase
PF01676	1	1	1	1	1	1	2	Metalloenzyme superfamily
PF06415	1	1	1	1	1	1	2	BPG-independent PGAM N-terminus (iPGM_N)
PF00648	1	1	1	3	2	2	7	Calpain family cysteine protease
PF25435	1	1	1	1	1	2	4	Calpain-like protease palB-like, C-terminal domain
PF22893	3	1	4	2	1	5	10	Ubiquitin-like domain
PF06687	10	7	8	7	8	5	15	SUR7/PalI family
PF12351	3	2	2	1	1	1	4	Ca2+ regulator and membrane fusion protein Fig1
PF16487	1	1	1	1	1	1	2	Mid domain of argonaute
PF16488	1	2	1	2	1	3	4	Argonaute linker 2 domain
PF00587	3	5	5	7	5	6	10	tRNA synthetase class II core domain (G, H, P, S and T)
PF02824	2	3	3	3	3	3	6	TGS domain
PF07973	2	3	3	4	3	2	6	Threonyl and Alanyl tRNA synthetase second additional domain
PF04410	2	2	2	2	2	2	4	Gar1/Naf1 RNA binding region
PF01189	4	3	3	3	5	2	8	16S rRNA methyltransferase RsmB/F
PF02889	5	5	5	3	5	4	8	Sec63 Brl domain
PF23074	1	2	1	2	2	0	2	PH domain found in tandem in fungal proteins
PF23076	1	2	1	2	2	0	2	PH domain found in tandem in fungal proteins
PF28459	1	1	1	1	1	1	2	Protein PET54 N-terminal domain
PF09295	1	1	1	1	2	2	2	ChAPs (Chs5p-Arf1p-binding proteins)
PF27584	1	1	1	1	1	1	2	Histone transcription regulator 3 helical domain
PF27595	1	1	1	1	1	1	2	HIR3 helical bundle domain
PF27596	1	1	1	1	1	1	2	HIR3 N-terminal domain
PF11696	0	1	1	1	2	1	2	Protein of unknown function (DUF3292)
PF00781	2	2	2	2	2	2	3	Diacylglycerol kinase catalytic domain
PF00611	5	5	5	5	7	5	9	Fes/CIP4, and EFC/F-BAR homology domain
PF01636	16	13	12	25	40	9	25	Phosphotransferase enzyme family
PF23544	1	2	2	4	4	2	11	AtuA ferredoxin-like domain
PF01765	1	1	1	1	2	1	2	Ribosome recycling factor
PF01096	5	5	5	4	4	3	8	Transcription factor S-II (TFIIS)
PF11374	10	11	10	4	8	3	15	Protein of unknown function (DUF3176)
PF00656	5	7	7	2	4	2	7	Caspase domain
PF00676	3	3	3	6	4	3	8	Dehydrogenase E1 component
PF16870	1	1	1	2	1	2	1	2-oxoglutarate dehydrogenase C-terminal
PF00658	1	1	1	1	1	1	3	MLLE domain
PF07842	1	1	1	1	1	1	2	GC-rich sequence DNA-binding factor-like protein
PF12656	3	3	3	4	4	2	4	G-patch domain
PF01566	1	1	1	0	3	2	2	Natural resistance-associated macrophage protein-like
PF04146	3	3	3	1	4	3	5	YT521-B-like domain
PF12893	0	0	0	0	0	1	2	Putative lumazine-binding
PF10360	1	1	1	1	2	1	2	Protein of unknown function (DUF2433)
PF25061	1	1	1	1	2	1	1	Fungal RNA-binding domain
PF09073	1	0	0	1	1	1	2	BUD22
PF20628	1	0	0	1	1	0	2	Dyp-type peroxidase, C-terminal

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF21105	1	0	0	0	1	0	2	DyP dimeric alpha+beta barrel domain
PF01388	3	3	3	4	4	4	4	ARID/BRIGHT DNA binding domain
PF03525	1	1	1	0	0	0	2	Meiotic recombination protein Rec7 N-terminal domain
PF01380	2	2	2	2	2	2	4	SIS domain
PF04366	2	3	3	5	4	3	6	Las17-binding protein actin regulator
PF00632	7	5	5	6	10	6	10	HECT-domain (ubiquitin-transferase)
PF25579	1	1	1	1	2	2	2	E3 ubiquitin-protein ligase TRIP12-like, TPR repeats
PF08636	1	1	1	1	2	1	2	ER protein Pkr1
PF14531	4	5	5	4	4	4	4	Kinase-like
PF05347	7	5	7	9	7	6	11	Complex 1 protein (LYR family)
PF00198	3	3	3	7	4	2	6	2-oxoacid dehydrogenases acyltransferase (catalytic domain)
PF28449	0	0	0	1	1	0	2	YKP1 C-terminal domain
PF04034	1	1	1	1	1	1	2	Ribosome biogenesis protein, C-terminal
PF04068	3	2	2	2	3	2	3	Possible Fer4-like domain in RNase L inhibitor, RLI
PF00790	4	4	4	6	4	4	8	VHS domain
PF03127	3	3	3	4	5	3	4	GAT domain
PF00199	6	6	6	4	5	4	12	Catalase
PF06628	5	5	5	3	4	4	10	Catalase-related immune-responsive
PF12464	5	3	3	5	4	1	6	Maltose acetyltransferase hexapeptide capping motif
PF14602	4	3	3	4	4	2	6	Hexapeptide repeat of succinyl-transferase
PF09745	1	1	1	1	1	1	2	Nuclear speckle splicing regulatory protein 1, N-terminal
PF10257	1	1	1	1	1	1	2	Retinoic acid induced 16-like protein
PF20168	1	1	1	1	1	1	2	Sister chromatid cohesion protein PDS5 protein
PF03981	1	1	1	1	1	1	2	Ubiquinol-cytochrome C chaperone
PF01331	1	1	1	1	1	1	2	mRNA capping enzyme, catalytic domain
PF03919	1	1	1	1	1	1	2	mRNA capping enzyme, C-terminal domain
PF05764	1	1	1	1	1	1	2	YL1 nuclear protein
PF08265	2	2	2	2	3	2	4	YL1 nuclear protein C-terminal domain
PF03096	1	1	1	2	1	0	1	Ndr family
PF02297	2	2	2	2	4	2	6	Cytochrome oxidase c subunit VIb
PF02492	6	5	5	5	4	3	6	CobW/HypB/UreG, nucleotide-binding domain
PF08118	1	1	1	1	1	2	2	Yeast mitochondrial distribution and morphology (MDM) proteins
PF17903	1	1	1	2	2	1	4	Krr1 KH1 domain
PF22891	2	2	2	2	2	2	4	Eukaryotic type KH-domain (KH-domain type I)
PF01063	4	4	4	6	6	5	6	Amino-transferase class IV
PF04777	2	2	2	2	2	2	4	Erv1 / Alr family
PF00487	7	7	7	9	5	4	14	Fatty acid desaturase
PF01717	2	3	3	2	3	3	5	Cobalamin-independent synthase, Catalytic domain
PF00450	13	10	10	8	16	7	20	Serine carboxypeptidase
PF14534	1	1	1	1	6	0	3	Domain of unknown function (DUF4440)
PF00044	1	1	1	1	1	1	1	Glyceraldehyde 3-phosphate dehydrogenase, NAD binding domain
PF02800	1	1	1	1	1	1	2	Glyceraldehyde 3-phosphate dehydrogenase, C-terminal domain
PF00562	3	4	4	3	3	3	6	RNA polymerase Rpb2, domain 6
PF04560	3	4	4	3	3	3	6	RNA polymerase Rpb2, domain 7
PF04561	3	4	4	3	3	3	6	RNA polymerase Rpb2, domain 2
PF04563	3	4	4	3	3	3	6	RNA polymerase beta subunit
PF04565	3	4	4	3	3	3	6	RNA polymerase Rpb2, domain 3
PF04566	2	3	3	2	2	1	4	RNA polymerase Rpb2, domain 4
PF04567	2	3	3	2	2	2	4	RNA polymerase Rpb2, domain 5
PF00886	1	1	1	1	1	1	2	Ribosomal protein S16
PF08588	3	3	3	1	3	1	4	Domain of unknown function at the cortex 1 (Duc1)
PF01144	1	1	1	4	1	1	4	Coenzyme A transferase
PF04628	2	3	3	3	2	2	4	Sedlin, N-terminal conserved region
PF13532	6	6	6	6	9	7	12	2OG-Fe(II) oxygenase superfamily
PF10650	1	1	1	0	2	1	1	Putative zinc-finger domain
PF02736	1	1	2	1	0	1	2	Myosin N-terminal SH3-like domain
PF24319	1	1	2	1	1	0	2	Coiled-coil region of unknown function (DUF7491)
PF00102	1	1	1	1	2	1	1	Protein-tyrosine phosphatase
PF01729	1	1	1	1	1	1	2	Quinolinate phosphoribosyl transferase, C-terminal domain
PF02749	1	1	1	1	1	1	2	Quinolinate phosphoribosyl transferase, N-terminal domain
PF04419	0	2	2	2	0	0	2	Small EDRK-rich factor 1/2-like, N-terminal
PF12907	0	1	1	1	0	0	1	Zinc-binding
PF06212	1	1	1	1	1	1	2	GRIM-19 protein
PF27710	1	1	1	1	2	1	2	tRNA (guanine(9)-N(1))-methyltransferase TRM10/TRM10A
PF13622	3	3	3	8	9	2	8	Acyl-CoA thioesterase N-terminal domain
PF03097	3	2	3	2	2	3	4	BRO1-like domain
PF08799	2	2	2	2	2	2	4	pre-mRNA processing factor 4 (PRP4) like
PF25812	1	1	1	1	1	1	2	Checkpoint protein RAD24-like, helical bundle
PF05405	2	2	2	1	1	2	2	Mitochondrial ATP synthase B chain precursor (ATP-synt_B)
PF03914	3	3	3	3	3	3	6	CBF/Mak21 family
PF26702	1	1	1	1	1	1	2	Nucleolar complex protein 4-like, TPR repeats
PF19326	1	1	1	1	1	0	2	AMP deaminase
PF21138	1	1	1	2	2	1	2	Helicase SMUBP-2/HCS1, 1B domain
PF27934	1	1	1	1	1	1	1	PSI+ induction protein 2
PF00232	4	4	4	3	4	1	9	Glycosyl hydrolase family 1
PF07350	1	1	1	5	4	2	5	Gig2-like
PF13013	2	2	2	0	4	0	5	F-box-like domain
PF01172	2	2	2	2	2	4	4	Shwachman-Bodian-Diamond syndrome (SBDS) N-terminal domain
PF09423	6	4	4	2	3	2	4	PhoD-like phosphatase
PF07928	1	1	1	1	1	0	2	Vps54-like protein
PF21933	1	1	1	1	1	1	2	MCM5, C-terminal domain
PF26733	1	2	2	2	1	1	2	Adenylate-forming reductase 03009, C-terminal domain
PF13833	9	7	7	6	7	10	8	EF-hand domain pair
PF00319	4	2	3	2	2	2	2	SRF-type transcription factor (DNA-binding and dimerisation domain)
PF04912	0	0	0	1	1	1	2	Dynamitin
PF03702	2	2	2	3	3	3	5	Anhydro-N-acetylmuramic acid kinase
PF00230	11	12	11	4	14	18	21	Major intrinsic protein
PF15460	1	1	1	1	2	1	2	Something about silencing, SAS, complex subunit 4
PF01822	13	11	12	11	16	10	14	WSC domain
PF03881	2	1	1	6	4	2	3	Fructosamine kinase
PF01222	3	3	3	3	5	3	3	Ergosterol biosynthesis ERG4/ERG24 family
PF01118	3	3	3	2	2	3	6	Semialdehyde dehydrogenase, NAD binding domain
PF02774	2	1	1	1	1	1	2	Semialdehyde dehydrogenase, dimerisation domain
PF02469	3	3	3	3	11	3	11	Fasciclin domain
PF00042	1	1	1	2	1	1	2	Globin
PF11563	1	1	1	1	1	0	2	Protoglobin
PF00390	2	2	2	2	4	2	4	Malic enzyme, N-terminal domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF03949	2	2	2	2	4	2	4	Malic enzyme, NAD binding domain
PF06244	1	1	1	1	1	1	2	Coiled-coil domain-containing protein 124 /Oxs1
PF22048	1	1	1	1	1	1	2	LSO1/2-like
PF15404	1	1	1	0	2	1	2	Pleckstrin homology domain
PF15407	1	1	1	0	0	1	2	Sporulation protein family 7
PF23207	1	1	1	0	2	1	2	Prospore membrane adapter protein SPO71 PH domain
PF24541	1	1	1	1	1	1	2	PDIA6-like, C-terminal thioredoxin-like domain
PF04652	1	1	1	1	1	1	2	Vta1 like
PF18097	1	1	1	1	1	1	2	Vta1 C-terminal domain
PF03358	3	6	4	1	3	2	6	NADPH-dependent FMN reductase
PF13821	2	2	2	2	3	2	5	Domain of unknown function (DUF4187)
PF22586	1	1	1	1	1	1	2	ANCHR-like B-box zinc-binding domain
PF01644	6	6	6	9	9	7	14	Chitin synthase-like glycosyltransferase domain
PF03142	4	5	5	6	10	5	9	Chitin synthase
PF13632	16	15	15	15	22	11	20	Glycosyl transferase family group 2
PF13641	10	9	9	10	17	8	16	Glycosyltransferase like family 2
PF22997	1	1	1	1	1	1	4	Chitin synthase 4-like domain
PF03962	1	1	1	0	2	1	2	Mnd1 HTH domain
PF24137	1	0	0	0	0	0	2	Diels-Alderase N-terminal domain
PF01435	1	2	2	3	2	2	6	Peptidase family M48
PF16491	0	0	0	1	1	1	2	CAAX prenyl protease N-terminal, five membrane helices
PF00397	9	7	7	12	10	8	12	WW domain
PF19050	0	0	0	1	1	1	2	PhoD related phosphatase
PF09334	2	2	2	3	2	2	4	tRNA synthetases class I (M)
PF00313	2	2	2	0	1	0	6	Cold-shock' DNA-binding domain
PF03051	1	1	1	1	1	1	2	Peptidase C1-like family
PF16122	1	1	1	0	1	1	2	40S ribosomal protein SA C-terminus
PF00476	1	1	1	1	2	1	2	DNA polymerase family A
PF18136	1	1	1	1	2	1	2	DNA mitochondrial polymerase exonuclease domain
PF22939	3	6	9	7	2	1	6	GPI inositol-deacylase, winged helix domain
PF15370	1	1	1	0	1	1	2	NOP protein chaperone 1
PF00536	4	6	5	4	4	7	2	SAM domain (Sterile alpha motif)
PF00788	1	2	1	2	5	1	2	Ras association (RalGDS/AF-6) domain
PF07647	6	8	7	6	8	8	10	SAM domain (Sterile alpha motif)
PF25907	3	2	2	0	5	4	10	Domain of unknown function (DUF7962)
PF02585	0	0	0	1	1	1	2	GlcNAc-PI de-N-acetylase
PF09419	1	1	1	1	2	0	3	Mitochondrial PGP phosphatase
PF24841	0	0	0	1	3	0	2	Domain of unknown function (DUF7719)
PF12271	1	2	1	3	2	2	2	Chitin synthase export chaperone
PF10199	1	1	1	1	2	1	2	Alpha and gamma adaptin binding protein p34
PF11885	4	4	4	5	6	4	5	Protein of unknown function (DUF3405)
PF00163	2	2	2	2	2	2	5	Ribosomal protein S4/S9 N-terminal domain
PF01157	1	1	1	1	1	1	2	Ribosomal protein L21e
PF18388	0	0	0	1	1	1	2	Atg29 N-terminal domain
PF03447	4	3	3	3	2	2	5	Homoserine dehydrogenase, NAD binding domain
PF08666	1	1	1	1	1	0	2	SAF domain
PF21135	1	1	1	1	1	0	2	Oxidoreductase DRL, catalytic domain
PF03169	4	8	8	8	10	2	12	OPT oligopeptide transporter protein
PF02598	1	0	0	1	1	0	2	Putative RNA methyltransferase
PF16881	1	1	1	1	1	1	2	N-terminal domain of lipoyl synthase of Radical_SAM family
PF13382	0	0	0	0	0	0	2	Adenine deaminase C-terminal domain
PF11788	1	1	1	1	1	0	2	39S mitochondrial ribosomal protein L46
PF04880	1	1	1	1	1	1	4	NUDE protein, C-terminal conserved region
PF12298	1	1	1	1	1	2	4	Eukaryotic mitochondrial regulator protein
PF02809	2	1	1	4	3	1	4	Ubiquitin interaction motif
PF06722	9	9	9	7	6	8	5	Erythromycin biosynthesis protein CIII-like, C-terminal domain
PF18142	9	4	4	3	4	0	7	SMODS and SLOG-associating 2TM effector domain
PF11443	0	0	0	1	2	0	2	Domain of unknown function (DUF2828)
PF25043	0	0	0	1	2	0	2	Domain of unknown function (DUF7788)
PF11999	0	0	0	0	0	0	1	Ice-binding-like
PF00120	2	2	2	5	3	2	4	Glutamine synthetase, catalytic domain
PF01798	3	3	3	3	3	3	6	snoRNA binding domain, fibrillarin
PF08156	2	2	2	2	2	2	4	NOP5NT (NUC127) domain
PF04406	2	1	1	1	1	0	2	Type IIB DNA topoisomerase
PF21180	2	1	1	1	1	0	2	Topoisomerase 6 subunit A/Spo11, Toprim domain
PF12253	1	1	1	1	1	1	3	Chromatin assembly factor 1 subunit A dimerization domain
PF21796	1	1	1	1	1	1	3	Chromatin assembly factor 1 subunit Cac1, C-terminal domain
PF13625	1	1	1	1	1	1	2	Helicase conserved C-terminal domain
PF16203	1	1	1	1	1	1	2	ERCC3/RAD25/XPB C-terminal helicase
PF15932	1	1	1	1	1	1	2	Domain of unknown function (DUF4748)
PF22384	1	2	2	1	2	1	2	Ca3427-like PBP
PF04049	1	1	1	1	1	1	2	Anaphase promoting complex subunit 8 / Cdc23
PF00348	5	4	4	8	4	2	9	Polyprenyl synthetase
PF10373	1	1	1	2	3	1	2	Est1 DNA/RNA binding domain
PF10374	1	1	1	1	1	1	2	Telomerase activating protein Est1
PF00282	7	6	6	7	5	5	8	Pyridoxal-dependent decarboxylase conserved domain
PF05285	1	1	1	1	1	0	2	SDA1, conserved domain
PF08158	1	1	1	1	1	2	2	SDA1, HEAT repeat
PF21638	1	1	1	1	1	0	2	SDA1, C-terminal
PF03928	4	4	4	1	3	5	4	Haem degrading protein HbpS-like
PF00967	0	0	1	0	0	0	1	Barwin family
PF01269	1	1	1	1	1	2	2	Fibrillarin
PF00237	2	2	2	2	2	2	4	Ribosomal protein L22p/L17e
PF10273	1	1	1	1	1	1	2	Pre-rRNA-processing protein TSR2
PF01194	1	1	1	1	1	1	2	RNA polymerases N / 8 kDa subunit
PF03099	1	2	2	1	1	2	2	Biotin/lipoate A/B protein ligase family
PF09825	1	1	1	1	1	2	2	Biotin-protein ligase, N terminal
PF06420	1	1	1	1	2	2	2	Mitochondrial genome maintenance MGM101
PF07632	3	4	3	2	3	1	2	Cellulose-binding Sde182, nucleoside hydrolase-like domain
PF21027	3	4	3	2	3	1	2	Cellulose-binding protein Sde0182, C-terminal domain
PF03595	7	9	9	3	9	5	13	Voltage-dependent anion channel
PF00701	10	9	7	16	4	1	10	Dihydrodipicolinate synthetase family
PF01251	1	1	1	1	1	1	2	Ribosomal protein S7e
PF13664	1	1	0	1	1	2	2	Domain of unknown function (DUF4149)
PF01156	3	5	4	4	3	3	10	Inosine-uridine preferring nucleoside hydrolase
PF08508	1	1	1	1	2	1	2	Fungal domain of unknown function (DUF1746)
PF21960	3	2	2	3	3	2	4	RCF1/5-like, AAA+ ATPase lid domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF07716	5	7	7	4	7	6	5	Basic region leucine zipper
PF01756	2	2	2	1	3	3	8	Acyl-CoA oxidase
PF14749	2	2	2	1	3	3	8	Acyl-coenzyme A oxidase N-terminal
PF22924	2	3	3	1	4	3	9	Acyl-CoA oxidase, C-alpha1 domain
PF04910	1	1	1	1	1	1	2	Transcriptional repressor TCF25
PF01557	7	7	7	7	7	5	15	Fumarylacetoacetate (FAA) hydrolase C-terminal
PF00288	4	4	4	6	6	6	9	GHMP kinases N terminal domain
PF18376	1	1	1	1	1	1	2	Mevalonate 5-diphosphate decarboxylase C-terminal domain
PF22700	1	1	1	1	1	1	2	Diphosphomevalonate decarboxylase-like N-terminal domain
PF09637	1	1	1	1	2	0	2	Med18 protein
PF10937	1	1	1	1	1	1	2	Alpha-ketoglutarate dehydrogenase component 4/YMR-31
PF01042	13	10	10	16	13	3	15	Endoribonuclease L-PSP
PF05022	1	1	1	1	1	1	2	SRP40, C-terminal domain
PF02167	2	1	1	1	1	1	2	Cytochrome C1 family
PF02390	1	1	1	1	3	1	4	Putative methyltransferase
PF10236	1	1	1	1	1	1	2	Mitochondrial ribosomal death-associated protein 3
PF05176	1	1	1	1	1	1	2	ATP10 protein
PF12352	3	3	3	3	3	3	6	Snare region anchored in the vesicle membrane C-terminus
PF27017	1	1	1	1	1	1	2	GOSR1 N-terminal domain
PF00831	1	1	1	1	1	1	2	Ribosomal L29 protein
PF09774	1	1	1	1	1	0	2	Intermembrane space protein MIX23
PF04679	3	3	3	3	4	3	6	ATP dependent DNA ligase C terminal region
PF06966	6	4	4	4	5	2	7	Protein of unknown function (DUF1295)
PF14479	9	7	10	2	5	4	9	Prion-inhibition and propagation
PF08314	1	1	1	1	1	1	2	Secretory pathway protein Sec39
PF07944	1	1	1	1	3	0	1	Beta-L-arabinofuranosidase, GH127 catalytic domain
PF04182	1	0	0	1	1	1	1	B-block binding subunit of TFIIIC
PF20222	1	0	0	1	1	1	2	Family of unknown function (DUF6581)
PF08797	2	2	2	2	3	2	4	HIRAN domain
PF24975	1	1	1	1	2	1	2	Fungal Rad5 UBA-like domain
PF00174	5	7	7	3	5	4	11	Oxidoreductase molybdopterin binding domain
PF03404	5	7	7	3	5	3	10	Mo-co oxidoreductase dimerisation domain
PF07929	0	0	0	0	1	0	7	Plasmid pRiA4b ORF-3-like protein
PF06293	2	3	2	0	3	0	3	Lipopolysaccharide kinase (Kdo/WaaP) family
PF05047	3	3	3	3	4	6	5	Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain
PF12220	1	1	1	1	1	1	2	U1 small nuclear ribonucleoprotein of 70kDa MW N terminal
PF16177	4	4	4	5	4	4	9	Acetyl-coenzyme A synthetase N-terminus
PF00962	4	7	7	4	6	4	5	Adenosine deaminase
PF13329	1	1	1	1	1	1	2	Autophagy-related protein 2
PF03306	3	3	3	0	3	1	4	Alpha-acetolactate decarboxylase
PF25585	1	1	1	1	1	2	2	DUS3L CCCH zinc finger domain
PF17875	1	1	1	1	0	1	2	RPA43 OB domain in RNA Pol I
PF00185	2	2	2	2	2	2	4	Aspartate/ornithine carbamoyltransferase, Asp/Orn binding domain
PF02729	2	2	2	2	2	2	4	Aspartate/ornithine carbamoyltransferase, carbamoyl-P binding domain
PF06011	5	5	5	8	4	8	4	Transient receptor potential (TRP) ion channel
PF14558	5	6	6	7	6	8	5	ML-like domain
PF03983	1	1	1	1	1	2	2	SLA1 homology domain 1, SHD1
PF24081	1	1	1	1	1	1	2	SLA1-like, PH domain-like
PF01253	2	2	3	3	3	4	4	Translation initiation factor SUI1
PF21023	1	1	1	1	1	2	2	DENR, N-terminal
PF22241	2	2	2	2	2	2	5	PSMD12/CSN4, N-terminal
PF02270	1	1	1	1	1	1	2	TFIIF, beta subunit HTH domain
PF17683	1	1	1	1	1	1	2	TFIIF, beta subunit N-terminus
PF14388	0	0	0	1	0	0	3	Domain of unknown function (DUF4419)
PF06726	2	1	1	1	1	1	2	Bladder cancer-related protein BC10
PF01433	3	4	4	3	3	3	6	Peptidase family M1 domain
PF11838	2	2	2	1	2	2	2	ERAP1-like C-terminal domain
PF17900	3	4	4	3	3	3	6	Peptidase M1 N-terminal domain
PF01218	1	1	1	1	1	0	2	Coproporphyrinogen III oxidase
PF10443	1	1	1	1	1	1	2	RNA12 protein
PF08312	1	2	2	1	1	1	2	cwf21 domain
PF07065	1	2	2	1	1	2	2	D123
PF06723	5	5	5	5	6	6	12	MreB/Mbl protein
PF03443	11	10	10	23	2	1	4	Auxiliary Activity family 9 (formerly GH61)
PF01674	0	1	1	1	1	0	1	Lipase (class 2)
PF24894	1	1	1	1	1	0	2	GlmU-like, C-terminal hexapeptide
PF25084	2	1	1	3	3	1	4	EIF2B subunit epsilon LbH domain
PF03987	1	1	1	2	3	1	4	Autophagocytosis associated protein, active-site domain
PF02627	3	3	3	3	6	2	13	Carboxymuconolactone decarboxylase family
PF08790	1	1	1	2	1	1	2	LYAR-type C2HC zinc finger
PF08566	1	2	2	1	1	1	2	Mitochondrial import protein Pam17
PF27894	2	2	2	1	3	1	4	YJR115W helical domain
PF02330	1	1	1	1	1	1	4	Mitochondrial glycoprotein
PF08640	1	1	1	1	1	0	2	U3 small nucleolar RNA-associated protein 6
PF23021	1	1	1	2	1	1	2	PGAP2IP, second transmembrane domain
PF23022	1	1	1	2	1	1	2	PGAP2IP, first transmembrane domain
PF23226	1	1	1	2	1	1	2	PGAP2IP, C-terminal nuclease-like domain
PF12698	4	5	5	4	6	2	10	ABC-2 family transporter protein
PF25499	1	1	1	1	1	0	2	F-box protein pof12 beta-propeller
PF04248	2	2	2	2	2	1	3	Domain of unknown function (DUF427)
PF02538	1	3	3	11	7	1	9	Hydantoinase B/oxoprolinase
PF05089	0	0	0	0	2	0	2	Alpha-N-acetylglucosaminidase (NAGLU) tim-barrel domain
PF12971	0	0	0	0	2	0	2	Alpha-N-acetylglucosaminidase (NAGLU) N-terminal domain
PF12972	0	0	0	0	2	0	2	Alpha-N-acetylglucosaminidase (NAGLU) C-terminal domain
PF00344	1	1	1	1	1	1	2	SecY
PF10559	1	1	1	1	1	1	2	Plug domain of Sec61p
PF04950	2	2	2	2	2	2	4	40S ribosome biogenesis protein Tsr1 and BMS1 C-terminal
PF08142	2	2	2	2	2	2	4	AARP2CN (NUC121) domain
PF22298	1	1	1	1	1	0	2	Tsr1, G-like domain
PF01238	1	1	1	2	1	2	4	Phosphomannose isomerase type I C-terminal
PF20511	2	2	2	2	2	2	4	Phosphomannose isomerase type I, catalytic domain
PF01591	2	2	2	2	2	3	6	6-phosphofructo-2-kinase
PF13907	2	1	2	2	1	1	4	Chromodomain-helicase-DNA-binding protein 1-like, C-terminal
PF22788	1	1	1	1	1	0	2	COP9 signalosome complex subunit 3, N-terminal helical repeats
PF08662	2	4	3	4	3	3	4	Eukaryotic translation initiation factor eIF2A
PF25175	1	1	1	2	1	1	2	WDR5 beta-propeller domain
PF08171	1	1	1	1	1	2	2	Mad3/BUB1 homology region 2

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF08311	1	1	1	1	1	1	2	Mad3/BUB1 homology region 1
PF03398	1	1	1	1	1	1	2	Regulator of Vps4 activity in the MVB pathway
PF18271	2	2	2	1	3	0	2	Glycoside hydrolase 131 catalytic N-terminal domain
PF06733	2	2	2	2	2	2	4	DEAD_2
PF06777	1	1	1	1	1	1	2	Helical and beta-bridge domain
PF13307	2	2	2	2	2	2	4	Helicase C-terminal domain
PF22958	1	1	1	1	1	0	2	E3 ubiquitin-protein ligase listerin, N-terminal domain
PF16655	4	3	3	1	1	1	2	PhoD-like phosphatase, N-terminal domain
PF09415	1	1	1	1	1	1	4	CENP-S associating Centromere protein X
PF05859	0	0	1	1	1	1	2	Mis12 protein
PF00215	0	1	1	1	1	1	2	Orotidine 5'-phosphate decarboxylase / HUMPS family
PF03239	1	1	1	1	1	1	2	Iron permease FTR1 family
PF15630	0	0	0	2	1	1	2	CENP-S protein
PF08427	1	1	1	1	2	1	4	Armadillo-like helical domain-containing protein 3, C-terminal
PF05008	1	1	1	1	1	1	2	Vesicle transport v-SNARE protein N-terminus
PF00213	0	1	1	1	1	1	2	ATP synthase delta (OSCP) subunit
PF06068	1	1	2	2	2	2	4	TIP49 P-loop domain
PF17856	1	1	2	2	2	2	4	TIP49 AAA-lid domain
PF01521	3	3	3	2	3	1	4	Iron-sulphur cluster biosynthesis
PF10302	1	1	1	1	2	1	2	DSC E3 ubiquitin ligase complex subunit 3, ubiquitin-like domain
PF13373	1	1	1	1	1	1	2	DSC E3 ubiquitin ligase complex subunit 3, C-terminal domain
PF07876	8	9	9	7	6	0	4	Stress responsive A/B Barrel Domain
PF09347	3	4	3	1	5	2	5	Domain of unknown function (DUF1989)
PF00169	15	16	16	14	17	15	24	PH domain
PF26013	2	3	3	3	2	2	4	Domain of unknown function (DUF8004)
PF01039	4	4	4	3	4	3	3	Carboxyl transferase domain
PF00780	2	2	2	3	3	3	5	CNH domain
PF15405	2	2	2	2	2	2	4	Pleckstrin homology domain
PF23582	1	1	1	1	1	1	2	RGF3 winged helix domain
PF08324	2	2	2	2	2	2	4	PUL domain
PF09070	1	1	1	1	1	1	2	PFU (PLAA family ubiquitin binding)
PF08615	1	1	1	1	1	1	2	Ribonuclease H2 non-catalytic subunit (Ylr154p-like)
PF00399	1	1	1	1	7	1	3	Yeast PIR protein repeat
PF04908	0	0	0	0	1	0	2	SH3-binding, glutamic acid-rich protein
PF01956	1	1	1	1	2	1	2	Integral membrane protein EMC3/TMCO1-like
PF06703	1	1	1	1	1	1	2	Microsomal signal peptidase 25 kDa subunit (SPC25)
PF11160	2	2	2	1	3	4	6	Hypervirulence associated proteins TUDOR domain
PF08271	0	0	0	1	2	2	2	TFIIB zinc-binding
PF10775	1	0	0	1	2	2	2	ATP synthase complex subunit h
PF18086	1	1	1	1	2	1	2	Diphosphoinositol pentakisphosphate kinase 2 N-terminal domain
PF04192	1	1	1	1	1	1	2	Utp21 specific WD40 associated putative domain
PF25168	1	1	1	1	1	1	2	WDR36/Utp21 second beta-propeller domain
PF25171	1	1	1	1	1	1	2	WDR36/Utp21 first beta-propeller
PF05282	1	1	1	1	1	1	2	AAR2 C-terminal repeat region
PF20981	2	1	1	1	1	1	2	AAR2 N-terminal domain
PF10501	1	1	1	1	1	1	2	Ribosomal subunit 39S
PF09463	1	1	1	1	1	1	3	Opy2 protein
PF01168	2	2	2	4	2	1	3	Alanine racemase, N-terminal domain
PF08509	1	1	1	1	2	1	1	Adenylate cyclase G-alpha binding domain
PF08172	1	1	1	1	1	1	2	CASP C terminal
PF25398	1	1	1	1	1	1	2	CUX1-like, N-terminal tRNA-binding arm
PF11937	3	2	2	2	2	2	4	Protein of unknown function (DUF3455)
PF23024	1	1	1	1	1	1	2	Disco-interacting protein 2-like, AMP domain
PF24919	1	1	1	1	1	1	2	Meiotically up-regulated gene 62 protein-like domain
PF08826	0	0	0	0	0	0	2	DMPK coiled coil domain like
PF10780	1	1	1	1	1	1	2	39S ribosomal protein L53/MRP-L53
PF14474	1	1	1	1	1	1	2	RTC4-like domain
PF02787	2	2	2	2	2	2	4	Carbamoyl-phosphate synthetase large chain, oligomerisation domain
PF25596	2	2	2	2	3	3	4	Carbamoyl phosphate synthase preATP-grasp domain
PF04119	2	1	2	0	2	2	3	Heat shock protein 9/12
PF10415	1	1	1	3	1	1	2	Fumarase C C-terminus
PF00957	5	4	4	4	6	4	8	Synaptobrevin
PF02900	3	3	3	1	4	2	4	Catalytic LigB subunit of aromatic ring-opening dioxygenase
PF02230	3	5	5	4	5	5	9	Phospholipase/Carboxylesterase
PF00128	14	20	20	5	12	6	8	Alpha amylase, catalytic domain
PF04000	3	3	3	3	4	3	6	Sas10/Utp3/C1D family
PF09368	1	1	1	1	1	1	2	Sas10 C-terminal domain
PF17648	0	1	1	1	2	1	3	Luciferase domain
PF26021	1	1	1	1	1	0	2	C144.05-like, ferritin-like domain
PF00982	2	3	3	4	4	3	5	Glycosyltransferase family 20
PF02358	1	1	1	3	2	2	4	Trehalose-phosphatase
PF08544	2	3	3	4	4	6	4	GHMP kinases C terminal
PF24901	1	1	1	1	1	1	2	DNA replication licensing factor MCM7, winged helix
PF00244	2	2	2	2	2	1	2	14-3-3 protein
PF08389	3	3	3	4	4	4	5	Exportin 1-like protein
PF24138	1	1	1	1	1	1	2	Transportin-3/Importin-13 second TPR domain
PF24139	1	1	1	1	1	1	2	Transportin-3/Importin-13 fourth TPR domain
PF24140	2	2	2	2	3	1	3	Transportin-3/Importin-13 third TPR domain
PF01812	1	2	1	2	1	0	2	5-formyltetrahydrofolate cyclo-ligase family
PF10681	1	1	1	0	1	0	2	Chaperone for protein-folding within the ER, fungal
PF20411	1	2	2	0	1	2	1	Domain of unknown function (DUF6697)
PF00696	3	3	3	3	3	3	6	Amino acid kinase family
PF01472	3	3	3	2	5	2	6	PUA domain
PF03473	6	6	6	6	8	4	10	MOSC domain
PF03476	6	4	5	5	7	4	10	MOSC N-terminal beta barrel domain
PF01488	6	2	3	2	3	2	6	Shikimate / quinate 5-dehydrogenase
PF14833	4	5	5	14	5	4	17	NAD-binding of NADP-dependent 3-hydroxyisobutyrate dehydrogenase
PF04129	1	1	1	2	1	1	2	Vps52/Sac2 family, coiled-coil
PF20655	1	1	1	2	1	1	2	Vps52, C-terminal
PF00689	10	12	12	15	7	6	7	Cation transporting ATPase, C-terminus
PF12325	1	1	1	1	1	1	2	TATA element modulatory factor 1 TATA binding
PF12329	1	1	1	1	1	1	2	TATA element modulatory factor 1 DNA binding
PF07200	1	1	1	1	1	0	2	Modifier of rudimentary (Mod(r)) protein
PF01633	4	3	3	2	3	2	4	Choline/ethanolamine kinase
PF13086	10	6	6	7	12	5	11	AAA domain
PF20173	1	1	1	1	1	2	2	RZ type zinc finger domain
PF07927	0	0	0	0	0	0	5	HicA toxin of bacterial toxin-antitoxin,

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF00339	6	5	6	3	4	2	4	Arrestin (or S-antigen), N-terminal domain
PF02383	3	3	3	4	6	4	7	SacI homology domain
PF05786	1	1	1	1	1	1	2	Condensin complex subunit 2
PF00370	5	5	5	3	5	3	9	FGGY family of carbohydrate kinases, N-terminal domain
PF02782	5	5	5	3	5	4	9	FGGY family of carbohydrate kinases, C-terminal domain
PF21137	2	2	2	1	1	1	2	Protein arginine N-methyltransferase 3, C2H2 zinc finger domain
PF05183	3	3	3	4	4	2	5	RNA dependent RNA polymerase
PF01569	7	6	6	7	9	7	9	PAP2 superfamily
PF04874	1	1	1	1	1	1	2	Mak16 protein C-terminal region
PF04061	1	2	2	1	1	2	2	ORMDL family
PF13419	9	10	11	11	10	6	18	Haloacid dehalogenase-like hydrolase
PF16983	1	1	1	1	1	1	2	Molybdate transporter of MFS superfamily
PF09444	1	1	2	1	1	1	2	MRC1-like domain
PF08587	1	1	1	1	1	1	2	Ubiquitin associated domain (UBA)
PF01284	6	7	7	6	8	6	6	Membrane-associating domain
PF04564	2	3	3	2	3	3	6	U-box domain
PF01027	2	2	2	2	2	2	4	Inhibitor of apoptosis-promoting Bax1
PF04525	5	6	6	1	4	0	8	LURP-one-related
PF04939	1	0	0	1	2	1	2	Ribosome biogenesis regulatory protein (RRS1)
PF04166	1	1	1	1	0	0	3	Pyridoxal phosphate biosynthetic protein PdxA
PF06398	2	2	2	2	2	2	4	Integral peroxisomal membrane peroxin
PF13185	2	2	2	3	2	1	6	GAF domain
PF09420	1	1	1	1	1	0	2	Ribosome biogenesis protein Nop16
PF08784	1	1	1	1	1	1	5	Replication protein A C terminal
PF03625	0	0	0	0	0	0	1	Domain of unknown function DUF302
PF13302	7	10	10	7	14	4	17	Acetyltransferase (GNAT) domain
PF13420	1	1	1	0	0	0	4	Acetyltransferase (GNAT) domain
PF18444	1	1	1	0	0	1	2	RNA recognition motif
PF22602	1	1	1	1	1	1	2	Nuclear RNA export factor, NTF2 domain
PF24048	1	1	1	1	1	1	2	NXF1/2/3/5 leucine-rich repeat domain
PF25540	3	3	3	2	3	1	6	Domain of unknown function (DUF7923)
PF25542	2	2	2	1	2	1	4	CCCH zinc finger domain
PF25543	3	3	3	2	3	1	6	Tandem CCCH zinc finger domains
PF04938	1	1	1	1	2	2	2	Survival motor neuron (SMN) interacting protein 1 (SIP1)
PF00191	1	1	1	1	2	1	2	Annexin
PF10197	1	2	2	2	4	1	4	N-terminal domain of CBF1 interacting co-repressor CIR
PF12542	1	1	1	1	2	1	2	Pre-mRNA splicing factor
PF02012	0	0	0	0	0	0	2	BNR/Asp-box repeat
PF13088	1	1	1	0	3	0	1	BNR repeat-like domain
PF23155	4	3	3	4	4	3	7	Domain of unknown function (DUF7053)
PF18101	0	0	0	1	1	1	2	Pan3 C-terminal knob domain
PF10336	2	1	1	1	2	1	1	Protein of unknown function (DUF2420)
PF10275	2	1	1	0	2	2	1	Peptidase C65 Otubain
PF01667	1	1	1	1	2	1	2	Ribosomal protein S27
PF11719	1	1	1	1	1	1	3	DNA replication and checkpoint protein
PF08883	1	1	1	1	0	1	2	Dopa 4,5-dioxygenase family
PF02450	1	1	1	1	1	1	2	Lecithin:cholesterol acyltransferase
PF05388	1	1	1	2	1	1	2	Carboxypeptidase Y pro-peptide
PF01142	1	1	1	1	1	1	2	tRNA pseudouridine synthase D (TruD)
PF04030	2	2	2	2	1	1	3	D-arabinono-1,4-lactone oxidase
PF03297	1	1	1	1	1	1	2	S25 ribosomal protein
PF04719	1	1	1	1	1	1	2	hTAFII28-like protein conserved region
PF00573	2	2	2	2	2	2	4	Ribosomal protein L4/L1 family
PF14374	1	1	1	1	1	1	2	60S ribosomal protein L4 C-terminal domain
PF07969	3	4	5	2	0	0	4	Amidohydrolase family
PF11915	7	3	3	3	2	4	4	Protein of unknown function (DUF3433)
PF13249	1	1	1	2	1	1	2	Squalene-hopene cyclase N-terminal domain
PF03648	1	1	1	2	1	0	2	Glycosyl hydrolase family 67 N-terminus
PF07477	2	1	1	2	1	0	2	Glycosyl hydrolase family 67 C-terminus
PF07488	2	1	1	2	1	0	2	Glycosyl hydrolase family 67 middle domain
PF07080	1	1	1	1	1	1	2	Protein of unknown function (DUF1348)
PF12680	4	3	3	5	5	2	9	SnoaL-like domain
PF12333	1	1	1	1	1	1	2	Rix1 complex component involved in 60S ribosome maturation
PF08045	1	1	1	1	1	1	2	Cell division control protein 14, SIN component
PF09802	1	1	1	1	1	1	2	Preprotein translocase subunit Sec66
PF05020	1	1	1	1	1	0	2	NPL4 family, putative zinc binding region
PF05021	1	1	1	1	1	1	2	NPL4 family
PF08920	1	1	1	1	1	1	2	Splicing factor 3B subunit 1
PF22646	2	2	2	2	2	2	4	PPP2R1A-like HEAT repeat
PF04145	8	5	4	7	3	3	10	Ctr copper transporter family
PF07034	1	1	1	1	1	0	2	Origin recognition complex (ORC) subunit 3 N-terminus
PF18137	1	1	1	1	1	0	2	Origin recognition complex winged helix C-terminal
PF00659	0	0	0	0	1	0	2	POLO box duplicated region
PF16499	2	5	5	1	2	1	9	Alpha galactosidase A
PF17801	3	8	8	1	2	2	9	Alpha galactosidase C-terminal beta sandwich domain
PF07544	1	1	1	1	2	1	2	RNA polymerase II transcription mediator complex subunit 9
PF08585	1	1	1	1	1	1	2	RMI1, N-terminal OB-fold domain
PF21000	1	1	1	1	1	1	2	RMI1, N-terminal helical domain
PF01161	4	3	3	2	8	3	7	Phosphatidylethanolamine-binding protein
PF06912	9	8	7	2	8	1	7	Protein of unknown function (DUF1275)
PF17120	2	1	1	1	0	0	2	RING/Ubox like zinc-binding domain
PF02732	1	1	1	3	1	1	2	ERCC4 domain
PF07960	1	1	1	1	1	2	2	CBP4
PF01894	1	1	1	2	1	1	2	UPF0047 protein YjbQ-like
PF10276	1	1	1	1	1	1	2	Zinc-finger domain
PF16187	1	1	1	1	1	1	2	Middle or third domain of peptidase_M16
PF22456	1	1	1	1	1	1	2	PQQ synthase PqqF-like, C-terminal lobe domain 4
PF02678	2	2	2	3	2	2	5	Pirin
PF17954	1	1	1	0	1	1	3	Quercetinase C-terminal cupin domain
PF23276	1	1	1	2	1	3	2	Pentatricopeptide repeat-containing proteins
PF16200	1	1	1	1	1	1	2	C-terminal region of band_7
PF04855	3	2	2	2	2	4	4	SNF5 / SMARCB1 / INI1
PF03223	1	1	1	1	1	1	2	V-ATPase subunit C
PF01571	3	2	2	2	2	2	2	GCVT N-terminal domain
PF08669	3	2	2	2	2	2	2	Glycine cleavage T-protein C-terminal barrel domain
PF00534	5	9	8	4	9	7	11	Glycosyl transferases group 1
PF08288	1	1	1	1	2	1	2	PIGA (GPI anchor biosynthesis)

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF13439	3	4	3	3	4	2	3	Glycosyltransferase Family 4
PF13579	1	1	1	3	3	2	2	Glycosyl transferase 4-like domain
PF13692	6	10	9	6	7	7	12	Glycosyl transferases group 1
PF20706	0	0	0	0	0	2	2	Family 4 Glycosyltransferase in conflict systems
PF17100	0	0	0	5	0	1	2	N-terminal domain of NWD NACHT-NTPase
PF00664	17	18	18	27	20	18	27	ABC transporter transmembrane region
PF01987	2	2	2	3	5	1	6	Mitochondrial biogenesis AIM24
PF00398	1	1	1	1	1	1	2	Ribosomal RNA adenine dimethylase
PF02269	2	2	2	3	4	3	4	Transcription initiation factor IID, 18kD subunit
PF00590	2	2	2	2	2	2	2	Tetrapyrrole (Corrin/Porphyrin) Methylases
PF13515	5	5	5	4	3	2	6	Fusaric acid resistance protein-like
PF02852	4	4	4	3	3	3	4	Pyridine nucleotide-disulphide oxidoreductase, dimerisation domain
PF20917	1	1	1	1	1	1	2	Asparaginal-tRNA synthetase, N-terminal domain
PF08647	2	2	1	2	1	1	4	BRE1 E3 ubiquitin ligase
PF26095	2	2	1	2	1	1	4	Bre1, coiled-coil containing domain
PF15963	1	1	1	1	1	1	2	Myb DNA-binding like
PF05460	1	1	1	1	1	1	2	Origin recognition complex subunit 6 (ORC6)
PF00447	5	4	4	3	4	4	6	HSF-type DNA-binding
PF12848	4	3	3	3	4	2	3	ABC transporter
PF02421	2	2	2	2	2	1	4	Ferrous iron transport protein B
PF16897	2	2	2	2	2	2	4	C-terminal region of MMR_HSR1 domain
PF00817	5	4	4	4	5	4	8	impB/mucB/samB family
PF11799	3	4	4	4	3	4	6	impB/mucB/samB family C-terminal domain
PF18439	1	1	1	1	1	1	2	Ubiquitin-Binding Zinc Finger
PF21704	1	1	1	1	1	1	2	DNApol eta/Rev1, HhH motif
PF04108	2	2	2	3	2	1	4	Autophagy protein ATG17-like domain
PF01554	5	4	6	3	4	2	6	MatE
PF00141	9	5	5	3	6	15	5	Peroxidase
PF28221	1	1	1	1	2	1	2	Verrucosidin biosynthesis cluster protein U3 C-terminal domain
PF08689	1	1	1	2	0	1	2	Mediator complex subunit Med5
PF00317	1	1	1	1	1	1	2	Ribonucleotide reductase, all-alpha domain
PF02867	1	1	1	1	1	1	2	Ribonucleotide reductase, barrel domain
PF03477	1	1	1	1	1	1	2	ATP cone domain
PF01264	1	1	1	1	1	1	2	Chorismate synthase
PF00490	1	1	1	1	1	1	2	Delta-aminolevulinic acid dehydratase
PF25534	7	6	7	1	8	1	20	Domain of unknown function (DUF7918)
PF08559	1	1	1	1	2	2	2	Cut8, nuclear proteasome tether protein
PF14441	0	1	1	5	0	0	3	OTT_1508-like deaminase
PF06870	1	1	1	1	1	1	2	A49-like RNA polymerase I associated factor
PF08698	1	1	1	1	1	1	2	Fcf2 pre-rRNA processing
PF01048	2	3	6	6	3	7	4	Phosphorylase superfamily
PF00338	2	2	2	2	2	2	3	Ribosomal protein S10p/S20e
PF07286	0	1	1	3	2	1	2	D-glutamate cyclase
PF02727	6	6	7	5	3	3	4	Copper amine oxidase, N2 domain
PF00815	0	1	1	2	1	1	2	Histidinol dehydrogenase
PF27434	1	1	1	1	1	1	2	3-isopropylmalate dehydratase small subunit C-terminal domain
PF11709	1	1	1	1	1	1	2	Mitochondrial ribosomal protein subunit
PF01828	0	1	1	0	3	0	2	Peptidase A4 family
PF25809	1	1	1	0	2	1	2	STEEP1 domain
PF08153	1	1	1	1	1	1	1	NGP1NT (NUC091) domain
PF26163	1	1	1	1	1	1	1	Small ribosomal subunit protein mS26
PF10394	1	1	1	1	1	1	2	Histone acetyl transferase HAT1 N-terminus
PF21184	0	1	1	0	0	1	2	Fungal HAT1, C-terminal
PF09325	2	2	2	2	3	3	9	Vps5 C terminal like
PF00679	6	6	6	6	8	7	12	Elongation factor G C-terminus
PF03144	10	9	9	9	11	8	18	Elongation factor Tu domain 2
PF14492	4	4	4	6	6	5	7	Elongation Factor G, domain III
PF09174	1	1	1	1	2	1	2	Maf1 regulator
PF01217	6	7	7	7	8	5	8	Clathrin adaptor complex small chain
PF12830	1	1	1	1	1	1	2	Sister chromatid cohesion C-terminus
PF01262	2	1	1	1	1	0	2	Alanine dehydrogenase/PNT, C-terminal domain
PF02233	2	1	1	1	1	0	2	NAD(P) transhydrogenase beta subunit
PF05222	3	1	1	2	2	1	4	Alanine dehydrogenase/PNT, N-terminal domain
PF12769	2	1	1	1	1	0	2	4TM region of pyridine nucleotide transhydrogenase, mitoch
PF06026	1	1	1	1	1	1	2	Ribose 5-phosphate isomerase A (phosphoriboisomerase A)
PF04383	3	5	5	3	5	4	4	KilA-N domain
PF02115	1	1	1	1	1	0	2	RHO protein GDP dissociation inhibitor
PF21032	0	0	0	0	1	0	1	PROPPIN
PF04072	1	1	1	1	3	2	4	Leucine carboxyl methyltransferase
PF08007	0	0	0	0	2	1	2	JmjC domain
PF13418	0	0	0	1	2	1	2	tRNA wybutosine-synthesizing protein 4, beta-propeller
PF13621	5	5	5	5	6	6	11	Cupin-like domain
PF00782	8	10	10	6	11	5	15	Dual specificity phosphatase, catalytic domain
PF05208	1	1	1	1	2	1	2	ALG3 protein
PF00520	3	3	2	5	5	4	5	Ion transport protein
PF23317	3	4	4	7	5	4	5	Calcium channel YVC1-like, C-terminal
PF13774	4	3	3	3	5	3	6	Regulated-SNARE-like domain
PF09180	1	1	1	1	1	1	2	Prolyl-tRNA synthetase, C-terminal
PF00320	8	8	8	9	6	8	10	GATA zinc finger
PF14260	2	2	2	2	2	2	3	C4-type zinc-finger of DNA polymerase delta
PF00888	5	6	6	4	3	3	6	Cullin alpha solenoid domain
PF10557	5	6	6	4	3	4	6	Cullin protein neddylation domain
PF26557	6	7	7	5	4	5	7	Cullin alpha+beta domain
PF07780	1	1	1	1	1	1	2	Spb1 C-terminal domain
PF11861	1	1	1	1	1	1	2	Ribosomal RNA methyltransferase Spb1, DUF3381
PF07971	6	5	5	2	9	2	8	Glycosyl hydrolase family 92 catalytic domain
PF17678	6	4	4	2	8	3	10	Glycosyl hydrolase family 92 N-terminal domain
PF03676	1	1	1	1	2	0	2	Phagosome assembly factor 1
PF12861	3	2	2	6	3	2	6	Anaphase-promoting complex subunit 11 RING-H2 finger
PF01184	7	7	7	7	13	4	18	GPR1/FUN34/yaaH family
PF02582	3	4	4	3	4	2	6	RMND1/Sif2-Sif3/Mrx10, DUF155
PF23556	1	1	1	1	1	1	2	Vps41 TPR-like region
PF04402	0	0	0	0	2	0	4	Protein of unknown function (DUF541)
PF04209	1	1	1	2	3	1	3	Homogentisate 1,2-dioxygenase C-terminal
PF09696	1	1	1	1	2	0	2	Ctf8
PF04191	5	3	3	4	3	4	6	Phospholipid methyltransferase
PF08567	1	1	1	1	1	1	3	TFIIH p62 subunit, N-terminal domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF10198	1	2	2	1	1	1	2	Histone acetyltransferases subunit 3
PF24853	1	1	1	1	1	1	2	Domain of unknown function (DUF7727)
PF13298	1	1	1	1	2	2	2	DNA Ligase D 3'-phosphoesterase domain
PF00406	3	2	2	2	5	2	7	Adenylate kinase
PF13353	0	1	1	0	0	0	1	4Fe-4S single cluster domain
PF25522	2	1	1	2	1	1	1	Mitochondrial protein cyt-4, OB-fold domain
PF08493	0	2	1	1	2	0	1	Aflatoxin regulatory protein
PF26785	1	1	1	0	1	1	9	Domain of unknown function (DUF8257)
PF01595	2	2	2	1	2	1	2	Cyclin M transmembrane N-terminal domain
PF08164	1	1	1	1	1	2	2	Apoptosis-antagonizing transcription factor, C-terminal
PF13339	1	1	1	1	1	2	2	Apoptosis antagonizing transcription factor
PF03909	2	2	2	2	2	2	5	BSD domain
PF04189	1	1	1	1	1	2	2	Gcd10p family
PF08634	1	1	1	1	1	1	2	Mitochondrial protein Pet127
PF00709	1	1	1	2	1	1	2	Adenylosuccinate synthetase
PF10513	3	3	3	2	2	2	5	Enhancer of polycomb-like
PF00579	3	3	3	5	4	5	6	tRNA synthetases class I (W and Y)
PF23489	1	2	1	1	1	1	2	V-type proton ATPase subunit f-like
PF12456	1	1	1	1	2	1	2	Inositol phosphatase
PF08424	0	0	0	1	1	1	2	NRDE-2, necessary for RNA interference
PF08146	1	1	1	1	1	1	2	BP28CT (NUC211) domain
PF12397	1	1	1	1	1	1	2	U3 small nucleolar RNA-associated protein 10
PF23243	0	1	1	1	0	1	1	HEATR1-like, HEAT repeats
PF24055	1	2	2	2	1	1	2	DNA polymerase delta catalytic subunit-like, N-terminal domain
PF24065	1	1	1	1	1	1	2	DNA polymerase zeta catalytic subunit, N-terminal
PF00840	2	2	2	2	3	0	2	Glycosyl hydrolase family 7
PF02194	3	3	3	3	3	2	4	PXA domain
PF28561	1	1	1	0	3	1	2	Required for respiratory growth protein 1 C-terminal domain
PF01230	3	4	4	4	6	2	9	HIT domain
PF02984	3	3	3	3	3	4	5	Cyclin, C-terminal domain
PF03947	2	2	2	2	2	2	3	Ribosomal Proteins L2, C-terminal domain
PF00533	10	10	10	11	10	6	20	BRCA1 C Terminus (BRCT) domain
PF05916	4	4	4	4	6	4	8	GINS complex protein helical bundle domain
PF24997	1	1	1	1	1	1	2	PSF1 C-terminal domain
PF01920	4	4	4	4	4	5	7	Prefoldin subunit
PF05875	3	2	2	3	3	1	4	Ceramidase
PF01509	3	2	2	3	5	2	4	TruB family pseudouridylate synthase (N terminal domain)
PF11969	2	2	2	4	4	2	6	Scavenger mRNA decapping enzyme C-term binding
PF16278	1	1	1	1	1	0	2	C2HE / C2H2 / C2HC zinc-binding finger
PF13926	1	1	1	0	1	1	2	Domain of unknown function (DUF4211)
PF01459	2	2	2	1	1	1	4	Eukaryotic porin
PF13430	1	1	1	1	1	1	1	Domain of unknown function (DUF4112)
PF06814	3	1	1	1	1	1	1	GOST, seven transmembrane domain
PF21902	3	1	1	1	1	1	1	PTM1-like, N-terminal domain
PF01180	2	2	2	2	1	2	4	Dihydroorotate dehydrogenase
PF01302	4	4	4	4	5	3	8	CAP-Gly domain
PF16835	1	1	1	1	2	1	2	Pre-mRNA-splicing factor SF3a complex subunit 2 (Prp11)
PF28298	1	1	1	1	1	1	2	Stationary phase protein 5 C-terminal domain
PF13638	2	1	1	1	1	1	2	PIN domain
PF17215	1	1	1	1	1	1	2	S1 domain
PF17216	2	3	3	1	1	1	2	Rrp44-like cold shock domain
PF17849	2	3	3	3	2	2	2	Dis3-like cold-shock domain 2 (CSD2)
PF08624	2	2	2	3	2	2	4	Chromatin remodelling complex Rsc7/Swp82 subunit
PF11699	1	2	2	1	1	1	2	Mif2/CENP-C like
PF15624	1	2	2	1	1	1	2	Kinetochore CENP-C fungal homologue, Mif2, N-terminal
PF19047	1	1	1	2	1	1	2	HOOK domain
PF22974	2	0	0	2	2	1	4	Domain of unknown function (DUF7029)
PF02026	0	0	0	0	1	0	2	RyR domain
PF21274	2	2	2	2	1	2	7	Aromatic-ring hydroxylase, C-terminal
PF08443	0	1	1	0	0	0	1	RimK-like ATP-grasp domain
PF10642	0	0	0	0	1	0	2	Mitochondrial import receptor subunit or translocase
PF00285	3	3	3	4	4	3	4	Citrate synthase, C-terminal domain
PF04100	1	1	1	1	1	1	2	Vps53, N-terminal
PF10475	1	0	0	0	1	1	2	Vacuolar-sorting protein 54, of GARP complex
PF14608	2	3	3	4	2	4	6	RNA-binding, Nab2-type zinc finger
PF08590	2	2	2	2	2	2	4	Domain of unknown function (DUF1771)
PF28536	1	1	1	1	1	1	2	Domain of unknown function (DUF8432)
PF06991	0	0	0	1	1	1	2	Microfibril-associated/Pre-mRNA processing
PF14382	2	2	1	2	3	2	4	Exosome complex exonuclease RRP4 N-terminal region
PF17035	1	1	1	1	2	3	6	Bromodomain extra-terminal - transcription regulation
PF20305	3	2	3	2	2	2	2	prokaryotic YEATS domain
PF01151	2	2	2	3	2	3	4	GNS1/SUR4 family
PF02284	2	1	1	1	1	1	2	Cytochrome c oxidase subunit Va
PF09734	1	1	1	1	1	1	2	RNA polymerase III transcription factor (TF)IIIC subunit HTH domain
PF17682	1	1	1	1	1	0	2	Tau95 Triple barrel domain
PF01603	4	3	3	2	1	1	2	Protein phosphatase 2A regulatory B subunit (B56 family)
PF02769	2	2	2	2	2	2	3	AIR synthase related protein, C-terminal domain
PF13507	1	1	1	1	1	1	2	CobB/CobQ-like glutamine amidotransferase domain
PF18072	1	1	1	1	1	0	2	Formylglycinamide ribonucleotide amidotransferase linker domain
PF18076	1	1	1	1	1	0	2	Formylglycinamide ribonucleotide amidotransferase N-terminal
PF22689	1	1	1	1	1	1	2	FGAR-AT PurM_N-like domain
PF02386	4	2	2	3	5	4	4	Cation transport protein
PF04188	1	1	1	1	1	0	2	Mannosyltransferase (PIG-V)
PF04615	1	1	1	1	1	1	2	Utp14 protein
PF09809	1	1	1	1	1	1	2	Mitochondrial ribosomal protein L27
PF08327	1	1	1	1	1	1	2	Activator of Hsp90 ATPase homolog 1-like protein
PF09229	1	1	1	1	1	1	2	Activator of Hsp90 ATPase, N-terminal
PF25005	1	1	1	1	2	1	2	PSF2 N-terminal domain
PF04922	1	1	1	1	2	1	3	DIE2/ALG10 family
PF04614	1	1	1	2	1	1	4	Pex19 protein family
PF06862	1	1	1	1	1	1	2	Utp25, C-terminal domain
PF22916	1	1	1	1	1	1	2	UTP25, NTP hydrolase-like domain
PF01398	5	8	8	7	8	6	13	JAB1/Mov34/MPN/PAD-1 ubiquitin protease
PF13012	3	3	3	3	3	3	6	Maintenance of mitochondrial structure and function
PF00164	2	2	2	2	3	2	4	Ribosomal protein S12/S23
PF00408	1	2	2	1	2	4	1	Phosphoglucomutase/phosphomannomutase, C-terminal domain
PF21404	1	1	1	1	1	2	1	Phosphoacetylglucosamine mutase AMG1, domain III

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF21405	1	1	1	1	1	2	1	Phosphoacetylglucosamine mutase AMG1, domain II
PF19189	1	1	1	1	1	1	2	Mtf2 family
PF12849	0	0	0	0	0	0	1	PBP superfamily domain
PF19278	1	2	2	7	3	1	3	Hydantoinase/oxoprolinase C-terminal domain
PF00438	1	1	1	1	1	1	2	S-adenosylmethionine synthetase, N-terminal domain
PF02772	1	1	1	1	1	1	2	S-adenosylmethionine synthetase, central domain
PF02773	1	1	1	1	1	1	2	S-adenosylmethionine synthetase, C-terminal domain
PF12859	1	1	1	1	1	0	2	Anaphase-promoting complex subunit 1 WD40 beta-propeller domain
PF28370	1	1	0	1	1	1	2	Nucleoporin NUP37 N-terminal domain
PF18564	1	1	1	1	1	1	2	Glycoside hydrolase family 5 C-terminal domain
PF19273	1	1	1	1	1	0	2	Exportin-5 family
PF00930	2	2	2	2	4	1	2	Dipeptidyl peptidase IV (DPP IV) N-terminal region
PF02129	6	4	3	4	7	2	4	X-Pro dipeptidyl-peptidase (S15 family)
PF08243	0	0	0	1	1	1	2	SPT2 chromatin protein
PF00428	3	3	3	3	3	3	6	60s Acidic ribosomal protein
PF00203	2	2	2	2	3	3	4	Ribosomal protein S19
PF03876	2	2	2	2	2	2	4	SHS2 domain found in N terminus of Rpb7p/Rpc25p/MJ0397
PF09298	4	3	3	2	4	1	5	Fumarylacetoacetase N-terminal
PF05691	0	0	0	0	0	0	2	Raffinose synthase or seed imbibition protein Sip1
PF10510	0	0	0	1	1	1	2	Phosphatidylinositol-glycan biosynthesis class S protein
PF07727	0	0	0	1	2	1	2	Reverse transcriptase (RNA-dependent DNA polymerase)
PF14223	0	2	3	1	0	0	2	gag-polypeptide of LTR copia-type
PF03439	1	1	1	1	1	1	2	Early transcription elongation factor of RNA pol II, NGN section
PF11942	1	1	1	1	1	1	2	Spt5 transcription elongation factor, acidic N-terminal
PF12815	1	1	0	1	0	1	1	Spt5 C-terminal nonapeptide repeat binding Spt4
PF23037	1	1	1	1	1	1	2	Transcription elongation factor SPT5, KOWx domain
PF23042	1	1	1	1	1	1	2	Transcription elongation factor SPT5, KOW1 domain
PF23290	1	1	1	1	1	1	2	Transcription elongation factor SPT5, fifth KOW domain
PF23291	1	1	1	1	1	1	2	Transcription elongation factor SPT5, fourth KOW domain
PF16714	1	1	1	1	2	2	2	Tyrosyl-tRNA synthetase C-terminal domain
PF28122	0	0	0	1	1	1	2	Domain of unknown function (DUF8369)
PF04934	0	0	0	2	1	1	2	MED6 mediator sub complex component
PF00425	1	1	1	2	2	2	4	chorismate binding enzyme
PF04715	1	1	1	2	2	2	4	Anthranilate synthase component I, N terminal region
PF07722	1	1	1	2	1	0	4	Peptidase C26
PF13919	1	1	1	1	1	1	2	Asx homology domain
PF10483	1	1	1	1	1	1	2	Elongator subunit Iki1
PF21936	1	1	1	1	0	2	2	Pcf11, C-terminal domain
PF13563	1	1	1	0	2	1	2	2'-5' RNA ligase superfamily
PF01416	2	2	2	2	2	2	5	tRNA pseudouridine synthase
PF04495	1	1	1	1	2	1	4	GRASP55/65 PDZ-like domain
PF03941	1	1	1	1	1	1	2	Inner centromere protein, ARK binding region
PF23681	1	1	1	1	1	0	2	ATP-dependent rRNA helicase SPB4-like, C-terminal tail
PF07691	1	2	3	5	2	2	2	PA14 domain
PF01226	2	1	1	0	2	1	9	Formate/nitrite transporter
PF00639	2	2	2	2	3	2	3	PPIC-type PPIASE domain
PF13616	2	2	2	2	3	2	3	PPIC-type PPIASE domain
PF11274	2	2	2	2	2	1	2	Protein of unknown function (DUF3074)
PF09995	1	3	3	4	2	1	2	ER-bound oxygenase mpaB/B'/Rubber oxygenase, catalytic domain
PF00617	4	4	4	4	5	3	7	RasGEF domain
PF00618	4	4	4	4	5	2	5	RasGEF N-terminal motif
PF06320	1	1	1	1	1	1	2	GCN5-like protein 1 (GCN5L1)
PF26410	3	2	2	1	0	0	2	GH family 5 beta-mannosidase-like
PF00111	3	5	4	5	6	2	8	2Fe-2S iron-sulfur cluster binding domain
PF00941	1	1	1	2	2	1	2	FAD binding domain in molybdopterin dehydrogenase
PF01315	1	1	1	2	2	1	2	Aldehyde oxidase and xanthine dehydrogenase, a/b hammerhead domain
PF01799	1	1	1	2	2	0	2	[2Fe-2S] binding domain
PF02738	1	1	1	2	2	1	2	Molybdopterin cofactor-binding domain
PF03450	1	1	1	2	2	1	2	CO dehydrogenase flavoprotein C-terminal domain
PF20256	1	1	1	2	2	1	2	Molybdopterin cofactor-binding domain
PF03343	1	1	1	1	1	1	2	SART-1 family
PF05712	1	1	1	1	1	1	2	MRG
PF11717	2	2	2	2	2	2	4	RNA binding activity-knot of a chromodomain
PF22732	1	1	1	1	1	1	2	MSL3 chromodomain-like
PF02338	2	2	2	2	3	2	5	OTU-like cysteine protease
PF06421	1	1	1	2	1	1	2	GTP-binding protein LepA C-terminus
PF08407	3	3	3	5	5	3	8	Chitin synthase N-terminal
PF00723	2	2	2	2	2	5	2	Glycosyl hydrolases family 15
PF09924	1	1	1	2	1	2	2	Phosphatidylglycerol lysyltransferase, C-terminal
PF00989	7	4	4	3	4	5	9	PAS fold
PF03874	2	2	2	2	3	2	2	RNA polymerase Rpb4
PF00412	5	4	4	4	6	2	6	LIM domain
PF00620	9	10	10	8	10	10	13	RhoGAP domain
PF15901	1	1	1	1	1	1	2	Sortilin, neurotensin receptor 3, C-terminal
PF15902	1	1	1	1	1	0	4	Sortilin, neurotensin receptor 3,
PF26053	5	3	3	1	1	1	2	Scytalone dehydratase-like protein Arp1, N-terminal domain
PF00931	1	8	11	5	5	2	1	NB-ARC domain
PF25000	2	4	6	1	0	2	2	Domain of unknown function (DUF7779)
PF25376	1	1	1	1	2	1	2	NSUN2 Pre-PUA domain
PF25378	1	1	1	1	2	1	2	NSUN2 PUA domain
PF16495	1	1	1	1	1	1	2	SWIRM-associated region 1
PF18031	1	1	2	1	1	1	2	Ubiquitin carboxyl-terminal hydrolases
PF00298	2	2	2	2	3	2	2	Ribosomal protein L11, RNA binding domain
PF03946	2	2	2	2	3	2	3	Ribosomal protein L11, N-terminal domain
PF03839	1	1	1	1	1	1	2	Translocation protein Sec62
PF03453	1	1	1	1	2	1	3	MoeA N-terminal region (domain I and II)
PF03454	1	1	1	1	2	1	2	MoeA C-terminal region (domain IV)
PF02268	1	1	1	2	1	1	2	Transcription initiation factor IIA, gamma subunit, helical domain
PF02751	1	1	1	2	1	1	2	Transcription initiation factor IIA, gamma subunit
PF09429	1	1	1	1	1	1	2	WW domain binding protein 11
PF07956	0	1	0	1	1	1	2	Protein of Unknown function (DUF1690)
PF01849	2	2	2	2	2	2	4	NAC domain
PF00255	1	0	0	1	1	1	3	Glutathione peroxidase
PF07819	1	1	1	2	2	1	2	PGAP1-like alpha/beta domain
PF02854	4	4	4	5	5	5	10	MIF4G domain
PF04050	1	1	1	2	1	1	4	Up-frameshift suppressor 2
PF08676	1	1	1	1	3	0	2	MutL C terminal dimerisation domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF07541	1	1	1	1	1	1	2	Eukaryotic translation initiation factor 2 alpha subunit
PF01213	1	1	1	1	1	2	4	CAP N-terminal conserved motif
PF08603	1	1	1	1	1	2	4	Adenylate cyclase associated (CAP) C terminal
PF21938	1	1	1	1	1	2	4	CAP, N-terminal domain
PF11707	1	1	1	1	1	0	2	Ribosome 60S biogenesis N-terminal
PF16201	1	1	1	1	1	1	2	Nucleolar pre-ribosomal-associated protein 1
PF26140	1	1	1	1	1	1	2	URB1, central HEAT repeat domain
PF20566	0	0	0	1	0	0	3	eIF4E-associated protein
PF05625	1	1	1	1	1	1	2	PAXNEB protein
PF24969	0	0	0	0	0	1	1	Leucine-rich repeat domain
PF05603	1	1	1	1	3	1	2	Hikeshi-like, N-terminal domain
PF21057	1	1	1	1	3	1	2	Hikeshi-like, C-terminal domain
PF02845	5	5	5	5	6	5	8	CUE domain
PF04153	2	3	3	3	4	2	6	NOT2/NOT3/NOT5 C-terminal
PF02502	1	1	1	2	3	0	2	Ribose/Galactose Isomerase
PF04161	1	1	1	1	1	1	2	Arv1-like family
PF05493	1	1	1	1	1	1	2	ATP synthase subunit H
PF03853	2	2	2	3	2	2	3	YjeF-related protein N-terminus
PF00456	4	3	3	5	4	3	4	Transketolase, thiamine diphosphate binding domain
PF13292	1	1	1	3	0	0	2	1-deoxy-D-xylulose-5-phosphate synthase
PF22613	4	3	3	5	4	3	5	Transketolase-like TK C-terminal domain
PF18477	1	1	1	1	1	1	2	PIN like domain
PF28230	1	1	1	1	1	1	2	Vacoular membrane protein SCY_4732
PF08538	2	2	2	1	3	1	2	Protein of unknown function (DUF1749)
PF03982	1	1	1	1	1	1	2	Diacylglycerol acyltransferase
PF10494	1	1	1	1	1	1	2	Inactive serine-threonine protein kinase 19
PF08229	1	1	1	1	1	0	2	ER membrane protein SH3
PF12710	5	5	5	6	3	6	8	haloacid dehalogenase-like hydrolase
PF13889	2	1	1	1	2	1	2	Chromosome segregation during meiosis
PF13915	2	1	1	1	2	1	2	Domain of unknown function (DUF4210)
PF03619	3	4	4	1	5	2	11	Organic solute transporter Ostalpha
PF09362	5	5	6	6	3	5	6	Domain of unknown function (DUF1996)
PF03907	1	1	1	1	1	1	2	Spo7-like protein
PF00264	13	12	12	6	17	6	7	Common central domain of tyrosinase
PF14634	2	4	4	5	4	5	6	zinc-RING finger domain
PF14447	0	0	0	0	0	0	2	Prokaryotic RING finger family 4
PF16679	1	1	1	1	1	0	2	DNA replication factor Cdt1 C-terminal domain
PF26121	1	1	1	1	1	0	2	Cell division cycle protein CDT1-like, helix-turn-helix domain
PF01504	3	3	3	3	4	2	1	Phosphatidylinositol-4-phosphate 5-Kinase
PF00786	2	3	3	2	3	2	3	P21-Rho-binding domain
PF08293	1	1	1	1	1	1	2	Mitochondrial ribosomal subunit S27
PF01960	1	1	1	1	1	1	2	ArgJ family
PF01321	2	1	1	3	1	1	2	Creatinase/Prolidase N-terminal domain
PF16188	1	1	1	1	1	1	2	C-terminal region of peptidase_M24
PF16189	1	1	1	1	1	1	2	Creatinase/Prolidase N-terminal domain
PF02201	3	2	2	2	3	3	4	SWIB/MDM2 domain
PF02453	1	1	1	1	1	1	2	Reticulon
PF15950	0	0	0	0	0	0	2	Putative sperm flagellar membrane protein
PF01323	3	3	3	6	10	3	9	DSBA-like thioredoxin domain
PF04695	2	2	2	2	1	2	4	Pex14 N-terminal domain
PF04795	2	1	1	1	2	1	2	PAPA-1-like conserved region
PF02719	4	2	2	2	2	2	2	Polysaccharide biosynthesis protein
PF01019	2	2	2	5	2	2	3	Gamma-glutamyltranspeptidase
PF14378	2	2	2	3	5	3	3	PAP2 superfamily
PF00928	4	4	4	4	4	4	6	Adaptor complexes medium subunit family
PF02586	1	1	1	2	1	1	2	SOS response associated peptidase (SRAP)
PF24948	1	1	1	1	1	1	1	ATP-citrate synthase ATP-grasp domain
PF01650	1	1	1	1	1	1	2	Peptidase C13 family
PF10417	2	2	2	1	2	4	6	C-terminal domain of 1-Cys peroxiredoxin
PF00887	2	2	2	2	3	2	4	Acyl CoA binding protein
PF00833	1	1	1	1	1	1	2	Ribosomal S17
PF02463	6	6	6	7	5	7	14	RecF/RecN/SMC N terminal domain
PF06470	4	4	4	6	4	4	6	SMC proteins Flexible Hinge Domain
PF13476	4	4	5	7	5	4	9	AAA domain
PF04768	2	2	2	2	2	2	5	NAT, N-acetyltransferase, of N-acetylglutamate synthase
PF12068	0	0	0	0	1	1	2	Rab-binding domain (RBD)
PF28376	1	1	1	1	1	1	2	Nucleoporin NUP53 C-terminal domain
PF02969	2	2	2	4	2	2	4	TATA box binding protein associated factor (TAF)
PF07571	1	1	1	1	1	1	2	TAF6 C-terminal HEAT repeat domain
PF08082	1	1	1	1	1	1	2	PRO8NT (NUC069), PrP8 N-terminal domain
PF08083	1	1	1	1	1	0	2	PROCN (NUC071) domain
PF08084	1	1	1	1	1	1	2	PROCT (NUC072) domain
PF10596	1	1	1	0	1	1	2	U6-snRNA interacting domain of PrP8
PF10597	1	1	1	1	1	1	2	U5-snRNA binding site 2 of PrP8
PF10598	1	1	1	1	1	0	2	RNA recognition motif of the spliceosomal PrP8
PF12134	1	1	1	1	1	1	2	PRP8 domain IV core
PF01199	1	1	1	1	1	1	2	Ribosomal protein L34e
PF10615	1	1	1	1	1	1	2	Domain of unknown function (DUF2470)
PF01791	1	1	1	1	0	2	7	DeoC/LacD family aldolase
PF00854	5	6	6	4	4	1	9	POT family
PF00703	7	10	9	9	5	0	5	Glycosyl hydrolases family 2
PF22666	1	7	6	3	5	0	3	Glycosyl hydrolase 2 galactose-binding domain-like
PF07542	0	0	0	1	1	1	2	ATP12 chaperone protein
PF21762	2	4	3	4	5	2	16	DNA polymerase III subunit epsilon-like, C-terminal domain
PF01967	1	1	1	1	1	1	3	MoaC family
PF06463	1	1	1	1	1	1	2	Molybdenum Cofactor Synthesis C
PF08550	3	3	3	4	3	3	4	Nitrogen regulatory protein areA, GATA-like domain
PF11702	1	1	1	1	1	1	2	Protein of unknown function (DUF3295)
PF01393	1	1	1	1	1	1	2	Chromo shadow domain
PF00347	2	2	2	2	3	2	4	Ribosomal protein L6
PF07950	1	1	1	1	2	1	2	MDM10-complementing protein 1, transmembrane domain
PF12813	1	1	1	1	1	0	2	XPG domain containing
PF00235	1	1	1	1	2	1	2	Profilin
PF03694	2	2	2	2	1	1	3	Erg28 like protein
PF03234	1	1	1	1	1	1	2	Cdc37 N terminal kinase binding
PF08564	1	1	1	1	1	1	2	Cdc37 C terminal domain
PF08565	1	1	1	1	1	1	2	Cdc37 Hsp90 binding domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF24802	2	2	2	3	2	0	5	Domain of unknown function (DUF7703)
PF06858	1	1	1	1	1	1	2	Nucleolar GTP-binding protein 1 (NOG1)
PF08155	1	1	1	1	1	1	2	NOGCT (NUC087) domain
PF17835	1	1	1	1	1	1	2	NOG1 N-terminal helical domain
PF00622	3	2	3	2	4	4	3	SPRY domain
PF15469	1	1	1	1	1	1	2	Exocyst complex component Sec5
PF23191	1	1	1	1	1	2	2	MCM3-like, winged helix domain
PF10436	3	3	3	3	3	2	6	Mitochondrial branched-chain alpha-ketoacid dehydrogenase kinase
PF10281	0	1	1	1	1	1	4	Putative nuclear envelope organisation protein
PF04547	2	2	2	3	2	1	2	Calcium-activated chloride channel
PF20877	2	2	2	3	2	1	2	Alpha-beta plait domain in TMEM16 lipid scramblase
PF02878	2	2	2	1	2	2	4	Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain I
PF02879	2	2	2	1	2	2	4	Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain II
PF02880	2	2	2	1	2	2	4	Phosphoglucomutase/phosphomannomutase, alpha/beta/alpha domain III
PF24947	1	1	1	1	1	1	2	Phosphoglucomutase-1, C-terminal domain
PF10377	1	1	1	2	1	1	2	Autophagy-related protein 11
PF22580	2	2	2	1	2	1	2	Kynureninase C-terminal domain
PF14880	1	1	1	1	1	1	1	Cytochrome oxidase c assembly
PF12855	1	2	2	2	2	2	4	TORC1 inhibitor Ecl family
PF03824	1	1	1	1	1	5	2	High-affinity nickel-transport protein
PF14570	1	1	1	1	1	2	2	RING/Ubox like zinc-binding domain
PF00329	1	1	1	1	1	1	3	Respiratory-chain NADH dehydrogenase, 30 Kd subunit
PF05983	1	1	1	1	1	1	2	MED7 protein
PF00194	2	2	2	1	4	1	2	Eukaryotic-type carbonic anhydrase
PF00410	2	2	2	2	2	2	2	Ribosomal protein S8
PF10446	1	1	1	1	1	1	2	Protein of unknown function (DUF2457)
PF07792	1	1	1	2	1	1	2	Docking domain of Afi1 for Arf3 in vesicle trafficking
PF08616	2	1	1	2	2	1	4	Stabilization of polarity axis
PF00177	2	2	2	2	2	2	4	Ribosomal protein S7p/S5e
PF25318	1	2	2	1	1	1	2	GDS1 winged helix domain
PF20219	1	1	0	0	0	0	2	Family of unknown function (DUF6579)
PF07962	1	1	1	1	1	0	2	Replication Fork Protection Component Swi3
PF11957	1	1	1	1	1	0	2	THO complex subunit 1 transcription elongation factor
PF04699	1	1	1	1	2	1	2	ARP2/3 complex 16 kDa subunit (p16-Arc)
PF13816	0	1	0	1	2	0	2	Haem-containing dehydratase
PF08528	4	3	3	3	3	3	4	Whi5 like
PF09260	7	7	7	0	4	1	7	Alpha-amylase, domain C
PF00189	1	1	1	1	1	1	2	Ribosomal protein S3, C-terminal domain
PF07650	1	1	1	1	1	1	2	KH domain
PF10509	1	1	1	1	1	2	2	Galactokinase galactose-binding signature
PF10255	2	1	1	1	1	1	2	RNA polymerase I-associated factor PAF67
PF11705	1	1	1	1	1	1	2	DNA-directed RNA polymerase III subunit Rpc31
PF05179	1	1	1	1	1	1	2	RNA pol II accessory factor, Cdc73 family, C-terminal
PF01428	2	2	2	2	2	2	6	AN1-like Zinc finger
PF25327	1	1	1	1	1	1	2	ZFAND1-like ubiquitin-like domain
PF20789	3	3	3	7	8	2	8	Acyl-CoA thioesterase C-terminal domain
PF15377	1	1	1	1	2	1	2	Domain of unknown function (DUF4604)
PF22062	1	1	1	1	1	1	2	DNA polymerase alpha subunit B, OB domain
PF02847	2	2	2	2	3	3	4	MA3 domain
PF01058	2	1	1	2	2	1	2	NADH ubiquinone oxidoreductase, 20 Kd subunit
PF04420	1	1	1	1	1	1	2	CHD5-like protein
PF00733	3	3	3	2	3	2	4	Asparagine synthase
PF13537	6	6	6	4	5	4	8	Glutamine amidotransferase domain
PF13716	3	3	3	5	4	3	5	Divergent CRAL/TRIO domain
PF06202	1	0	0	2	1	1	4	Amylo-alpha-1,6-glucosidase
PF03101	1	1	1	0	1	0	2	FAR1 DNA-binding domain
PF12006	1	1	1	1	1	1	2	Protein of unknown function (DUF3500)
PF12511	0	2	2	2	1	0	2	Protein of unknown function (DUF3716)
PF27041	0	2	2	0	0	1	1	ZBED1 RNase-like domain
PF03060	3	4	4	4	6	6	7	Nitronate monooxygenase
PF04750	1	0	0	1	2	1	2	FAR-17a/AIG1-like protein
PF03571	1	1	1	1	2	1	3	Peptidase family M49
PF16455	1	1	1	1	1	1	2	Ubiquitin-binding domain
PF16413	1	1	1	1	1	1	2	DNA mismatch repair protein Mlh1 C-terminus
PF22956	1	1	1	2	3	3	2	Phosphatase 2A Regulatory Subunit A, helical domain
PF00995	4	4	4	4	5	4	7	Sec1 family
PF12513	1	1	1	1	1	1	2	ATP-dependent RNA helicase SUV3 C-terminal domain
PF18147	0	0	0	1	1	1	2	Suv3 C-terminal domain 1
PF22527	3	3	3	3	4	2	5	DEXQ-box helicase domain of Suv3
PF01817	1	1	1	2	1	1	2	Chorismate mutase type II
PF24564	4	5	4	1	7	1	9	Domain of unknown function (DUF7605)
PF14475	1	2	1	1	2	1	2	Sec1-binding region of Mso1
PF20233	5	2	3	1	8	0	10	Family of unknown function (DUF6590)
PF05224	4	2	2	3	3	2	2	NDT80 / PhoG like DNA-binding family
PF00478	3	6	6	4	6	3	7	IMP dehydrogenase / GMP reductase domain
PF00809	1	1	1	1	2	1	2	Pterin binding enzyme
PF01288	1	1	1	1	2	1	2	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase (HPPK)
PF04181	1	1	1	1	1	1	2	Rtr1/RPAP2 family
PF21666	2	3	3	1	1	0	2	Domain of unknown function DUF4246, N-terminal
PF04096	1	1	1	1	1	1	2	Nup98-96 autopeptidase S59
PF12110	1	1	1	1	1	1	1	Nuclear protein 96
PF01434	2	2	2	2	3	2	4	Peptidase family M41
PF21232	1	1	1	1	2	1	2	Yme1-like, N-terminal
PF00432	4	5	5	3	3	3	8	Prenyltransferase alpha-alpha toroid domain
PF12931	1	1	1	2	2	1	2	Sec16 Sec23-binding domain
PF12932	1	1	1	1	1	1	2	Vesicle coat trafficking protein Sec16 mid-region
PF08539	1	1	1	1	1	1	2	HbrB-like
PF24810	0	1	1	1	1	0	1	Leucine--tRNA ligase, RagD-binding domain
PF05153	0	1	1	1	1	1	2	Myo-inositol oxygenase
PF12843	0	0	0	0	0	0	1	Putative quorum-sensing-regulated virulence factor
PF08656	1	1	1	1	1	1	2	DASH complex subunit Dad3
PF02752	3	4	4	2	4	5	6	Arrestin (or S-antigen), C-terminal domain
PF12928	1	2	2	1	1	1	2	tRNA-splicing endonuclease subunit sen54 N-term
PF05011	2	2	2	1	1	1	1	Lariat debranching enzyme, C-terminal domain
PF17832	1	1	2	1	2	1	4	Pre-PUA-like domain
PF26292	1	1	2	0	2	1	4	eIF2D, PUA domain
PF16546	1	1	1	1	1	2	2	Homodimerisation domain of SGTA

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF00725	4	4	4	3	6	3	4	3-hydroxyacyl-CoA dehydrogenase, C-terminal domain
PF02737	4	5	5	3	6	3	4	3-hydroxyacyl-CoA dehydrogenase, NAD binding domain
PF06314	1	1	1	0	1	1	1	Acetoacetate decarboxylase (ADC)
PF04280	1	1	1	1	1	1	2	Tim44-like domain
PF11635	1	1	1	3	1	1	1	Mediator complex subunit 16, N-terminal
PF20719	1	1	1	3	1	1	2	Mediator complex subunit 16, C-terminal
PF08598	2	2	2	3	2	2	2	Sds3-like
PF00275	2	2	1	1	1	1	4	EPSP synthase (3-phosphoshikimate 1-carboxyvinyltransferase)
PF01202	2	3	2	3	3	2	4	Shikimate kinase
PF01487	3	5	5	4	4	3	5	Type I 3-dehydroquinase
PF01761	2	2	2	2	2	2	4	3-dehydroquinate synthase N-terminal
PF08501	7	7	7	6	3	5	12	Shikimate dehydrogenase substrate binding domain
PF18317	5	3	3	2	1	3	6	Shikimate 5'-dehydrogenase C-terminal domain
PF24621	2	2	2	2	2	1	4	3-dehydroquinate synthase C-terminal
PF13810	0	0	0	1	1	0	1	Domain of unknown function (DUF4185)
PF02872	2	2	2	2	3	1	2	5'-nucleotidase, C-terminal domain
PF08490	1	1	1	1	1	1	2	Domain of unknown function (DUF1744)
PF10108	1	1	1	1	1	0	2	Predicted 3'-5' exonuclease related to the exonuclease domain of PolB
PF22634	1	1	1	1	1	0	2	DNA polymerase epsilon catalytic subunit A, thumb domain
PF22912	1	1	1	1	1	1	2	Zinc finger domain of DNA polymerase-epsilon
PF23250	1	1	1	1	1	1	2	Zinc finger domain of DNA polymerase-epsilon
PF12597	1	1	1	1	1	1	4	Cytochrome c oxidase assembly protein COX20
PF08969	1	2	2	1	1	1	2	USP8 dimerisation domain
PF18808	1	1	1	1	1	2	2	Importin repeat
PF18816	1	1	1	1	1	2	2	Importin repeat
PF18829	1	1	1	1	1	2	2	Importin repeat 6
PF07524	3	4	4	3	4	4	6	Bromodomain associated
PF25118	1	1	1	1	1	2	2	Elongation factor-like GTPase 1-like domain
PF04006	1	1	1	1	1	1	2	Mpp10 protein
PF03222	0	1	1	2	1	0	4	Tryptophan/tyrosine permease family
PF08445	11	10	8	8	11	8	13	FR47-like protein
PF19031	1	1	1	1	1	1	4	First Longin domain of INTU, CCZ1 and HPS4
PF03656	2	2	2	1	1	1	2	Pam16
PF01220	1	1	1	2	2	1	2	Dehydroquinase class II
PF05978	10	7	8	6	4	1	5	Ion channel regulatory protein UNC-93
PF16158	1	1	2	1	1	1	2	Ig-like domain from next to BRCA1 gene
PF09405	1	1	1	1	1	1	2	CASC3/Barentsz eIF4AIII binding
PF01105	4	4	4	4	4	6	8	emp24/gp25L/p24 family/GOLD
PF10744	1	1	1	1	1	1	2	Mediator of RNA polymerase II transcription subunit 1
PF13091	5	3	3	5	6	1	5	PLD-like domain
PF00626	4	3	3	5	4	3	7	Gelsolin repeat
PF25480	1	2	1	1	1	1	2	Domain of unknown function (DUF7904)
PF05236	1	1	1	1	0	1	2	Transcription initiation factor TFIID component TAF4 family
PF07521	1	1	1	2	1	2	3	Zn-dependent metallo-hydrolase RNA specificity domain
PF10996	2	2	2	2	2	2	4	Beta-Casp domain
PF11718	1	1	1	1	1	1	2	Pre-mRNA 3'-end-processing endonuclease polyadenylation factor C-term
PF16661	2	2	2	2	2	2	4	Metallo-beta-lactamase superfamily domain
PF23023	1	3	3	2	1	0	3	Anti-Pycsar protein Apyc1
PF21148	1	1	1	1	1	0	2	NOL1/NOP2/Sun domain family member 5, ferredoxin-like domain
PF21153	1	1	1	1	1	0	2	NOL1/NOP2/Sun domain family member 5, N-terminal domain
PF27508	1	1	1	1	1	1	2	HYOU1-like, C-terminal domain
PF28428	1	1	1	2	1	1	3	TAM12
PF02544	4	6	6	2	4	1	6	3-oxo-5-alpha-steroid 4-dehydrogenase
PF01201	2	2	2	2	2	2	4	Ribosomal protein S8e
PF26113	6	5	5	3	6	5	10	XgeA-like, catalytic GH16 domain
PF04681	3	3	3	3	2	2	4	Blastomyces yeast-phase-specific protein
PF20882	1	1	1	1	2	1	2	Kinetochore protein Sos7
PF02046	1	2	1	1	2	2	2	Cytochrome c oxidase subunit VIa
PF28404	0	0	0	1	1	0	1	Uncharacterised secreted protein ARB_05178
PF05026	1	1	1	1	1	1	2	Dcp2, box A domain
PF01263	3	3	3	5	6	3	6	Aldose 1-epimerase
PF28522	1	1	1	1	1	1	1	ELL1 C-terminal domain
PF00154	2	2	2	1	2	2	4	RecA N-terminal domain
PF08438	1	1	1	1	1	2	2	Obg-like GTPase YGR210-like, G4 motif-containing domain
PF10487	0	1	1	1	1	0	2	Nucleoporin Nup188, N-terminal
PF18378	1	1	1	1	1	0	2	Nuclear pore protein NUP188 C-terminal domain
PF21093	0	0	0	1	1	0	2	Nucleoporin Nup188, N-terminal subdomain III
PF21094	1	1	1	1	1	1	1	Nup188 SH3-like domain
PF10340	3	3	3	1	3	0	6	Steryl acetyl hydrolase
PF01084	1	1	1	1	1	0	2	Ribosomal protein S18
PF01896	1	2	2	1	1	1	2	DNA primase small subunit
PF08939	1	1	1	1	2	1	2	Basophilic leukemia-expressed protein Bles03
PF02537	1	2	2	1	2	1	2	CrcB-like protein, Camphor Resistance (CrcB)
PF19566	1	1	1	1	1	1	2	Sorting nexin 8/Mvp1 BAR domain
PF27512	0	0	0	1	1	0	1	LeuD_N
PF15055	1	1	1	1	1	0	2	DMAC1/Dmo2-like domain
PF08523	1	1	1	1	1	1	2	Multiprotein bridging factor 1
PF04037	1	1	1	1	1	1	2	Domain of unknown function (DUF382)
PF04046	1	1	1	1	1	1	2	PSP
PF02806	1	1	1	1	1	2	2	Alpha amylase, C-terminal all-beta domain
PF02922	1	1	1	1	1	1	2	Carbohydrate-binding module 48 (Isoamylase N-terminal domain)
PF10431	2	3	3	3	3	3	5	C-terminal, D2-small domain, of ClpB protein
PF03378	1	1	1	1	1	1	2	CAS/CSE protein, C-terminus
PF08506	1	1	1	1	1	1	2	Cse1
PF04707	2	2	2	2	3	1	4	PRELI-like family
PF03177	2	2	2	2	2	2	4	Non-repetitive/WGA-negative nucleoporin C-terminal
PF08801	2	2	2	2	2	2	4	Nup133 N terminal like
PF05093	1	1	1	1	1	1	2	Cytokine-induced anti-apoptosis inhibitor 1, Fe-S biogenesis
PF16803	1	1	1	1	1	1	2	Fe-S cluster assembly protein DRE2 N-terminus
PF10309	1	1	1	1	2	1	2	Nuclear cap-binding protein subunit 3
PF04488	4	5	5	9	5	2	5	Glycosyltransferase sugar-binding region containing DXD motif
PF15801	2	0	1	2	1	1	2	zf-MYND-like zinc finger, mRNA-binding
PF03311	1	1	1	2	1	1	2	Cornichon protein
PF01233	1	1	1	1	2	1	2	Myristoyl-CoA:protein N-myristoyltransferase, N-terminal domain
PF02799	1	1	1	1	2	1	2	Myristoyl-CoA:protein N-myristoyltransferase, C-terminal domain
PF01040	2	3	3	5	3	2	4	UbiA prenyltransferase family
PF14008	0	2	2	0	3	0	6	Iron/zinc purple acid phosphatase-like protein C

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF16656	0	1	1	0	4	0	6	Purple acid Phosphatase, N-terminal domain
PF24845	1	1	1	1	1	1	2	Domain of unknown function (DUF7721)
PF10187	1	2	2	1	1	1	2	FAM192A/Fyv6, N-terminal domain
PF22807	1	1	1	2	0	1	3	TrAA12-like
PF09804	1	1	1	1	2	1	2	DENN domain-containing protein 11
PF14831	1	1	1	1	1	1	2	Domain of unknown function (DUF4484)
PF08514	2	2	2	1	1	1	2	STAG domain
PF21581	2	2	2	1	1	1	2	Stromalin conservative domain
PF24571	2	2	2	1	1	1	2	Cohesin subunit SCC3/SA, HEAT-repeats domain
PF01774	1	1	1	1	1	3	2	UreD urease accessory protein
PF03999	1	1	1	1	1	1	2	Microtubule associated protein (MAP65/ASE1 family)
PF00380	2	2	2	2	2	2	4	Ribosomal protein S9/S16
PF00647	1	1	1	1	1	1	2	Elongation factor 1 gamma, conserved domain
PF00838	1	1	1	1	1	2	2	Translationally controlled tumour protein
PF04080	1	1	1	1	2	1	3	Per1-like family
PF07452	2	1	1	3	1	0	4	CHRD domain
PF21269	0	0	0	1	1	1	2	Trehalose synthase, N-terminal domain
PF27036	0	0	0	1	1	1	2	Trehalose phosphorylase-like, N-terminal domain
PF09339	0	0	0	0	0	0	1	IclR helix-turn-helix domain
PF04083	2	2	2	2	2	2	4	Partial alpha/beta-hydrolase lipase region
PF10203	1	1	1	1	1	1	2	Cytochrome c oxidase assembly protein PET191
PF24803	2	3	3	3	7	1	4	Domain of unknown function (DUF7704)
PF20512	1	1	1	1	1	1	2	Phosphomannose isomerase type I, helical insertion domain
PF10358	1	1	1	2	1	1	2	N-terminal C2 in EEIG1 and EHBP1 proteins
PF09451	1	1	1	1	1	1	4	Autophagy-related protein 27
PF10153	1	1	1	1	1	1	2	rRNA-processing protein Efg1
PF17034	1	1	1	1	2	0	2	Zinc-ribbon like family
PF21719	1	1	1	1	2	0	2	MIOS, alpha-solenoid
PF00925	2	2	2	2	2	2	4	GTP cyclohydrolase II
PF01713	1	1	1	1	1	1	2	Smr domain
PF04430	1	1	1	1	2	1	2	Protein of unknown function (DUF498/DUF598)
PF04722	1	1	1	1	1	1	2	Ssu72-like protein
PF03248	1	1	1	1	1	1	2	Rer1 family
PF11899	1	1	1	1	1	0	2	Protein of unknown function (DUF3419)
PF10785	1	1	1	1	1	1	2	NADH-ubiquinone oxidoreductase complex I, 21 kDa subunit
PF12853	1	1	1	1	1	1	2	C-terminal of NADH-ubiquinone oxidoreductase 21 kDa subunit
PF16399	1	1	1	1	2	1	2	Intron-binding protein aquarius N-terminal
PF21143	1	1	1	1	2	1	2	Intron-binding protein aquarius, beta-barrel
PF21144	1	1	1	1	2	1	2	Intron-binding protein aquarius insert domain
PF03485	1	1	1	1	1	1	2	Arginyl tRNA synthetase N terminal domain
PF05746	1	1	1	1	1	1	2	DALR anticodon binding domain
PF17107	3	14	9	2	6	0	3	N-terminal domain on NACHT_NTPase and P-loop NTPases
PF05726	1	1	1	2	1	1	2	Pirin C-terminal cupin domain
PF10382	1	1	1	1	1	1	2	DNA helicase ZGRF1-like, N-terminal domain
PF00830	1	1	1	1	1	1	2	Ribosomal L28 family
PF08690	1	1	1	1	1	1	2	GET complex subunit GET2
PF10469	1	1	1	1	1	1	2	AKAP7 2'5' RNA ligase-like domain
PF07304	1	1	1	1	1	0	2	Steroid receptor RNA activator (SRA1)
PF03403	3	4	4	4	4	2	4	Platelet-activating factor acetylhydrolase, isoform II
PF08991	0	0	0	1	1	0	3	Cx9C motif-containing protein 4
PF10300	1	1	1	1	1	1	2	Iml2/Tetratricopeptide repeat protein 39
PF17877	1	2	2	2	1	1	2	DIS3-like exonuclease 2 C terminal
PF01363	5	5	4	6	6	3	8	FYVE zinc finger
PF21154	1	1	1	1	1	1	2	26S proteasome regulatory subunit RPN7/PSMD6 C-terminal helix
PF27751	2	1	0	2	0	1	4	ATEG_07667 C-terminal domain
PF05648	4	5	5	3	5	1	5	Peroxisomal biogenesis factor 11 (PEX11)
PF10403	2	1	1	2	2	3	2	Rad4 beta-hairpin domain 1
PF10404	2	1	1	2	2	3	2	Rad4 beta-hairpin domain 2
PF10405	2	1	1	2	2	3	4	Rad4 beta-hairpin domain 3
PF13241	2	3	3	2	3	2	5	Putative NAD(P)-binding
PF22099	1	1	2	1	1	1	2	Magnesium transporter MRS2-like
PF24984	3	3	3	3	4	3	5	Elongation factor 3/GNC1 HEAT repeat
PF24987	3	3	3	3	4	4	5	EF3 N-terminal HEAT repeat
PF04258	1	1	1	1	1	1	2	Signal peptide peptidase
PF02676	0	0	0	1	0	0	2	Methyltransferase TYW3
PF09365	1	1	1	1	1	0	2	Conserved hypothetical protein (DUF2461)
PF02002	0	0	0	1	1	1	2	TFIIE alpha subunit
PF08743	1	1	1	1	2	1	1	Nse4 C-terminal
PF15412	1	1	1	1	2	1	1	Binding domain of Nse4/EID3 to Nse3-MAGE
PF00454	7	8	8	11	11	8	10	Phosphatidylinositol 3- and 4-kinase
PF00613	2	2	2	2	3	3	3	Phosphoinositide 3-kinase family, accessory domain (PIK domain)
PF00792	1	1	1	1	1	1	1	Phosphoinositide 3-kinase C2
PF13793	3	3	3	3	3	3	4	N-terminal domain of ribose phosphate pyrophosphokinase
PF24684	0	0	0	0	5	0	3	Virginiamycin B lyase family
PF06999	2	2	2	4	2	2	4	Sucrase/ferredoxin-like
PF00926	1	1	1	1	1	2	2	3,4-dihydroxy-2-butanone 4-phosphate synthase
PF05486	2	1	1	1	2	1	2	Signal recognition particle 9 kDa protein (SRP9)
PF07000	1	1	1	0	1	0	2	Protein of unknown function (DUF1308)
PF08661	1	1	1	1	1	1	2	Replication factor A protein 3
PF12829	1	1	1	1	1	0	2	Transcriptional regulation of mitochondrial recombination
PF10186	2	2	2	1	3	1	3	Vacuolar sorting 38 and autophagy-related subunit 14
PF17649	1	1	1	1	2	1	2	Vacuolar protein sorting 38
PF12265	2	2	2	2	4	2	3	Histone-binding protein RBBP4 or subunit C of CAF1 complex
PF13401	10	17	18	9	12	8	11	AAA domain
PF22606	2	2	2	2	2	2	4	Cdc6/ORC-like, ATPase lid domain
PF28274	1	2	2	1	1	1	2	INA17 C-terminal domain
PF20408	1	1	1	0	1	0	2	Alpha/beta hydrolase domain
PF18005	0	0	0	1	1	1	2	eIF3 subunit M, C-terminal helix
PF13238	2	3	4	5	6	3	6	AAA domain
PF00416	2	2	2	2	1	1	4	Ribosomal protein S13/S18
PF07039	0	0	0	1	1	1	3	SGF29 tudor-like domain
PF01409	2	2	2	1	2	1	4	tRNA synthetases class II core domain (F)
PF18553	1	1	1	1	1	1	2	PheRS DNA binding domain 3
PF00204	1	1	1	1	2	1	2	DNA gyrase B
PF00521	1	1	1	1	2	1	2	DNA gyrase/topoisomerase IV, subunit A
PF16898	1	1	1	1	2	1	2	C-terminal associated domain of TOPRIM
PF14342	0	1	0	0	1	0	2	Domain of unknown function (DUF4396)

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF00804	2	2	2	2	2	1	4	Syntaxin
PF04733	1	1	1	1	1	1	2	Coatomer epsilon subunit
PF11312	2	2	2	1	1	1	2	Putative SAM-dependent methyltransferase
PF03114	3	3	3	5	6	4	8	BAR domain
PF21314	2	0	0	0	0	0	1	Epidermal growth factor receptor transmembrane-juxtamembrane segment
PF00281	2	2	2	1	3	2	3	Ribosomal protein L5
PF00673	2	2	2	2	3	2	2	ribosomal L5P family C-terminus
PF11815	3	4	4	3	3	4	5	Domain of unknown function (DUF3336)
PF01875	1	1	1	1	1	1	2	Memo-like protein
PF28332	1	1	1	1	2	1	2	C2H2-type transcription factor zfpA C-terminal domain
PF23256	1	1	1	0	1	1	2	Plant cation/H(+) antiporter domain
PF24807	1	1	1	2	3	2	1	CDC20/Fizzy WD40 domain
PF16335	4	5	5	0	7	1	5	Glutaminase A six helical-hairpin domain
PF17168	5	6	6	0	6	1	7	Domain of unknown function (DUF5127)
PF04051	4	3	3	3	3	3	6	Transport protein particle (TRAPP) component
PF08583	2	2	2	2	2	1	3	Cytochrome c oxidase biogenesis protein Cmc1 like
PF02939	1	1	1	1	3	1	3	UcrQ family
PF07576	1	1	1	1	2	2	2	BRCA1-associated protein 2
PF13881	2	2	2	3	3	2	6	Ubiquitin-2 like Rad60 SUMO-like
PF08552	1	1	1	1	1	1	2	Inositolphosphorylceramide synthase subunit Kei1
PF07767	1	1	1	1	1	1	2	Nop53 (60S ribosomal biogenesis)
PF15916	1	1	1	1	1	1	2	Domain of unknown function (DUF4743)
PF03870	1	1	1	1	1	1	2	RNA polymerase Rpb8
PF00764	1	1	1	2	1	1	2	Arginosuccinate synthase N-terminal HUP domain
PF20979	1	1	1	2	1	1	2	Arginosuccinate synthase C-terminal domain
PF11595	1	1	1	0	0	1	2	Protein of unknown function (DUF3245)
PF10454	1	1	1	0	1	1	2	Protein of unknown function (DUF2458)
PF08633	1	1	1	1	1	1	2	Rox3 mediator complex subunit
PF03834	1	1	1	1	1	1	2	Binding domain of DNA repair protein Ercc1 (rad10/Swi10)
PF08145	1	1	1	1	1	1	2	BOP1NT (NUC169) domain
PF03381	2	1	1	1	1	1	2	LEM3 (ligand-effect modulator 3) family / CDC50 family
PF05572	1	2	2	2	2	1	2	Pregnancy-associated plasma protein-A
PF13688	1	1	1	2	3	1	4	Metallo-peptidase family M12
PF03641	1	1	1	1	3	1	2	Possible lysine decarboxylase
PF20521	4	1	0	0	0	0	1	Family of unknown function (DUF6736)
PF01743	1	1	1	1	2	1	2	Poly A polymerase head domain
PF10521	1	1	1	1	2	1	2	Tti2 family
PF12627	1	1	1	1	2	1	2	Probable RNA and SrmB- binding site of polymerase A
PF12739	1	1	1	1	1	1	2	ER-Golgi trafficking TRAPP I complex 85 kDa subunit
PF04057	1	1	1	1	2	1	4	Replication factor-A protein 1, N-terminal domain
PF08646	1	1	1	1	1	1	4	Replication factor-A C terminal domain
PF16900	1	1	1	1	2	1	4	Replication protein A OB domain
PF17135	1	1	1	1	2	2	2	Ribosomal protein 60S L18 and 50S L18e
PF12734	0	0	0	1	0	0	2	Cysteine-rich TM module stress tolerance
PF07045	0	0	0	0	0	0	2	Domain of unknown function (DUF1330)
PF06424	2	1	1	1	1	1	4	PRP1 splicing factor, N-terminal
PF13428	4	4	4	2	2	4	8	Tetratricopeptide repeat
PF00828	2	2	2	2	2	2	4	Ribosomal proteins 50S-L15, 50S-L18e, 60S-L27A
PF12868	2	1	1	0	1	1	2	Domain of unknwon function (DUF3824)
PF01086	1	1	1	1	1	1	2	Clathrin light chain
PF23002	1	1	1	1	1	0	2	ATP-dependent RNA helicase DDX60, PIN-like domain
PF24120	0	0	0	0	0	0	2	Single-strand DNA deaminase toxin A, C-terminal
PF07366	0	0	0	3	0	2	2	SnoaL-like polyketide cyclase
PF09445	2	1	1	3	2	2	4	RNA cap guanine-N2 methyltransferase
PF16242	3	3	2	1	1	2	4	Pyridoxamine 5'-phosphate oxidase like
PF00574	1	1	1	1	2	1	2	Clp protease
PF17403	1	1	1	1	1	1	2	Nrap protein PAP/OAS-like domain
PF17404	1	1	1	1	1	1	2	Nrap protein domain 3
PF17405	1	1	1	1	1	1	2	Nrap protein nucleotidyltransferase domain 4
PF17406	1	1	1	1	1	1	2	Nrap protein PAP/OAS1-like domain 5
PF17407	1	1	1	1	1	1	2	Nrap protein domain 6
PF06280	1	1	1	2	0	0	2	Fn3-like domain
PF04275	1	1	1	1	0	0	2	Phosphomevalonate kinase
PF01227	3	3	3	2	2	0	5	GTP cyclohydrolase I
PF01823	0	0	0	0	2	0	1	MAC/Perforin domain
PF06842	1	1	1	1	1	1	2	Protein of unknown function (DUF1242)
PF04815	3	3	3	4	3	3	6	Sec23/Sec24 helical domain
PF08033	3	3	3	4	3	3	4	Sec23/Sec24 beta-sandwich domain
PF05495	3	2	2	3	2	1	3	CHY zinc finger
PF02221	2	2	2	1	5	1	3	ML domain
PF15456	1	1	1	3	1	1	2	Up-regulated During Septation
PF25078	1	1	1	0	1	1	2	Domain of unknown function (DUF7801)
PF15879	1	1	1	1	1	1	1	NADH-ubiquinone oxidoreductase MWFE subunit
PF08316	1	1	1	1	2	1	4	Pal1 cell morphology protein
PF05669	1	1	1	1	1	0	2	SOH1
PF03820	1	1	1	1	1	1	2	Siderophore-interacting
PF09280	1	1	1	1	1	1	1	XPC-binding domain
PF07923	1	1	1	1	1	2	2	N1221-like protein
PF11882	1	1	1	1	1	1	2	Domain of unknown function (DUF3402)
PF12449	1	1	1	1	1	1	2	Protein of unknown function (DUF3684)
PF23120	2	1	1	1	1	1	2	Peroxisomal ATPase 6 N-terminal
PF23315	2	1	1	1	1	1	2	PEX6 fourth domain
PF10295	2	2	2	1	1	1	2	Uncharacterised protein (DUF2406)
PF09446	1	1	1	1	1	0	2	VMA21-like domain
PF00262	1	1	1	1	1	1	2	Calreticulin family
PF09749	1	1	1	1	1	0	2	Uncharacterised conserved protein
PF11831	1	1	1	1	1	1	2	pre-mRNA splicing factor component
PF05042	0	1	1	0	0	2	2	Caleosin related protein
PF04446	1	1	1	2	1	2	2	tRNAHis guanylyltransferase
PF14413	1	1	1	2	1	2	2	Thg1 C terminal domain
PF00672	1	1	1	1	1	2	2	HAMP domain
PF18947	1	1	1	1	1	2	2	HAMP domain
PF25331	2	2	2	2	4	3	3	Third C2 domain of meiotically up-regulated Mug190 protein
PF09262	1	1	1	1	1	1	2	Peroxisome biogenesis factor 1, N-terminal
PF09079	1	0	0	1	1	1	1	CDC6, C terminal winged helix domain
PF18972	1	1	1	1	1	2	2	Cns1/TTC4 Wheel domain
PF01257	1	1	1	1	2	1	2	Thioredoxin-like [2Fe-2S] ferredoxin

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF01781	1	1	1	2	1	1	2	Ribosomal L38e protein family
PF12706	4	4	4	4	6	3	7	Beta-lactamase superfamily domain
PF13483	4	3	3	1	4	3	4	Beta-lactamase superfamily domain
PF27504	0	1	0	1	0	0	4	Domain of unknown function (DUF8348)
PF01256	1	1	1	2	2	1	2	NAD(P)H-hydrate dehydratase
PF00565	2	2	2	2	2	1	4	Staphylococcal nuclease homologue
PF04499	1	1	1	1	2	3	2	SIT4 phosphatase-associated protein
PF05960	0	1	1	1	1	0	2	Bacterial protein of unknown function (DUF885)
PF03330	3	0	0	1	1	0	2	Lytic transglycolase
PF13558	1	0	0	1	0	1	1	SbcC/RAD50-like, Walker B motif
PF06229	1	1	1	1	1	1	1	FRG1-like domain
PF08911	0	0	0	0	0	1	2	NUP50 (Nucleoporin 50 kDa)
PF28325	2	1	1	1	4	1	4	Fungal beta-trefoil domain
PF04178	2	2	2	2	2	1	3	Got1/Sft2-like family
PF00793	2	1	1	2	2	2	4	DAHP synthetase I family
PF00572	2	3	3	2	2	2	4	Ribosomal protein L13
PF01014	1	1	1	1	1	1	2	Uricase
PF02185	2	2	2	2	2	2	4	Hr1 repeat
PF14664	1	1	1	1	1	1	2	Rapamycin-insensitive companion of mTOR, N-term
PF14666	1	1	1	1	1	0	2	Rapamycin-insensitive companion of mTOR, middle domain
PF14617	1	1	1	1	1	1	2	U3-containing 90S pre-ribosomal complex subunit
PF05971	1	1	1	1	1	0	2	RNA methyltransferase
PF14823	2	2	2	2	2	1	3	Sirohaem biosynthesis protein C-terminal
PF14824	2	2	2	2	2	2	3	Sirohaem biosynthesis protein central
PF11464	2	2	1	1	1	0	2	Rabenosyn Rab binding domain
PF03074	1	1	1	1	2	2	2	Glutamate-cysteine ligase
PF21711	1	1	1	0	1	1	3	Dynactin subunit 5
PF00388	5	5	5	6	7	3	3	Phosphatidylinositol-specific phospholipase C, X domain
PF22039	0	0	0	0	0	0	1	Imidazolonepropionase-like composite domain, bacteria
PF03795	3	3	3	1	2	1	2	YCII-related domain
PF08557	1	1	1	1	1	1	2	Sphingolipid Delta4-desaturase (DES)
PF07557	1	1	1	1	2	0	2	Shugoshin C terminus
PF07558	1	1	1	1	2	1	2	Shugoshin N-terminal coiled-coil region
PF08654	1	1	1	1	2	1	2	DASH complex subunit Dad2
PF13812	4	5	5	5	6	7	6	Pentatricopeptide repeat domain
PF08315	1	1	1	1	1	1	2	cwf18 pre-mRNA splicing factor
PF25889	1	1	1	1	1	1	1	Fungal-differentiation regulator winged helix domain
PF17137	1	1	1	1	1	1	3	Domain of unknown function (DUF5110)
PF00334	1	1	1	2	2	2	4	Nucleoside diphosphate kinase
PF12505	1	2	2	5	0	0	3	Protein of unknown function (DUF3712)
PF03517	0	0	0	1	1	1	2	Regulator of volume decrease after cellular swelling
PF09402	1	1	1	1	1	1	2	Man1-Src1p-C-terminal domain
PF12949	1	1	1	1	1	1	2	HeH/LEM domain
PF02862	1	1	1	1	1	1	2	DDHD domain
PF23463	1	1	1	1	1	0	2	WWE domain
PF23465	1	1	1	1	1	1	2	Domain of unknown function (DUF7131)
PF04758	1	1	1	1	1	1	2	Ribosomal protein S30
PF13883	1	1	1	1	1	1	2	CREG, beta-barrel
PF00024	1	5	5	0	8	1	10	PAN domain
PF13454	1	0	0	3	1	0	3	FAD-NAD(P)-binding
PF16078	1	1	1	2	1	1	1	2-oxoglutarate dehydrogenase N-terminus
PF01255	1	1	1	2	1	2	1	Putative undecaprenyl diphosphate synthase
PF12719	1	1	1	1	1	1	2	Nuclear condensing complex subunits, C-term domain
PF01536	1	1	1	1	1	1	2	Adenosylmethionine decarboxylase
PF23867	2	2	2	1	1	1	1	Mmc1 N-terminal domain
PF23868	2	2	2	1	2	1	1	Mmc1 C-terminal domain
PF07297	1	0	0	1	2	1	2	Dolichol phosphate-mannose biosynthesis regulatory protein (DPM2)
PF10408	1	1	1	1	1	1	2	Ubiquitin elongating factor core
PF08432	1	1	1	2	2	1	2	AAA-ATPase Vps4-associated protein 1
PF14698	1	1	1	5	1	1	2	Argininosuccinate lyase C-terminal
PF04884	1	1	1	1	1	1	2	Vitamin B6 photo-protection and homoeostasis domain
PF22784	2	2	2	0	2	2	4	Swiss Army Knife protein, DSP-PTPase phosphatase domain
PF03162	1	1	1	1	1	1	2	Tyrosine phosphatase family
PF26729	1	0	0	1	2	1	2	TMA17 helical domain
PF01694	6	5	5	3	4	3	8	Rhomboid domain
PF08234	1	1	1	1	1	1	2	Chromosome segregation protein Spc25
PF10214	1	1	1	1	1	0	3	Rrn6, beta-propeller
PF20639	1	1	1	1	1	0	2	RRN6, K-rich C-terminal domain
PF20640	1	1	1	1	1	0	2	Rrn6, helical bundle domain
PF02679	0	0	0	0	1	1	2	(2R)-phospho-3-sulfolactate synthase (ComA)
PF11735	4	6	6	1	2	1	2	Cryptococcal mannosyltransferase 1
PF08752	1	1	1	1	1	1	2	Coatomer gamma subunit appendage platform subdomain
PF13646	7	7	7	8	6	6	6	HEAT repeats
PF16381	1	1	1	1	1	1	2	Coatomer subunit gamma-1 C-terminal appendage platform
PF02114	2	2	2	2	2	3	4	Phosducin
PF09763	1	2	2	1	1	1	3	Exocyst complex component Sec3, coiled-coil
PF15277	1	1	1	1	1	1	3	Exocyst complex component SEC3 N-terminal PIP2 binding PH
PF20654	1	1	1	1	1	1	3	Exocyst complex component Sec3, C-terminal
PF01267	1	1	1	1	2	1	2	F-actin capping protein alpha subunit
PF13650	2	1	2	2	2	1	2	Aspartyl protease
PF13975	1	1	1	2	2	1	2	gag-polyprotein putative aspartyl protease
PF00314	1	1	1	1	2	1	1	Thaumatin family
PF08589	1	1	1	1	1	1	2	Autophagy receptor ATG43
PF01261	6	4	4	9	4	3	7	Xylose isomerase-like TIM barrel
PF01902	1	1	1	0	2	1	2	Diphthamide synthase N-terminal domain
PF28410	0	0	0	1	2	1	2	Diphthamide synthase C-terminal domain
PF12757	1	1	1	1	1	2	2	Eisosome protein 1
PF04133	1	1	1	1	1	1	2	Vacuolar protein sorting 55
PF10345	1	1	2	2	1	1	2	Cohesin loading factor
PF28225	1	1	1	1	2	1	2	LOC1 helical domain
PF05255	1	1	1	1	1	1	2	Uncharacterised protein family (UPF0220)
PF08626	1	1	1	1	1	0	1	Trs120/TRAPPC9, N-terminal domain
PF26251	1	1	1	1	1	0	2	Trs120/TRAPPC9 TPR
PF26254	1	1	1	1	1	0	2	Trs120/TRAPPC9, first Ig-like domain
PF03645	1	1	1	1	2	1	1	Tctex-1 family
PF16016	2	2	2	2	3	3	4	VAD1 Analog of StAR-related lipid transfer domain
PF16746	2	3	3	2	2	2	4	BAR domain of APPL family

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF07569	2	1	1	1	1	1	2	TUP1-like enhancer of split
PF09453	2	1	1	1	1	1	2	HIRA B motif
PF24105	2	2	2	1	2	1	4	CAF1B/HIR1 beta-propeller domain
PF08513	2	4	4	4	2	2	5	LisH
PF01245	1	1	1	1	1	1	2	Ribosomal protein L19
PF28374	1	1	1	1	1	1	3	Mitochondrial ribosomal protein mS27
PF03815	1	1	1	1	1	1	2	LCCL domain
PF03105	2	2	2	2	2	2	5	SPX domain
PF03124	2	2	2	2	2	2	3	EXS family
PF11625	1	0	0	0	3	0	4	Protein of unknown function (DUF3253)
PF02580	1	2	2	1	2	1	4	D-Tyr-tRNA(Tyr) deacylase
PF04065	1	1	1	1	2	1	2	Not1 N-terminal domain, CCR4-Not complex component
PF10180	1	1	1	1	1	1	2	WKF domain
PF00616	2	2	2	6	2	4	3	GTPase-activator protein for Ras-like GTPase
PF03836	2	2	2	3	2	2	3	RasGAP C-terminus
PF03464	2	2	2	2	2	2	4	eRF1 domain 2
PF03465	2	2	2	2	2	2	4	eRF1 domain 3
PF26356	1	1	1	1	1	1	2	Pelota N-terminal domain
PF14735	1	2	1	0	1	1	2	HAUS augmin-like complex subunit 4
PF07896	1	1	1	1	2	1	2	Protein of unknown function (DUF1674)
PF03664	2	2	2	1	1	0	4	Glycosyl hydrolase family 62
PF03291	1	1	1	1	1	1	2	mRNA (guanine-N(7))-methyltransferase domain
PF09427	1	1	1	1	1	1	2	Domain of unknown function (DUF2014)
PF02765	2	2	2	2	2	0	2	Telomeric single stranded DNA binding POT1/CDC13
PF00956	2	2	2	3	2	1	4	Nucleosome assembly protein (NAP)
PF08605	1	1	1	0	2	1	2	Fungal Rad9-like Rad53-binding
PF18115	1	1	1	1	2	1	2	DNA repair protein Crb2 Tudor domain
PF08214	1	1	1	1	2	0	2	Histone acetylation protein
PF00641	1	1	1	1	3	1	1	Zn-finger in Ran binding protein and others
PF28255	1	1	1	1	1	1	1	CIP1 HTH domain
PF04109	1	1	1	1	2	0	2	Autophagy protein ATG9
PF09424	1	1	1	1	1	1	2	Yqey-like protein
PF00514	2	2	2	2	2	3	2	Armadillo/beta-catenin-like repeat
PF04826	1	1	1	1	1	1	2	Armadillo-like
PF08632	2	1	1	1	1	1	2	Activator of mitotic machinery Cdc14 phosphatase activation C-term
PF00459	2	3	2	6	5	5	4	Inositol monophosphatase family
PF21356	1	1	1	2	1	1	2	Vacuolar protein sorting-associated protein 27, GAT-like domain
PF00762	1	1	1	1	1	0	2	Ferrochelatase
PF02735	1	2	1	2	2	2	2	Ku70/Ku80 beta-barrel domain
PF03730	1	1	1	1	1	1	2	Ku70/Ku80 C-terminal arm
PF03731	1	2	1	2	2	2	3	Ku70/Ku80 N-terminal alpha/beta domain
PF06418	1	1	1	1	1	1	2	CTP synthase N-terminus
PF02150	2	2	2	2	2	1	3	RNA polymerases M/15 Kd subunit
PF01909	3	3	3	3	2	1	8	Nucleotidyltransferase domain
PF03828	4	3	3	3	3	1	8	Cid1 family poly A polymerase
PF22600	3	3	3	3	4	4	10	Poly(A) RNA polymerase, mitochondrial-like, central palm domain
PF09793	1	1	1	0	1	1	2	Anticodon-binding domain
PF01280	1	1	1	1	1	1	2	Ribosomal protein L19e, N-terminal domain
PF25476	1	1	1	1	1	1	2	Ribosomal protein L19e, C-terminal domain
PF04568	1	1	1	1	2	1	2	Mitochondrial ATPase inhibitor, IATP
PF10274	0	0	0	1	0	0	1	Parkin co-regulated protein
PF25786	1	1	1	1	1	1	2	GCN1-like, C-terminal HEAT repeats
PF25801	1	1	1	1	1	1	2	Stalled ribosome sensor GCN1-like, HEAT repeats
PF05680	1	1	1	1	1	1	2	ATP synthase E chain
PF14027	2	2	2	3	2	2	3	Questin oxidase-like
PF00498	11	9	9	16	12	10	10	FHA domain
PF16508	1	1	1	1	1	1	2	Second BRCT domain on Nijmegen syndrome breakage protein
PF01878	1	1	1	1	1	1	2	EVE domain
PF20263	2	1	1	1	2	2	3	LYR motif-containing protein 2-like
PF00584	1	1	1	1	1	1	1	SecE/Sec61-gamma subunits of protein translocation complex
PF13772	0	0	0	0	2	0	2	AIG2-like family
PF26112	1	1	1	1	1	1	2	RNF216-like, UBA domain
PF26191	1	1	1	1	1	1	2	RNF216 RING finger HC subclass domain
PF26200	1	1	2	1	2	2	4	RNF216 Rcat domain
PF13188	3	3	4	4	7	4	4	PAS domain
PF17947	1	1	1	1	1	1	2	Four helical bundle domain
PF23271	2	1	1	2	3	3	3	Stalled ribosome sensor GCN1-like, HEAT repeats
PF02089	1	2	2	1	1	1	2	Palmitoyl protein thioesterase
PF01020	1	1	1	1	1	1	2	Ribosomal L40e family
PF23305	2	2	2	2	2	1	3	Domain of unknown function (DUF7082)
PF09531	1	1	1	1	2	2	2	Nucleoporin protein Ndc1-Nup
PF14523	1	1	1	2	1	1	2	Syntaxin-like protein
PF01975	2	2	2	3	3	1	4	Survival protein SurE
PF24550	1	1	1	1	1	1	2	Dynamin-like GTPase MGM1-like, lipid interacting stalk
PF12246	1	2	2	1	2	1	2	Temperature dependent protein affecting M2 dsRNA replication
PF12247	1	2	2	1	2	1	1	Temperature dependent protein affecting M2 dsRNA replication
PF05903	2	2	2	2	2	1	6	PPPDE putative peptidase domain
PF01150	2	2	2	2	3	2	4	GDA1/CD39 (nucleoside phosphatase) family
PF08317	2	2	2	1	1	1	2	Spc7 kinetochore protein
PF15402	2	2	2	1	1	1	2	MELT motif
PF18210	2	2	2	1	1	1	2	Knl1 RWD C-terminal domain
PF00366	2	2	2	2	2	1	4	Ribosomal protein S17
PF16205	1	1	1	1	1	0	2	Ribosomal_S17 N-terminal
PF18264	1	1	1	2	0	0	2	CXC domain
PF27980	1	1	1	0	1	1	1	Embryogenesis-like protein helical domain
PF09792	4	2	2	0	6	5	6	Ubiquitin 3 binding protein But2 C-terminal domain
PF01432	2	3	3	2	5	2	3	Peptidase family M3
PF04979	1	1	1	1	1	1	2	Protein phosphatase inhibitor 2 (IPP-2)
PF00734	18	20	20	3	1	1	4	Fungal cellulose binding domain
PF13840	3	4	4	3	5	2	6	ACT domain
PF07522	1	1	1	1	1	1	2	DNA repair metallo-beta-lactamase
PF11579	1	0	0	0	0	0	1	Protein of unknown function (DUF3238)
PF16347	3	5	5	11	4	2	2	N-sulphoglucosamine sulphohydrolase, C-terminal
PF00585	1	1	1	1	2	1	4	C-terminal regulatory domain of Threonine dehydratase
PF07651	2	2	2	2	2	2	4	ANTH domain
PF01265	2	3	3	2	4	1	1	Cytochrome c/c1 heme lyase
PF02145	1	1	1	1	1	1	2	Rap/ran-GAP

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF03542	0	0	0	1	1	1	2	Tuberin
PF08767	1	1	1	1	1	1	2	CRM1 C terminal
PF18787	1	1	1	1	1	1	2	CRM1 / Exportin repeat 3
PF03540	1	1	1	1	1	1	2	Transcription initiation factor TFIID 23-30kDa subunit
PF08608	0	0	0	1	1	1	2	Wyosine base formation
PF01938	1	1	1	0	1	1	2	TRAM domain
PF06792	1	1	1	1	2	1	2	Uncharacterised protein family (UPF0261) N-terminal domain
PF23189	1	1	1	1	2	1	2	Uncharacterised protein family (UPF0261) C-terminal domain
PF09370	1	1	1	1	1	1	2	Phosphoenolpyruvate hydrolase-like
PF09949	4	4	5	3	4	3	6	Phosphatidate phosphatase APP1, catalytic domain
PF10176	1	2	2	1	1	1	2	NEDD4/Bsd2
PF10237	0	0	0	0	1	0	2	Probable N6-adenine methyltransferase
PF00305	0	0	0	0	1	0	1	Lipoxygenase
PF02391	1	1	1	1	1	1	2	MoaE protein
PF28272	1	1	1	1	2	1	2	AIM11 N-terminal domain
PF06432	1	1	1	1	1	1	2	Phosphatidylinositol N-acetylglucosaminyltransferase
PF12585	1	1	1	2	1	1	2	Protein of unknown function (DUF3759)
PF17068	0	0	0	0	1	0	2	Required for respiratory growth protein 8 mitochondrial
PF24355	2	2	2	2	2	2	2	Domain of unknown function (DUF7514)
PF03851	1	1	1	1	1	1	2	UV-endonuclease UvdE
PF03849	1	1	1	1	1	1	2	Transcription factor Tfb2
PF18307	1	1	1	1	1	1	2	Transcription factor Tfb2 (p52) C-terminal domain
PF27536	1	1	1	1	1	1	2	UbiB N-terminal domain
PF12807	0	1	1	1	1	1	2	Translation initiation factor eIF3 subunit 135
PF13236	0	1	1	1	1	1	2	Clustered mitochondria
PF15044	0	1	1	1	1	1	2	Mitochondrial function, CLU-N-term
PF24913	0	1	1	1	1	1	2	Fungal AAA protein, C-terminal winged helix domain
PF02179	2	1	2	1	1	1	2	BAG domain
PF17042	1	1	1	3	2	1	2	Nucleotide-binding C-terminal domain
PF08511	1	1	1	1	2	1	2	COQ9
PF00690	11	12	12	14	8	8	4	Cation transporter/ATPase, N-terminus
PF04824	1	1	1	2	2	2	2	Conserved region of Rad21 / Rec8 like protein
PF04825	2	2	2	2	2	2	4	N terminus of Rad21 / Rec8 like protein
PF17753	0	1	1	2	2	0	2	Ig-fold domain
PF17786	1	7	6	3	4	1	2	Mannosidase Ig/CBM-like domain
PF00200	1	1	1	2	1	1	2	Disintegrin
PF13574	1	1	1	2	1	1	2	Metallo-peptidase family M12B Reprolysin-like
PF13582	1	2	2	2	3	1	2	Metallo-peptidase family M12B Reprolysin-like
PF13583	1	2	2	2	1	1	2	Metallo-peptidase family M12B Reprolysin-like
PF01239	1	1	1	3	3	2	4	Protein prenyltransferase alpha subunit repeat
PF11522	1	1	1	2	1	1	2	Yeast phosphatidylinositol-4-OH kinase Pik1
PF21245	1	1	1	2	1	1	2	PI4KB/PIK1, accessory (PIK) domain
PF28357	1	2	2	3	2	1	2	Domain of unknown function (DUF8383)
PF07171	0	0	0	0	1	0	2	MlrC C-terminus
PF07364	0	0	0	0	1	0	2	Metallopeptidase family M81
PF23190	1	1	1	4	3	4	4	TRPY1 N-terminal linker helical domain
PF00871	1	1	1	2	1	1	2	Acetokinase family
PF13535	0	0	0	0	0	0	1	ATP-grasp domain
PF18130	0	0	0	0	0	0	1	ATP-grasp N-terminal domain
PF05346	1	1	1	1	1	1	2	Eukaryotic membrane protein family
PF17800	1	1	1	1	1	1	3	Nucleoplasmin-like domain
PF14377	2	2	2	2	3	2	4	Ubiquitin binding region
PF16727	1	1	1	1	1	1	2	DNA repair protein REV1 C-terminal domain
PF21999	1	1	1	1	1	1	2	DNA polymerase-iota, thumb domain
PF14420	5	4	5	5	2	1	5	Clr5 domain
PF02602	1	1	1	1	2	1	2	Uroporphyrinogen-III synthase HemD
PF21803	0	0	0	0	0	0	2	Nab2-type CCCH zinc finger 4
PF22683	1	0	0	1	1	1	2	Nab2-like CCCH zinc finger
PF00393	4	4	4	1	4	3	5	6-phosphogluconate dehydrogenase, C-terminal domain
PF12751	1	0	0	1	0	0	2	Vacuolar segregation subunit 7
PF00977	2	2	2	2	2	2	3	Histidine biosynthesis protein
PF08375	1	1	1	1	1	1	2	Proteasome regulatory subunit C-terminal
PF25573	1	1	1	1	1	1	2	PSMD3-like, N-terminal TPR repeats
PF04438	3	3	3	3	3	3	4	HIT zinc finger
PF04442	1	1	1	1	1	1	2	Cytochrome c oxidase assembly protein CtaG/Cox11
PF02873	1	1	1	0	0	0	2	UDP-N-acetylenolpyruvoylglucosamine reductase, C-terminal domain
PF06772	1	1	1	1	5	1	3	Bacterial low temperature requirement A protein (LtrA)
PF02755	1	1	1	0	2	0	1	RPEL repeat
PF01036	4	5	5	1	5	3	3	Bacteriorhodopsin-like protein
PF01191	1	1	1	1	1	1	2	RNA polymerase Rpb5, C-terminal domain
PF03871	1	1	1	1	1	1	2	RNA polymerase Rpb5, N-terminal domain
PF00731	1	1	1	1	1	1	2	AIR carboxylase
PF17769	1	1	1	1	1	1	2	Phosphoribosylaminoimidazole carboxylase C-terminal domain
PF22660	1	1	1	1	1	1	2	Ribonucleotide synthetase preATP-grasp domain
PF10419	1	1	1	1	1	0	1	TFIIIC subunit triple barrel domain
PF05705	3	4	5	2	2	0	1	Eukaryotic protein of unknown function (DUF829)
PF04821	1	1	1	1	1	1	2	Timeless protein
PF05029	1	1	1	1	1	1	2	Timeless-like, PAB domain
PF27570	1	1	1	1	1	1	2	PF3D7_0210200 fifth domain
PF00742	1	1	1	1	1	1	2	Homoserine dehydrogenase
PF13300	1	1	1	1	1	1	2	Domain of unknown function (DUF4078)
PF08058	1	2	2	1	2	1	2	Nuclear pore complex component
PF09791	2	1	1	1	1	1	2	Oxidoreductase-like protein, N-terminal
PF01853	2	2	2	3	2	3	4	MOZ/SAS family
PF17772	3	3	3	2	4	3	6	MYST family zinc finger domain
PF01223	1	1	1	1	1	1	2	DNA/RNA non-specific endonuclease
PF01733	1	1	0	1	0	0	1	Nucleoside transporter
PF01988	2	2	2	0	3	0	3	VIT family
PF17254	1	1	1	1	2	1	2	Family of unknown function (DUF5321)
PF01182	4	2	2	2	3	2	4	Glucosamine-6-phosphate isomerases/6-phosphogluconolactonase
PF04468	1	1	1	1	1	1	2	PSP1 C-terminal conserved region
PF06658	1	1	1	1	2	2	2	Protein of unknown function (DUF1168)
PF02893	2	2	2	1	2	2	3	GRAM domain
PF03033	7	8	8	3	2	5	2	Glycosyltransferase family 28 N-terminal domain
PF02637	1	1	1	0	1	1	2	GatB domain
PF02934	1	1	1	1	1	1	2	GatB/GatE catalytic domain
PF15511	2	1	1	3	1	2	2	Centromere kinetochore component CENP-T histone fold

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF00125	8	9	9	11	8	8	9	Core histone H2A/H2B/H3/H4 domain
PF09810	1	1	1	1	2	1	2	Exonuclease V - a 5' deoxyribonuclease
PF12624	1	1	1	1	1	0	2	VPS13-like family N-terminal region
PF25033	1	1	1	1	1	0	2	VPS13-like family middle region
PF25036	1	1	1	1	1	1	2	Vacuolar-sorting associated protein 13, adaptor binding domain
PF11911	1	1	1	1	2	1	2	Protein of unknown function (DUF3429)
PF05348	1	1	1	1	2	1	2	Proteasome maturation factor UMP1
PF04981	1	1	1	1	1	1	2	NMD3 family
PF21192	1	1	1	1	1	0	2	NMD3 OB-fold domain
PF21193	1	1	1	1	1	1	2	NMD3 SH3 domain
PF14661	1	1	1	1	1	1	2	HAUS augmin-like complex subunit 6 N-terminus
PF12917	1	1	1	1	1	0	3	5'-deoxynucleotidase YfbR-like
PF13023	1	1	1	2	1	1	3	HD domain
PF07904	1	1	1	1	2	1	2	Chromatin modification-related protein EAF7
PF18400	1	1	1	1	1	0	2	Thioredoxin-like domain
PF18401	1	1	1	1	1	0	2	Thioredoxin-like domain
PF01592	1	1	1	1	1	1	2	NifU-like N terminal domain
PF18158	1	1	1	2	2	1	2	Adaptive response protein AidB N-terminal domain
PF12090	1	2	2	1	1	1	2	Spt20, SEP domain
PF11917	0	0	0	1	2	1	2	Protein of unknown function (DUF3435)
PF12273	2	3	3	2	6	2	2	Chitin synthesis regulation, resistance to Congo red
PF10516	1	1	1	1	1	2	2	SHNi-TPR
PF12767	1	1	1	1	1	1	1	Transcriptional regulator of RNA polII, SAGA, subunit
PF08211	1	1	1	1	1	1	2	Cytidine and deoxycytidylate deaminase zinc-binding region
PF07743	1	1	1	1	1	1	2	HSCB C-terminal oligomerisation domain
PF12353	1	1	1	1	1	1	2	Eukaryotic translation initiation factor 3 subunit G
PF09369	1	1	1	1	1	1	2	MrfA Zn-binding domain
PF22982	1	1	1	1	1	1	2	ATP-dependent helicase HRQ1, winged helix domain
PF00002	0	0	0	5	3	0	5	7 transmembrane receptor (Secretin family)
PF08653	1	1	1	1	1	1	2	DASH complex subunit Dam1
PF01426	4	3	4	4	3	5	3	BAH domain
PF21403	1	1	1	1	1	1	1	OTU1, UBXL domain
PF24560	2	2	2	0	2	2	1	Ubiquitin thioesterase OTU1, C-terminal C2H2-type zinc finger
PF05002	1	1	1	1	1	1	2	SGS domain
PF01368	1	3	3	2	3	2	6	DHH family, N-terminal domain
PF02833	2	1	1	1	3	1	2	DHHA2 domain
PF03803	1	1	1	0	1	2	2	Scramblase
PF14748	4	3	3	3	3	1	2	Pyrroline-5-carboxylate reductase dimerisation
PF00484	1	1	1	4	1	1	5	Carbonic anhydrase
PF08148	2	2	2	2	3	2	2	DSHCT (NUC185) domain
PF13234	2	2	2	2	3	0	4	Mtr4-like, beta-barrel domain
PF21408	2	2	2	2	3	1	3	Exosome RNA helicase MTR4-like, stalk
PF15159	2	1	1	1	1	1	2	Phosphatidylinositol N-acetylglucosaminyltransferase subunit Y
PF07574	1	1	1	1	1	1	2	Nse1 non-SMC component of SMC5-6 complex
PF08746	1	1	1	1	1	1	2	RING-like domain
PF10096	0	2	2	1	0	0	1	Uncharacterized protein conserved in bacteria (DUF2334)
PF21236	1	1	1	2	2	2	2	26S proteasome regulatory subunit 7, OB domain
PF05132	0	0	0	1	1	1	2	RNA polymerase III RPC4
PF02359	1	1	1	1	1	1	2	Cell division protein 48 (CDC48), N-terminal domain
PF02933	2	2	2	2	2	2	4	Cell division protein 48 (CDC48), domain 2
PF24385	1	1	1	1	2	1	2	ATP-dependent RNA helicase DHX29, DSRM-like
PF26026	1	1	1	1	1	1	2	C-terminal domain in RNA helicases
PF27606	1	1	1	1	2	1	2	Ucp12-like, UBA domain
PF25539	1	3	3	1	4	0	2	Bacterial/Fungal Bestrophin protein
PF04841	1	1	1	1	1	1	2	Vps16, N-terminal region
PF06046	1	1	1	1	1	1	2	Exocyst complex component Sec6
PF00327	2	2	2	2	3	2	4	Ribosomal protein L30p/L7e
PF01583	2	2	2	3	2	2	4	Adenylylsulphate kinase
PF01747	1	1	1	1	1	1	2	ATP-sulfurylase
PF14306	1	1	1	1	1	1	2	PUA-like domain
PF01507	1	1	1	2	3	3	3	Phosphoadenosine phosphosulfate reductase domain
PF01984	1	1	1	1	1	1	2	Double-stranded DNA-binding domain
PF05019	1	1	1	1	1	1	2	Coenzyme Q (ubiquinone) biosynthesis protein Coq4
PF02558	10	6	6	8	11	4	9	Ketopantoate reductase PanE/ApbA
PF08546	11	6	6	9	11	4	9	Ketopantoate reductase PanE/ApbA C terminal
PF22749	1	1	1	2	1	1	2	Arb2 domain
PF00253	3	2	2	3	4	2	3	Ribosomal protein S14p/S29e
PF01777	1	1	1	1	1	1	2	Ribosomal L27e protein family
PF18132	3	3	3	2	4	3	4	Tyrosinase C-terminal domain
PF12409	1	1	1	2	1	0	3	P5-type ATPase cation transporter
PF08068	1	1	1	1	3	1	2	DKCLD (NUC011) domain
PF16198	3	1	1	1	3	1	2	tRNA pseudouridylate synthase B C-terminal domain
PF04303	2	3	3	3	4	0	2	PrpF protein
PF02464	1	1	1	0	1	1	2	Competence-damaged protein
PF00211	1	1	1	1	2	1	2	Adenylate and Guanylate cyclase catalytic domain
PF23598	0	0	0	1	2	0	1	Leucine-rich repeat region
PF07291	0	0	0	0	0	0	2	Methylamine utilisation protein MauE
PF07681	0	0	0	0	0	0	2	DoxX
PF13564	0	0	0	0	0	0	2	DoxX-like family
PF25129	1	1	1	1	1	0	2	Pyr4-like transmembrane terpene cyclases
PF05088	1	1	1	1	3	0	2	Bacterial NAD-glutamate dehydrogenase, catalytic domain
PF06881	1	1	1	1	1	1	2	RNA polymerase II transcription factor SIII (Elongin) subunit A
PF02970	1	1	1	1	1	0	2	Tubulin binding cofactor A
PF21128	1	1	1	1	1	1	2	MCM4, winged helix domain
PF05615	1	1	1	1	1	1	3	Tho complex subunit 7
PF14328	1	1	1	1	2	1	2	Domain of unknown function (DUF4385)
PF13500	1	2	2	0	2	1	1	AAA domain
PF02840	1	1	1	1	1	1	2	Prp18 domain
PF06487	1	1	1	0	1	1	2	Sin3 associated polypeptide p18 (SAP18)
PF10645	1	1	1	0	2	3	3	Carbohydrate binding
PF16641	0	0	0	1	0	0	2	CLIP1 zinc knuckle
PF03126	1	1	1	1	1	3	2	Plus-3 domain
PF02915	0	0	0	0	0	1	2	Rubrerythrin
PF03232	1	1	1	1	2	1	2	Ubiquinone biosynthesis protein COQ7
PF05724	1	1	1	1	1	1	2	Thiopurine S-methyltransferase (TPMT)
PF08323	1	4	4	1	3	1	2	Starch synthase catalytic domain
PF26108	1	4	4	0	1	0	2	Mok13-like, GH beta-sandwich domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF26111	1	4	4	0	3	0	2	Mok13, Ig-like beta-sandwich domain
PF26114	1	4	4	0	3	0	2	Mok13, second Ig-like beta-sandwich domain
PF26122	1	4	4	0	3	0	2	Mok13-like, CBM domain
PF26127	1	4	4	0	3	0	1	Mok13-like, transmembrane domain
PF26775	1	4	4	0	3	0	2	Mok13-like, helix-turn-helix domain
PF00682	2	3	3	4	4	1	5	HMGL-like
PF04893	3	3	3	3	3	3	5	Yip1 domain
PF10604	1	3	3	1	3	1	1	Polyketide cyclase / dehydrase and lipid transport
PF01450	1	1	1	1	1	1	1	Ketol-acid reductoisomerase, C-terminal domain
PF07991	1	2	2	1	1	1	1	Acetohydroxy acid isomeroreductase, NADPH-binding domain
PF04935	1	1	1	1	1	1	2	Surfeit locus protein 6
PF15459	1	1	1	1	1	1	2	60S ribosome biogenesis protein Rrp14
PF09359	3	2	2	3	3	2	4	VTC domain
PF05180	1	1	1	1	2	2	2	DNL zinc finger
PF08606	1	1	1	1	1	1	2	Prp19/Pso4-like
PF04387	3	1	1	1	1	1	2	Protein tyrosine phosphatase-like protein, PTPLA
PF01379	1	2	2	2	1	1	2	Porphobilinogen deaminase, dipyromethane cofactor binding domain
PF14538	1	1	1	1	2	1	2	Raptor N-terminal CASPase like domain
PF01344	7	4	4	5	6	4	11	Kelch motif
PF07646	4	2	2	5	4	3	6	Kelch motif
PF24681	9	7	7	9	13	7	13	KLHDC2/KLHL20/DRC7 Kelch-repeats domain
PF07978	1	1	1	1	1	1	2	NIPSNAP
PF01165	1	1	1	0	1	1	2	Ribosomal protein S21
PF14852	1	1	1	1	2	1	2	Fis1 N-terminal tetratricopeptide repeat
PF14853	1	1	1	1	2	1	2	Fis1 C-terminal tetratricopeptide repeat
PF08286	1	1	1	1	1	1	2	Spc24 subunit of Ndc80
PF01026	3	2	2	3	4	1	6	TatD related DNase
PF16503	1	1	1	1	1	1	2	Zinc-ribbon
PF28564	0	0	0	1	0	0	2	Genetic interactor of prohibitins 3 N-terminal domain
PF05637	2	2	2	2	3	4	4	galactosyl transferase GMA12/MNN10 family
PF23550	1	1	1	1	1	1	2	DNA repair protein rhp7 treble clef domain
PF10000	0	1	1	1	1	0	2	ACT domain
PF06480	1	1	1	1	1	0	2	FtsH Extracellular
PF05673	0	0	0	0	0	0	1	Protein of unknown function (DUF815)
PF26131	1	1	1	3	3	2	2	PAS-like domain
PF01773	1	1	1	1	2	1	2	Na+ dependent nucleoside transporter N-terminus
PF07662	1	1	1	1	2	1	2	Na+ dependent nucleoside transporter C-terminus
PF07670	1	1	1	1	2	1	2	Nucleoside recognition
PF24616	1	1	1	1	1	2	4	Domain of unknown function (DUF7624)
PF02223	1	1	1	1	1	2	2	Thymidylate kinase
PF01541	1	1	1	1	0	0	2	GIY-YIG catalytic domain
PF21202	1	1	1	1	2	0	2	Structure-specific endonuclease subunit SLX1, C-terminal
PF01722	4	3	3	4	3	2	7	BolA-like protein
PF01192	1	1	1	1	2	1	2	RNA polymerase Rpb6
PF05890	1	1	1	2	1	1	2	Eukaryotic rRNA processing protein EBP2
PF06825	1	1	1	1	1	1	2	Heat shock factor binding protein 1
PF08614	2	1	1	1	1	1	2	Autophagy protein 16 (ATG16)
PF16450	5	5	5	5	6	5	8	Proteasomal ATPase OB C-terminal domain
PF09497	1	1	1	1	1	2	2	Transcription mediator complex subunit Med12
PF03669	1	1	1	1	1	0	1	PAT complex subunit Asterix
PF06428	1	2	2	2	1	2	4	GDP/GTP exchange factor Sec2p
PF25555	1	1	1	1	1	1	2	Rabin 8-like C-terminal domain
PF02630	1	1	1	1	1	1	2	SCO1/SenC
PF27955	2	1	1	1	2	1	2	C1604.12 helical domain
PF10791	1	1	1	1	2	1	2	Mitochondrial F1-F0 ATP synthase subunit F of fungi
PF04800	1	1	1	1	1	2	2	NADH dehydrogenase ubiquinone Fe-S protein 4
PF03070	2	2	2	1	1	3	4	TENA/THI-4/PQQC family
PF03600	2	2	2	2	3	1	6	Citrate transporter
PF28480	2	1	1	1	3	2	4	Conidiation-specific protein 8
PF04056	2	2	2	2	2	3	4	Ssl1-like
PF07975	1	1	1	1	1	1	2	TFIIH C1-like domain
PF12584	1	1	1	1	1	3	2	Trafficking protein particle complex subunit 10, TRAPPC10
PF24965	1	1	1	1	1	3	2	TRS130-like four helical bundle domain
PF00166	1	1	1	1	1	0	2	Chaperonin 10 Kd subunit
PF25455	1	1	0	1	1	1	2	CAF17, C-terminal beta-barrel domain
PF01596	2	4	4	3	4	2	4	O-methyltransferase
PF13578	2	4	4	3	4	2	4	Methyltransferase domain
PF10639	1	1	1	1	1	1	2	Putative transmembrane family 234
PF15409	1	1	1	2	2	1	2	Pleckstrin homology domain
PF28419	1	1	1	1	1	1	2	WetA C-terminal domain
PF00037	3	2	2	2	3	2	3	4Fe-4S binding domain
PF23588	2	1	2	2	1	1	2	ATP-dependent helicase CHD1-2/hrp3 HTH domain
PF13365	2	1	1	4	1	1	4	Trypsin-like peptidase domain
PF09990	1	1	1	0	1	2	2	Predicted membrane protein (DUF2231)
PF06108	1	1	1	1	1	0	4	Protein of unknown function (DUF952)
PF26147	1	1	1	1	3	1	2	YMC0/YMC35 alpha/beta hydrolase domain
PF10395	0	1	1	1	1	0	2	Utp8, N-terminal beta propeller
PF13127	1	1	1	1	1	1	2	Protein of unknown function (DUF3955)
PF04229	1	2	2	1	2	0	1	GrpB protein
PF00113	1	2	2	1	2	1	3	Enolase, C-terminal TIM barrel domain
PF03952	1	2	2	1	3	1	3	Enolase, N-terminal domain
PF20974	2	2	2	3	4	3	1	tRNA synthetases class I (E and Q), anti-codon binding domain
PF11931	1	1	1	1	1	1	2	SF3a60/Prp9 C-terminal
PF12108	1	1	1	1	1	1	2	Splicing factor SF3a60 binding domain
PF16837	1	1	1	1	1	1	2	Pre-mRNA-splicing factor SF3A3, of SF3a complex, Prp9
PF07930	0	1	1	0	1	0	2	D-aminopeptidase, domain B
PF05148	1	1	1	1	1	0	2	Hypothetical methyltransferase
PF00303	1	1	1	1	1	1	2	Thymidylate synthase
PF02436	0	0	0	0	1	1	2	Conserved carboxylase domain
PF25917	0	0	0	0	2	1	2	RND MFP, barrel-sandwich hybrid domain
PF08367	1	1	1	1	1	2	2	Peptidase M16C associated
PF22516	1	1	1	1	1	2	2	PreP C-terminal domain
PF09728	1	1	1	2	1	1	2	Myosin-like coiled-coil protein
PF03576	0	0	0	1	1	0	2	Peptidase family S58
PF08502	1	1	1	1	1	1	2	LeuA allosteric (dimerisation) domain
PF22615	1	1	1	1	1	1	2	Alpha-isopropylmalate synthase, post-catalytic domain-like
PF07572	0	0	0	1	1	1	2	Bucentaur or craniofacial development

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF08726	1	1	1	2	1	1	2	Ca2+ insensitive EF hand
PF07676	0	0	1	1	7	0	2	WD40-like Beta Propeller Repeat
PF10471	0	1	1	0	0	1	2	Anaphase-promoting complex APC subunit CDC26
PF07047	1	1	1	1	2	1	2	Optic atrophy 3 protein (OPA3)
PF10444	2	2	1	1	1	2	2	Nbl1 / Borealin N terminal
PF03764	3	3	3	3	4	3	5	Elongation factor G, domain IV
PF27702	1	1	1	0	1	0	2	Uncharacterised conserved protein UCP007778
PF01187	0	0	0	1	1	0	2	Macrophage migration inhibitory factor (MIF)
PF01922	1	1	1	1	1	1	2	SRP19 protein
PF00158	1	2	2	3	2	2	3	Sigma-54 interaction domain
PF17871	1	2	2	2	2	2	4	AAA lid domain
PF23569	0	1	0	1	0	0	2	SMAX1 nucleotide binding domain
PF13254	1	2	1	1	1	0	2	Family of unknown function (DUF4045)
PF03055	2	2	2	7	4	2	7	Retinal pigment epithelial membrane protein
PF08558	1	1	1	1	1	1	2	Telomere repeat binding factor (TRF)
PF00485	5	1	1	5	2	0	4	Phosphoribulokinase / Uridine kinase family
PF00728	3	2	2	2	2	2	2	Glycosyl hydrolase family 20, catalytic domain
PF14845	2	1	2	1	1	2	2	beta-acetyl hexosaminidase like
PF07808	1	1	1	1	1	1	1	RED-like protein N-terminal region
PF17242	1	1	1	1	1	1	1	Disordered region of unknown function (DUF5315)
PF22943	1	1	1	1	2	1	1	Putative helix-turn-helix domain
PF09248	0	1	1	1	3	0	3	Domain of unknown function (DUF1965)
PF02545	1	1	1	1	2	1	2	Maf-like protein
PF02015	1	2	2	1	0	0	2	Glycosyl hydrolase family 45
PF23549	0	0	0	0	0	0	1	GRF-like zinc ribbon domain
PF28379	1	1	1	2	1	1	2	Acyl-CoA N-acyltransferase verG N-terminal domain
PF13976	0	0	0	1	0	0	1	GAG-pre-integrase domain
PF02005	1	1	1	1	1	1	2	N2,N2-dimethylguanosine tRNA methyltransferase
PF10311	1	1	1	1	1	0	2	Increased loss of mitochondrial DNA protein 1
PF01244	2	2	2	7	4	2	2	Membrane dipeptidase (Peptidase family M19)
PF06644	2	2	2	1	1	1	2	ATP11 protein
PF08704	1	1	1	2	2	0	2	tRNA methyltransferase complex GCD14 subunit
PF00467	2	2	2	3	1	4	5	KOW motif
PF22682	1	1	1	1	1	1	2	Large ribosomal subunit protein uL24m
PF04658	1	1	1	1	1	1	2	TAFII55 protein conserved region
PF03997	1	1	1	1	1	1	2	VPS28 protein
PF03715	1	1	1	1	1	1	1	Noc2p family
PF03998	1	1	1	1	1	1	2	Utp11 protein
PF01483	1	1	1	1	1	1	4	Proprotein convertase P-domain
PF01028	1	2	2	1	1	2	2	Eukaryotic DNA topoisomerase I, catalytic core
PF02919	1	2	2	1	1	1	2	Eukaryotic DNA topoisomerase I, DNA binding fragment
PF14370	1	2	2	1	1	2	2	C-terminal topoisomerase domain
PF00231	1	1	1	1	1	1	2	ATP synthase
PF10313	1	1	1	2	1	1	2	Uncharacterised protein domain (DUF2415)
PF01232	2	2	2	1	1	1	2	Mannitol dehydrogenase Rossmann domain
PF08125	2	2	2	1	1	1	2	Mannitol dehydrogenase C-terminal domain
PF21266	1	1	1	1	1	1	2	RRP4, S1 domain
PF25438	1	1	1	3	1	1	2	Domain of unknown function (DUF7896)
PF01016	2	1	1	1	1	1	2	Ribosomal L27 protein
PF05899	3	4	5	6	4	1	3	EutQ-like cupin domain
PF18261	1	1	1	1	1	1	2	Rpn9 C-terminal helix
PF22037	1	1	1	1	1	1	2	PSD13 N-terminal repeats
PF04603	1	1	1	1	1	0	2	Ran-interacting Mog1 protein
PF02990	2	2	2	2	2	2	4	Endomembrane protein 70
PF05328	0	1	0	1	1	1	2	CybS, succinate dehydrogenase cytochrome B small subunit
PF06978	1	1	1	1	2	1	2	Ribonucleases P/MRP protein subunit POP1, N-terminal
PF08170	1	1	1	1	2	1	2	POPLD (NUC188) domain
PF22770	1	1	1	1	2	1	2	POP1 C-terminal domain
PF02891	1	2	2	2	3	2	2	MIZ/SP-RING zinc finger
PF14324	1	1	1	2	1	1	2	PINIT domain
PF10338	2	1	1	1	1	1	1	YBL028C ribosome biogenesis factor, N-terminal domain
PF11262	1	1	1	1	1	1	2	Transcription factor/nuclear export subunit protein 2
PF11732	1	1	1	1	1	1	2	Transcription- and export-related complex subunit
PF16134	1	1	1	1	1	1	2	THO complex subunit 2 N-terminus
PF01246	2	2	2	2	2	2	4	Ribosomal protein L24e
PF01929	1	1	1	1	1	1	1	Ribosomal protein L14
PF19026	2	2	2	2	2	2	4	HYPK UBA domain
PF05873	1	1	1	1	1	1	2	ATP synthase D chain, mitochondrial (ATP5H)
PF25037	0	0	0	1	0	1	2	Intermembrane lipid transfer protein VPS13, C-terminal
PF01512	1	2	2	1	1	1	2	Nuo51 FMN-binding domain
PF10531	1	2	2	1	1	1	2	SLBB domain
PF10589	1	2	2	1	1	1	2	NADH-ubiquinone oxidoreductase-F iron-sulfur binding region
PF22461	1	2	2	1	1	1	2	SLBB domain
PF15786	1	1	1	1	2	1	2	PET assembly of cytochrome c oxidase, mitochondrial
PF03179	1	1	1	1	2	1	2	Vacuolar (H+)-ATPase G subunit
PF13523	2	2	2	3	3	1	2	Acetyltransferase (GNAT) domain
PF00766	1	1	1	2	1	1	2	Electron transfer flavoprotein FAD-binding domain
PF01012	2	2	2	3	2	2	4	Electron transfer flavoprotein domain
PF23143	1	1	1	1	2	1	2	P5A-ATPase, transmembrane helical hairpin
PF23097	1	1	1	1	1	1	2	Nucleolar protein 10-like, second domain
PF23098	3	2	2	2	4	2	2	Nucleolar protein 10-like, N-terminal domain
PF06333	1	1	1	1	1	0	2	Mediator complex subunit 13 C-terminal domain
PF11597	1	1	1	1	1	0	2	Mediator complex subunit 13 N-terminal
PF18296	1	1	1	1	1	1	2	MID domain of medPIWI
PF05033	1	1	1	1	2	0	3	Pre-SET motif
PF05997	1	1	1	1	1	1	2	Nucleolar protein,Nop52
PF08144	1	1	1	1	1	1	2	CPL (NUC119) domain
PF21312	0	1	1	1	1	1	2	Origin recognition complex subunit 1 C-terminal winged HTH domain
PF07823	0	0	0	0	2	1	2	Cyclic phosphodiesterase-like protein
PF12417	0	0	0	4	0	0	2	Zinc finger protein
PF17050	1	1	1	1	1	0	2	Altered inheritance of mitochondria 5
PF01196	1	1	1	1	1	1	2	Ribosomal protein L17
PF24586	1	1	1	1	1	0	2	Domain of unknown function (DUF7611)
PF24587	1	1	1	1	1	1	2	Domain of unknown function (DUF7612)
PF24588	1	1	1	1	1	1	2	Domain of unknown function (DUF7613)
PF24589	1	1	1	1	1	1	2	Domain of unknown function (DUF7614)
PF12569	1	1	1	1	1	1	2	N-terminal acetyltransferase A, auxiliary subunit

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF05719	1	1	1	1	1	1	2	Golgi phosphoprotein 3 (GPP34)
PF00089	1	1	1	6	1	2	2	Trypsin
PF00595	1	1	1	0	2	1	2	PDZ domain
PF12812	1	1	1	1	1	1	2	PDZ-like domain
PF17820	2	3	3	1	2	2	4	PDZ domain
PF05178	1	1	1	1	1	1	2	KRI1-like family
PF12936	1	1	1	1	1	1	2	KRI1-like family C-terminal
PF06968	2	1	1	0	1	1	2	Biotin and Thiamin Synthesis associated domain
PF08174	1	1	1	3	2	2	3	Cell division protein anillin
PF01282	1	1	1	1	1	1	2	Ribosomal protein S24e
PF12738	3	2	2	5	5	5	6	twin BRCT domain
PF02265	2	2	2	1	2	1	2	S1/P1 Nuclease
PF22980	2	2	2	3	0	2	4	Myb-like DNA-binding domain
PF08232	2	2	2	1	2	1	3	Striatin family
PF15375	1	1	1	0	1	1	2	40S small subunit processome assembly factor 1
PF12755	1	1	2	1	1	1	3	Vacuolar 14 Fab1-binding region
PF07264	2	2	2	1	1	1	2	Sulfate transporter CysZ/Etoposide-induced protein 2.4
PF01786	1	1	1	1	1	1	3	Alternative oxidase
PF00708	1	2	2	1	2	1	2	Acylphosphatase
PF09729	2	2	2	2	2	2	1	Gti1/Pac2 family
PF24800	1	2	3	0	1	0	2	Domain of unknown function (DUF7702)
PF00466	2	2	2	2	2	1	4	Ribosomal protein L10
PF17777	2	2	2	2	2	1	1	Insertion domain in 60S ribosomal protein L10P
PF04734	1	1	1	1	1	1	2	Neutral/alkaline non-lysosomal ceramidase, N-terminal
PF17048	1	1	1	1	1	1	2	Neutral/alkaline non-lysosomal ceramidase, C-terminal
PF05700	1	1	1	1	2	1	2	Breast carcinoma amplified sequence 2 (BCAS2)
PF02197	1	1	1	0	1	1	2	Regulatory subunit of type II PKA R-subunit
PF05071	2	3	3	2	2	0	4	NADH ubiquinone oxidoreductase subunit NDUFA12
PF02374	1	1	1	1	2	1	2	Anion-transporting ATPase
PF13614	1	1	1	1	0	1	2	AAA domain
PF07534	1	1	1	3	1	2	2	TLDc domain
PF19038	1	1	1	1	2	1	1	Third Longin domain of FUZ, MON1 and HPS1
PF28142	1	1	1	1	1	1	2	SPBC1E8.03c N-terminal domain
PF12612	2	1	1	1	1	1	2	Tubulin folding cofactor D C terminal
PF23579	2	1	1	1	1	1	2	Tubulin-specific chaperone D-like, ARM repeat
PF25767	2	1	1	1	1	1	2	Tubulin-specific chaperone D-like, ARM repeats
PF09507	1	1	1	1	2	1	2	DNA polymerase subunit Cdc27
PF14222	1	1	1	1	2	0	2	Cell morphogenesis N-terminal
PF14225	1	2	2	1	2	1	3	Cell morphogenesis C-terminal
PF03568	1	1	1	1	1	1	2	Separin, protease domain
PF09731	0	0	0	1	0	1	2	Mitochondrial inner membrane protein
PF02569	1	1	1	1	2	1	2	Pantoate-beta-alanine ligase
PF01588	1	1	1	1	1	1	2	Putative tRNA binding domain
PF21972	1	1	1	1	1	1	2	Nuclear-export cofactor Arc1p
PF08577	1	1	1	1	1	1	2	PI31 proteasome regulator
PF11566	1	1	1	1	1	1	2	PI31 proteasome regulator N-terminal
PF05270	1	1	1	1	2	0	1	Alpha-L-arabinofuranosidase B (ABFB) domain
PF09206	2	1	1	0	3	0	1	Alpha-L-arabinofuranosidase B, catalytic
PF08227	2	2	2	0	3	0	2	DASH complex subunit Hsk3 like
PF12331	1	1	1	1	2	1	2	Rad26-like, helical repeats
PF21046	1	1	1	1	2	1	2	Rad26-like, C-terminal domain
PF21048	1	1	1	1	2	1	2	Rad26-like, N-terminal domain
PF01148	1	1	1	2	1	1	2	Cytidylyltransferase family
PF00343	1	1	1	1	1	1	2	Carbohydrate phosphorylase
PF13506	0	1	1	3	3	2	2	Glycosyl transferase family 21
PF02291	1	1	1	1	2	1	2	Transcription initiation factor IID, 31kD subunit
PF24465	1	1	1	0	1	1	2	Tri-helical domain
PF24962	1	1	1	0	1	1	2	Domain of unknown function (DUF7767)
PF02724	1	1	1	1	1	1	2	CDC45
PF09084	2	2	2	1	2	2	8	NMT1/THI5 like
PF00463	2	3	3	3	4	1	6	Isocitrate lyase family
PF03650	2	1	1	2	2	2	5	Mitochondrial pyruvate carriers
PF13431	2	1	1	0	1	3	2	Tetratricopeptide repeat
PF10356	0	0	0	0	0	0	1	Required for respiratory growth protein 7
PF11221	1	1	1	1	1	1	2	Subunit 21 of Mediator complex
PF00875	3	4	3	3	4	3	6	DNA photolyase
PF03441	3	4	3	3	4	3	6	FAD binding domain of DNA photolyase
PF03878	1	1	1	1	1	1	2	YIF1
PF04086	1	1	1	1	1	1	2	Signal recognition particle, alpha subunit, N-terminal
PF05007	1	1	1	1	1	1	2	Mannosyltransferase (PIG-M)
PF06728	1	1	1	2	2	0	6	GPI transamidase subunit PIG-U
PF02116	1	1	1	1	1	0	2	Fungal pheromone mating factor STE2 GPCR
PF08555	1	1	1	1	1	1	2	FAM32A
PF05743	1	1	1	1	1	1	2	UEV domain
PF09454	1	1	1	1	1	1	2	Vps23 core domain
PF00218	1	1	1	1	2	0	2	Indole-3-glycerol phosphate synthase
PF00697	1	1	1	1	2	0	2	N-(5'phosphoribosyl)anthranilate (PRA) isomerase
PF05676	1	1	1	1	1	1	2	NADH-ubiquinone oxidoreductase B18 subunit (NDUFB7)
PF03856	1	1	1	2	1	1	2	Beta-glucosidase (SUN family)
PF07529	3	3	3	2	2	2	6	HSA domain
PF24866	1	1	1	1	1	1	3	Domain of unknown function (DUF7732)
PF05147	1	1	1	1	1	1	2	Lanthionine synthetase C-like protein
PF07934	1	1	1	1	2	1	2	8-oxoguanine DNA glycosylase, N-terminal domain
PF04324	1	1	1	1	1	1	2	BFD-like [2Fe-2S] binding domain
PF13806	2	2	2	2	2	0	4	Rieske-like [2Fe-2S] domain
PF27021	1	1	1	1	1	1	2	BOS1/GOSR2/MEM11, N-terminal domain
PF09770	1	1	1	1	1	1	2	Topoisomerase II-associated protein PAT1
PF08147	1	1	1	1	1	1	2	DBP10CT (NUC160) domain
PF01369	4	5	5	6	6	3	6	Sec7 domain
PF12783	3	3	3	4	4	2	4	Mon2/Sec7/BIG1-like, HUS domain
PF00635	1	1	1	1	1	1	3	MSP (Major sperm protein) domain
PF12009	1	1	1	0	1	1	2	Telomerase ribonucleoprotein complex - RNA binding domain
PF04676	3	2	2	2	2	2	4	Protein similar to Cwf] C-terminus 2
PF04677	4	2	2	3	2	2	4	Protein similar to Cwf] C-terminal
PF04078	0	0	0	1	1	2	2	Cell differentiation family, Rcd1-like
PF13175	3	4	4	2	4	3	7	AAA ATPase domain
PF03467	1	1	1	1	1	1	2	Smg-4/UPF3 family

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF19277	1	1	1	1	1	1	2	Glycerol-3-phosphate acyltransferase C-terminal region
PF05051	1	1	1	1	1	1	2	Cytochrome C oxidase copper chaperone (COX17)
PF02516	1	1	1	1	1	1	2	Oligosaccharyl transferase STT3, N-terminal
PF00515	3	3	4	6	6	7	10	Tetratricopeptide repeat
PF13414	2	2	2	4	6	7	10	TPR repeat
PF02104	1	2	2	1	1	1	2	SURF1 family
PF11970	3	4	4	1	4	1	4	G protein-coupled glucose receptor regulating Gpa2 C-term
PF00306	1	1	1	1	1	1	2	ATP synthase alpha/beta chain, C terminal domain
PF06127	1	1	1	1	1	1	2	2-hydroxy-palmitic acid dioxygenase Mpo1-like
PF07484	0	0	0	0	0	0	1	Phage Tail Collar Domain
PF13304	1	1	1	0	0	0	2	AAA domain, putative AbiEii toxin, Type IV TA system
PF08231	1	1	1	1	1	1	1	SYF2 splicing factor
PF01082	1	1	1	1	0	0	1	Copper type II ascorbate-dependent monooxygenase, N-terminal domain
PF03351	1	1	1	1	0	0	1	DOMON domain
PF03712	1	1	1	1	0	0	1	Copper type II ascorbate-dependent monooxygenase, C-terminal domain
PF08573	1	1	1	1	1	1	2	DNA endonuclease activator SAE2/CtIP C-terminus
PF09784	0	0	0	1	0	1	1	Mitochondrial ribosomal protein L31
PF23113	1	1	1	1	1	1	2	E3 ubiquitin-protein ligase MARCHF6-like, C-terminal domain
PF09088	1	1	1	1	1	1	2	MIF4G like
PF09090	1	1	1	1	1	1	2	MIF4G like
PF01125	1	1	1	1	2	1	2	Pre-mRNA-splicing factor BUD31
PF13892	1	1	1	1	1	1	2	DNA-binding domain
PF03098	2	3	3	0	3	1	2	Animal haem peroxidase
PF01869	0	0	0	0	0	0	2	BadF/BadG/BcrA/BcrD ATPase family
PF13580	0	0	0	0	0	0	1	SIS domain
PF22645	0	0	0	0	0	0	2	Glucokinase regulatory protein N-terminal SIS domain
PF07075	0	0	0	0	0	0	2	Exo-beta-N-acetylmuramidase NamZ, N-terminal
PF20732	0	0	0	0	0	0	2	Exo-beta-N-acetylmuramidase NamZ, C-terminal
PF10329	1	1	1	1	1	1	2	Region of unknown function (DUF2417)
PF13565	1	1	1	0	1	0	2	Homeodomain-like domain
PF13771	4	4	4	4	4	3	5	PHD-like zinc-binding domain
PF13832	4	4	4	4	4	3	5	PHD-zinc-finger like domain
PF10644	0	0	0	2	1	1	2	Misato Segment II tubulin-like domain
PF14881	0	0	0	1	1	0	2	Tubulin domain
PF09812	0	0	0	0	1	0	1	Mitochondrial ribosomal protein L28
PF01775	1	1	1	2	1	1	4	Ribosomal proteins 50S-L18Ae/60S-L20/60S-L18A
PF08530	4	3	3	2	2	1	4	X-Pro dipeptidyl-peptidase C-terminal non-catalytic domain
PF20776	1	1	1	1	1	1	2	SLS1 protein N-terminal domain
PF20777	0	0	0	0	0	0	1	SLS1 protein second KH domain
PF20778	1	1	1	1	1	1	2	SLS1 protein C-terminal beta barrel domain
PF00988	2	2	2	2	2	2	4	Carbamoyl-phosphate synthase small chain, CPSase domain
PF01248	4	4	5	5	6	4	9	Ribosomal protein L7Ae/L30e/S12e/Gadd45 family
PF04032	1	1	1	1	2	0	2	RNAse P Rpr2/Rpp21/SNM1 subunit domain
PF08209	1	1	1	0	1	1	2	Sgf11 (transcriptional regulation protein)
PF25773	1	1	1	1	1	1	2	ANAPC2-like, TPR repeats
PF22441	2	0	0	0	2	1	2	CLIC-like N-terminal domain
PF00056	3	3	3	3	2	2	5	lactate/malate dehydrogenase, NAD binding domain
PF02866	3	3	3	3	2	2	3	lactate/malate dehydrogenase, alpha/beta C-terminal domain
PF05426	0	0	0	2	0	0	1	Alginate lyase
PF22675	2	2	2	4	2	2	5	KHDC4/BBP-like, KH-domain type I
PF23469	3	2	3	2	3	2	5	KH-domain
PF10369	1	1	1	1	1	1	4	Small subunit of acetolactate synthase
PF22629	1	1	1	1	1	1	4	AHAS small subunit-like ACT domain
PF22786	1	1	1	1	2	1	2	Tag1 C-terminal domain
PF26150	1	1	1	1	2	1	2	Tag1-like fourth LEA-2 like domain
PF26153	1	1	1	1	2	1	2	Tag1-like fifth LEA-2 like domain
PF26174	1	1	1	1	2	1	2	Tag1-like first LEA-2 like domain
PF25757	1	1	1	1	1	2	2	Dynein axonemal assembly factor 5-like, TPR repeats
PF03483	2	2	2	1	3	1	2	B3/4 domain
PF03484	1	1	1	1	1	1	2	tRNA synthetase B5 domain
PF17759	1	1	1	1	1	1	2	Phenylalanyl tRNA synthetase beta chain CLM domain
PF18262	1	1	1	1	1	1	2	Phe-tRNA synthetase beta subunit B1 domain
PF00462	4	4	5	4	4	4	7	Glutaredoxin
PF02290	1	1	1	1	1	1	2	Signal recognition particle 14kD protein
PF17132	0	1	1	1	3	1	2	alpha-L-rhamnosidase
PF01805	1	2	2	2	2	2	4	Surp module
PF22466	1	1	1	1	1	1	2	PSF3 N-terminal domain
PF11919	1	1	1	1	1	1	2	Proteasome activator complex subunit 4-like, C-terminal
PF16507	1	1	1	1	1	1	2	Proteasome activator complex subunit 4, mid HEAT repeats region
PF16547	1	1	1	1	1	1	2	Proteasome-substrate-size regulator, N-terminal
PF01764	3	3	3	4	4	3	3	Lipase (class 3)
PF16123	1	2	2	1	1	1	3	Hydroxyacylglutathione hydrolase C-terminus
PF04281	1	1	1	1	1	1	2	Mitochondrial import receptor subunit Tom22
PF23459	1	1	1	1	1	2	2	RRP5 S1 domain
PF24685	1	1	1	1	1	0	2	RRP5 OB-fold domain
PF05742	1	1	1	1	1	2	2	Transport and Golgi organisation 2
PF03134	2	2	2	2	2	2	3	TB2/DP1, HVA22 family
PF08783	1	1	1	1	1	1	2	DWNN domain
PF13696	1	1	1	1	1	1	2	Zinc knuckle
PF03226	2	2	2	2	2	2	4	Yippee zinc-binding/DNA-binding /Mis18, centromere assembly
PF08766	5	3	3	3	4	4	4	DEK C terminal domain
PF13481	1	2	2	2	1	1	2	AAA domain
PF14520	1	1	1	1	1	3	2	Helix-hairpin-helix domain
PF11715	1	1	1	1	1	1	2	Nucleoporin Nup120/160, beta-propeller domain
PF21486	1	1	1	1	1	1	2	Nucleoporin NUP120, helical domain
PF23300	1	1	1	1	1	1	2	Nucleoporin Nup120, HEAT repeats
PF10334	3	2	2	3	2	2	4	Brefeldin A-sensitivity protein 4-like domain
PF10337	1	1	1	1	1	1	2	Putative ER transporter, 6TM, N-terminal
PF12519	1	1	1	1	1	1	2	Mitochondrial distribution and morphology protein 10
PF01465	1	2	2	1	1	1	2	GRIP domain
PF04063	1	1	1	1	1	1	2	Domain of unknown function (DUF383)
PF04064	1	1	1	1	1	1	2	Domain of unknown function (DUF384)
PF05496	1	1	1	2	3	1	2	Holliday junction DNA helicase RuvB P-loop domain
PF12002	1	1	1	1	2	1	2	MgsA AAA+ ATPase C terminal
PF16193	1	1	1	1	2	1	2	AAA C-terminal domain
PF18313	2	2	1	0	1	0	1	Thiolase-like protein type 1 additional C-terminal domain
PF10263	1	2	2	2	2	1	7	SprT-like family

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF00268	1	1	1	1	1	1	2	Ribonucleotide reductase, small chain
PF13422	1	1	1	1	3	1	2	Domain of unknown function (DUF4110)
PF24981	5	3	2	3	7	1	1	Attractin/LZTR1 beta-propeller
PF26747	1	1	1	1	1	1	2	AcrB ubiquitination network protein, Ig-like domain
PF28337	1	1	1	1	1	1	2	NNF2 middle helical domain
PF12708	3	3	3	2	8	4	5	Rhamnogalacturonase A/epimerase, pectate lyase-like
PF04802	2	1	1	2	1	1	2	Phosphatase 4 regulatory subunit 3
PF22972	2	1	1	2	1	1	2	EVH1-like domain in PP4R3 protein
PF09377	1	1	1	1	1	1	2	SBDS protein, domain II
PF20268	1	1	1	1	1	1	2	SBDS protein, C-terminal domain
PF23302	1	1	1	1	1	1	2	DNAJC9 HTH domain
PF04678	1	1	1	1	1	2	2	Mitochondrial calcium uniporter
PF10058	1	1	1	1	1	0	2	ER junction formation factor lunapark, zinc ribbon finger
PF08651	1	1	1	1	2	1	2	DASH complex subunit Duo1
PF00145	3	3	3	2	5	1	5	C-5 cytosine-specific DNA methylase
PF04911	1	0	0	1	1	1	1	ATP synthase j chain
PF08287	2	1	1	1	2	1	2	Spc19
PF11708	1	1	1	1	1	1	2	Pre-mRNA splicing Prp18-interacting factor
PF09118	3	2	2	1	4	1	1	Galactose oxidase-like, Early set domain
PF16755	1	1	1	1	1	1	2	NUP159/214 beta propeller
PF12465	1	1	1	1	1	1	2	Proteasome beta subunits C terminal
PF17110	1	1	1	1	1	1	2	Subunit 11 of the general transcription factor TFIIH
PF00436	1	1	1	1	1	1	2	Single-strand binding protein family
PF09816	1	1	1	1	1	1	2	RNA polymerase II transcription elongation factor
PF16420	1	1	1	1	1	1	1	Ubiquitin-like modifier-activating enzyme ATG7 N-terminus
PF05670	2	3	3	2	2	3	4	NFACT protein RNA binding domain
PF05833	1	1	1	1	1	0	2	NFACT N-terminal and middle domains
PF11923	1	1	1	1	1	1	2	NFACT protein C-terminal domain
PF05091	1	1	1	1	2	1	2	Eukaryotic translation initiation factor 3 subunit 7 (eIF-3)
PF04376	1	1	1	1	1	1	2	Arginine-tRNA-protein transferase, N terminus
PF04377	2	2	2	1	1	2	2	Arginine-tRNA-protein transferase, C terminus
PF22458	1	1	1	0	1	1	2	Methyltr_RsmF/B-like, ferredoxin-like domain
PF01466	1	1	1	1	1	2	2	Skp1 family, dimerisation domain
PF03931	2	2	2	2	2	2	3	Skp1 family, tetramerisation domain
PF01071	1	1	1	2	1	1	2	Phosphoribosylglycinamide synthetase, ATP-grasp (A) domain
PF02843	1	1	1	2	1	1	2	Phosphoribosylglycinamide synthetase, C domain
PF02844	1	1	1	2	1	1	2	Phosphoribosylglycinamide synthetase, N domain
PF04424	1	1	1	1	1	1	2	MINDY deubiquitinase
PF04921	1	1	1	1	1	1	2	XAP5, circadian clock regulator C-terminal domain
PF08551	0	1	1	2	2	1	2	Eukaryotic integral membrane protein (DUF1751)
PF23749	1	1	1	1	3	1	2	Domain of unknown function (DUF7165)
PF01625	3	2	2	1	3	2	2	Peptide methionine sulfoxide reductase
PF24554	1	1	1	1	2	1	2	Domain of unknown function (DUF7603)
PF03604	1	1	1	1	1	2	2	DNA directed RNA polymerase, 7 kDa subunit
PF02906	1	1	1	1	1	1	2	Iron only hydrogenase large subunit, C-terminal domain
PF14464	1	2	2	2	3	1	2	Prokaryotic homologs of the JAB domain
PF23594	1	1	1	1	3	0	2	26S proteasome regulatory subunit RPN11 C-terminal domain
PF01704	3	2	2	2	2	1	3	UTP--glucose-1-phosphate uridylyltransferase
PF02152	1	1	1	1	1	1	2	Dihydroneopterin aldolase
PF17830	1	1	1	1	1	1	2	STI1/HOP, DP domain
PF07540	1	1	1	1	1	1	2	Nucleolar complex-associated protein
PF03657	1	1	1	1	1	1	2	UPF0113 PUA domain
PF17833	1	1	1	1	1	1	2	NIP7/UPF0113, pre-PUA domain
PF15924	1	1	1	1	1	1	2	ALG11 mannosyltransferase N-terminus
PF25550	3	3	3	1	5	3	2	Domain of unknown function (DUF7928)
PF14612	1	1	1	1	1	1	2	IEC3 subunit of the Ino80 complex, chromatin re-modelling
PF24244	1	1	1	1	1	1	2	INO80 complex subunit 3-like, middle region
PF08652	1	1	1	1	1	1	2	RAI1 like PD-(D/E)XK nuclease
PF13824	1	1	1	1	1	1	2	Zinc-finger of mitochondrial splicing suppressor 51
PF04005	1	1	1	1	1	1	2	Hus1-like protein
PF02181	1	1	1	1	1	1	3	Formin Homology 2 Domain
PF06367	1	1	1	1	1	1	3	Diaphanous FH3 Domain
PF10396	1	1	1	2	2	2	2	GTP-binding protein TrmE N-terminus
PF12631	1	1	1	2	2	2	2	MnmE helical domain
PF01198	1	1	1	1	1	1	1	Ribosomal protein L31e
PF08426	1	1	1	1	1	1	2	ICE2
PF03690	1	2	2	2	1	2	4	Uncharacterised protein family (UPF0160)
PF01491	1	1	1	1	1	0	3	Frataxin-like domain
PF05207	2	2	2	2	3	1	3	CSL zinc finger
PF12152	1	1	1	1	1	1	1	Eukaryotic translation initiation factor 4G1
PF09458	1	1	1	1	1	3	5	H-type lectin domain
PF02136	3	2	2	2	2	3	6	Nuclear transport factor 2 (NTF2) domain
PF00996	2	2	2	2	2	2	2	GDP dissociation inhibitor
PF06984	1	1	1	1	1	1	2	Mitochondrial 39-S ribosomal protein L47 (MRP-L47)
PF16211	2	2	2	2	2	1	2	C-terminus of histone H2A
PF00800	1	1	1	1	0	1	4	Prephenate dehydratase
PF03463	1	1	1	1	1	1	2	eRF1 domain 1
PF18854	1	1	1	1	1	1	2	Bacterial archaeo-eukaryotic release factor family 10
PF03152	1	1	1	1	2	2	4	Ubiquitin fusion degradation protein UFD1, N-terminal subdomain 1
PF24842	2	2	2	2	2	2	4	Ubiquitin fusion degradation protein UFD1, N-terminal subdomain 2
PF06422	9	9	9	14	9	7	9	CDR ABC transporter
PF22698	1	1	1	1	1	1	2	Semialdehyde dehydrogenase, dimerisation domain
PF04180	1	1	1	1	1	1	2	Low temperature viability protein
PF01730	1	1	1	1	1	2	2	UreF
PF04101	1	1	1	1	1	0	2	Glycosyltransferase family 28 C-terminal domain
PF10213	1	1	1	1	1	1	2	Mitochondrial ribosomal subunit protein
PF06813	1	2	2	1	1	1	2	Nodulin-like
PF03348	0	0	0	1	1	2	2	Serine incorporator (Serinc)
PF08149	1	1	1	1	1	1	2	BING4CT (NUC141) domain
PF01627	2	2	2	1	1	1	4	Hpt domain
PF00623	3	3	3	3	3	3	5	RNA polymerase Rpb1, domain 2
PF04983	3	3	3	3	3	3	4	RNA polymerase Rpb1, domain 3
PF04997	3	3	3	3	3	3	4	RNA polymerase Rpb1, domain 1
PF05000	3	3	3	3	3	3	6	RNA polymerase Rpb1, domain 4
PF26253	0	1	1	0	2	0	1	RdRP, head domain
PF10032	1	1	1	1	2	1	1	Phosphate transport (Pho88)
PF24951	1	1	1	1	1	3	2	PAC1 LisH domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF21041	1	1	1	1	1	1	2	XMAP215/Dis1/CLASP, TOG domain
PF21042	1	1	1	1	1	1	2	Stu2, C-terminal segment
PF02460	2	2	2	2	4	2	3	Patched SSD
PF16414	1	1	1	1	2	1	2	Niemann-Pick C1 N terminus
PF22314	1	1	1	1	2	1	2	NPC1, middle luminal domain
PF10183	1	1	1	1	1	1	2	ESSS subunit of NADH:ubiquinone oxidoreductase (complex I)
PF02184	1	1	1	1	1	1	2	HAT (Half-A-TPR) repeat
PF23233	2	2	2	2	4	2	4	Pre-mRNA-splicing factor Syf1/CNRKL1 N-terminal HAT repeat
PF23240	5	4	4	4	4	4	7	PRP39 N-terminal HAT repeat
PF23241	3	2	2	2	2	2	3	PRP39 C-terminal HAT repeat
PF07942	2	2	2	2	2	1	2	Carnosine N-methyltransferase
PF16093	1	1	1	1	1	1	2	Proteasome assembly chaperone 4
PF04212	1	2	2	2	3	2	2	MIT (microtubule interacting and transport) domain
PF05843	3	2	2	2	2	2	4	Suppressor of forked protein (Suf)
PF05216	1	1	1	0	2	1	2	UNC-50 family
PF10355	3	3	3	1	4	4	4	Protein YTP1-like, C-terminal
PF05529	1	2	2	1	2	1	2	Bap31/Bap29 transmembrane region
PF18035	1	2	2	1	2	1	2	Bap31/Bap29 cytoplasmic coiled-coil domain
PF07021	1	1	1	0	6	1	2	Methionine biosynthesis protein MetW
PF05046	1	1	1	1	1	1	1	Mitochondrial large subunit ribosomal protein (Img2)
PF25574	2	1	1	2	2	1	2	Importin subunit beta-1-like, TPR repeats
PF28151	1	1	1	1	2	0	2	STT4, N-terminal TPR repeats
PF13679	2	2	2	1	1	1	2	Methyltransferase domain
PF09177	2	2	2	1	2	2	2	Syntaxin 6/10/61, N-terminal
PF00331	4	4	3	3	3	1	2	Glycosyl hydrolase family 10
PF23096	1	1	1	1	1	1	1	Proteasome activator complex subunit 4-like, HEAT repeat-like
PF03798	3	3	3	3	4	2	5	TLC domain
PF22468	1	1	1	1	1	1	2	ACT domain
PF02259	2	3	3	6	5	2	3	FAT domain
PF02260	3	4	4	6	6	2	4	FATC domain
PF08064	0	1	1	1	2	0	1	UME (NUC010) domain
PF23593	1	2	2	2	3	0	3	Serine/threonine-protein kinase ATR-like, HEAT repeats
PF25030	0	1	1	1	2	1	1	Serine/threonine-protein kinase ATR, M-HEAT region
PF14138	2	1	1	1	1	1	1	Cytochrome c oxidase assembly protein COX16
PF04157	2	2	2	2	2	2	3	EAP30/Vps36 family
PF03130	1	1	1	1	1	1	2	PBS lyase HEAT-like repeat
PF07933	1	1	1	1	1	1	2	Protein of unknown function (DUF1681)
PF05546	1	1	1	1	1	1	2	She9 / Mdm33 family
PF02403	2	2	2	3	2	2	4	Seryl-tRNA synthetase N-terminal domain
PF08122	1	1	1	2	1	2	2	NADH-ubiquinone oxidoreductase B12 subunit family
PF16906	1	1	1	1	1	2	2	Ribosomal proteins L26 eukaryotic, L24P archaeal
PF02373	5	5	5	5	6	7	7	JmjC domain, hydroxylase
PF03966	1	1	1	1	0	1	2	Trm112p-like protein
PF01740	6	5	5	4	3	1	5	STAS domain
PF16213	2	2	2	2	3	1	4	Mon2/Sec7/BIG1-like, dimerisation and cyclophilin-binding domain
PF25009	1	1	1	1	1	1	2	Domain of unknown function (DUF7785)
PF25289	1	1	1	1	1	1	2	Domain of unknown function (DUF7877)
PF00078	1	1	3	0	7	2	1	Reverse transcriptase (RNA-dependent DNA polymerase)
PF17917	0	0	0	0	2	1	1	RNase H-like domain found in reverse transcriptase
PF17919	0	0	0	0	2	1	1	RNase H-like domain found in reverse transcriptase
PF02550	1	1	1	1	1	1	2	Acetyl-CoA hydrolase/transferase N-terminal domain
PF13336	1	1	1	1	1	1	2	Acetyl-CoA hydrolase/transferase C-terminal domain
PF12854	1	1	1	1	3	1	2	PPR repeat
PF17177	1	0	0	2	0	1	2	Pentacotripeptide-repeat region of PRORP
PF24603	1	1	1	1	1	1	2	Tetratricopeptide repeat
PF05652	1	1	1	2	1	1	2	Scavenger mRNA decapping enzyme (DcpS) N-terminal
PF04081	1	1	1	1	1	2	2	DNA polymerase delta, subunit 4
PF08570	2	1	1	1	2	1	1	Protein of unknown function (DUF1761)
PF00885	1	0	0	0	0	0	2	6,7-dimethyl-8-ribityllumazine synthase
PF11764	1	1	1	1	1	1	2	COMPASS (Complex proteins associated with Set1p) component N
PF08701	1	1	1	1	1	1	2	GNL3L/Grn1 putative GTPase
PF10357	1	1	1	1	1	1	2	KIN17 WH-like domain
PF25095	1	1	1	1	1	0	2	KIN17 C2H2-type zinc finger domain
PF10262	1	1	1	1	1	0	2	Rdx family
PF01813	1	1	1	1	2	1	2	ATP synthase subunit D
PF23220	1	1	1	1	1	1	2	Pre-mRNA-splicing factor SYF1 middle HAT repeat
PF23231	1	1	1	1	1	2	2	Pre-mRNA-splicing factor Syf1/CRNKL1 C-terminal HAT repeat
PF12400	1	1	1	2	1	1	2	STIMATE family
PF00252	1	2	2	2	2	1	4	Ribosomal protein L16p/L10e
PF04727	1	2	1	1	1	1	2	ELMO/CED-12 family
PF11841	1	2	1	1	1	1	2	ELMO, armadillo-like helical domain
PF16457	1	2	1	1	1	1	2	Pleckstrin homology domain
PF03733	2	1	1	1	4	1	2	Inner membrane component domain
PF11017	0	0	0	2	0	0	1	Protein of unknown function (DUF2855)
PF10018	1	1	1	1	2	1	2	Vitamin-D-receptor interacting Mediator subunit 4
PF27975	1	1	1	1	2	1	2	NADH-ubiquinone oxidoreductase 17.8kDa helical domain
PF01758	3	4	2	2	2	2	3	Sodium Bile acid symporter family
PF02636	2	2	2	2	2	2	4	Putative S-adenosyl-L-methionine-dependent methyltransferase
PF13383	0	0	0	0	1	0	1	Methyltransferase domain
PF11968	1	1	1	1	1	0	2	25S rRNA (adenine(2142)-N(1))-methyltransferase, Bmt2
PF24357	1	2	2	4	2	1	3	ABC transporter TMD0 domain
PF08519	1	1	1	1	1	1	2	Replication factor RFC1 C terminal domain
PF25361	1	1	1	1	1	0	2	RFC1-like, AAA+ ATPase lid domain
PF26958	2	2	2	1	1	1	1	tRNA hydrolases-like, Thioredoxin-like domain
PF25390	2	2	2	4	3	2	4	RCC1-like domain
PF03980	2	1	1	1	1	1	2	Nnf1
PF13555	1	1	1	1	1	1	2	P-loop containing region of AAA domain
PF10998	1	1	1	1	1	1	4	Protein of unknown function (DUF2838)
PF09797	1	1	1	1	1	0	2	N-acetyltransferase B complex (NatB) non catalytic subunit
PF00384	1	1	1	1	2	2	2	Molybdopterin oxidoreductase
PF09326	1	1	1	1	1	1	2	NADH-ubiquinone oxidoreductase subunit G, C-terminal
PF10588	1	1	1	1	1	1	2	NADH-ubiquinone oxidoreductase-G iron-sulfur binding region
PF13510	1	1	1	1	1	1	2	2Fe-2S iron-sulfur cluster binding domain
PF22117	1	1	1	1	1	1	2	NADH-quinone oxidoreductase subunit 3, ferredoxin-like domain
PF22151	1	1	1	1	1	1	2	NADH-ubiquinone oxidoreductase NDSU1/NuoG-like, 4Fe-4S domain
PF09796	1	1	1	1	2	1	2	Ubiquinol-cytochrome-c reductase complex subunit (QCR10)
PF07335	0	1	1	2	1	0	1	Fungal chitosanase of glycosyl hydrolase group 75

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF28510	4	4	5	1	2	0	2	Domain of unknown function (DUF8419)
PF05922	2	2	2	13	1	2	4	Peptidase inhibitor I9
PF01274	2	2	2	2	1	2	1	Malate synthase, TIM barrel domain
PF20656	2	2	2	2	1	2	2	Malate synthase, N-terminal domain
PF20659	2	2	2	2	1	2	1	Malate synthase, C-terminal
PF03416	1	1	1	1	1	1	2	Peptidase C54 catalytic domain
PF01424	4	4	4	5	7	3	4	R3H domain
PF01871	1	1	1	1	1	1	2	AMMECR1
PF16004	1	1	1	1	1	1	2	116 kDa U5 small nuclear ribonucleoprotein component N-terminus
PF01411	1	1	1	1	1	1	2	tRNA synthetases class II (A)
PF02272	1	1	1	1	1	1	2	DHHA1 domain
PF26023	1	1	1	1	1	1	2	Alanine--tRNA ligase domain
PF15458	1	2	2	1	1	1	1	Nineteen complex-related protein 2
PF01115	1	1	1	1	1	1	1	F-actin capping protein, beta subunit
PF02541	2	2	2	2	1	1	2	Ppx/GppA phosphatase family
PF23566	2	2	2	2	1	1	2	RTG2 C-terminal domain
PF04998	3	3	3	3	3	4	6	RNA polymerase Rpb1, domain 5
PF04053	3	3	3	3	2	3	5	COPA/B second beta-propeller
PF23953	3	3	3	3	2	3	5	COPA/B TPR domain
PF01990	1	1	1	1	1	1	2	ATP synthase (F/14-kDa) subunit
PF16686	1	1	1	1	1	1	2	ssDNA-binding domain of telomere protection protein
PF05032	2	2	2	1	1	1	2	Spo12 family
PF01608	1	1	1	1	1	1	2	I/LWEQ domain
PF16121	1	1	1	1	1	1	1	40S ribosomal protein S4 C-terminus
PF02037	3	2	2	4	3	5	6	SAP domain
PF27815	1	2	1	1	1	1	2	C24B10.03
PF08639	1	1	1	1	1	1	2	DNA replication regulator SLD3, STD domain
PF25432	2	1	1	2	1	1	2	PRPF40A-like, FF domain
PF16892	1	1	1	1	1	1	2	Chitin biosynthesis protein CHS5 N-terminus
PF16893	1	1	1	1	1	1	2	Fibronectin type III domain
PF02213	2	2	2	2	2	3	2	GYF domain
PF11500	1	1	1	1	1	1	2	Cut12 conserved domain
PF01159	1	1	1	1	1	1	2	Ribosomal protein L6e
PF04683	1	1	1	1	1	1	2	Proteasome complex subunit Rpn13, Pru domain
PF01214	3	2	2	2	2	2	4	Casein kinase II regulatory subunit
PF02996	2	2	3	2	2	2	3	Prefoldin subunit
PF00318	1	2	2	1	1	1	2	Ribosomal protein S2
PF08729	1	1	1	1	1	1	2	HPC2 and ubinuclein domain
PF08620	1	1	1	1	1	1	2	RPAP1-like, C-terminal
PF08621	1	1	1	1	1	1	2	RPAP1-like, N-terminal
PF08755	1	1	1	1	1	2	2	Hemimethylated DNA-binding protein YccV like
PF12898	1	1	1	0	1	1	1	Stc1 domain
PF00034	1	1	1	1	1	1	2	Cytochrome c
PF13442	1	1	1	1	0	0	2	Cytochrome C oxidase, cbb3-type, subunit III
PF13949	3	2	3	2	2	2	3	ALIX V-shaped domain binding to HIV
PF09130	1	1	1	1	2	1	1	Domain of unknown function (DUF1932)
PF18126	1	1	1	1	2	1	2	Mitochondrial ribosomal protein mL59
PF13685	3	4	4	3	2	4	5	Iron-containing alcohol dehydrogenase
PF08123	1	1	1	1	3	1	2	Histone methylation protein DOT1
PF06544	2	2	2	2	2	1	2	Small nuclear ribonucleoprotein Prp3, C-terminal domain
PF08572	1	1	1	1	1	1	2	pre-mRNA processing factor 3 domain
PF09349	1	0	0	1	1	1	2	OHCU decarboxylase
PF01126	1	1	1	1	1	1	2	Heme oxygenase
PF09783	1	1	1	1	2	2	4	Vacuolar import and degradation protein
PF28515	0	1	1	0	2	0	1	Subtelomeric hrmA-associated cluster protein
PF23046	1	1	1	0	1	1	2	UBE2O, tandem tSH3-B domain
PF04124	1	1	1	1	1	1	2	Dor1-like family
PF10601	0	2	2	2	1	1	1	LITAF-like zinc ribbon domain
PF08561	1	1	1	1	1	2	2	Mitochondrial ribosomal protein L37
PF02045	1	1	1	1	1	1	1	CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B
PF02705	0	1	1	0	2	0	4	K+ potassium transporter integral membrane domain
PF22776	0	1	1	0	2	0	4	K+ potassium transporter C-terminal domain
PF00984	1	1	1	3	5	2	4	UDP-glucose/GDP-mannose dehydrogenase family, central domain
PF03720	1	1	1	1	3	1	6	UDP-glucose/GDP-mannose dehydrogenase family, UDP binding domain
PF04739	1	1	1	1	2	1	3	5'-AMP-activated protein kinase beta subunit, interaction domain
PF16561	3	3	3	2	4	3	4	Glycogen recognition site of AMP-activated protein kinase
PF09769	1	1	1	1	1	1	1	Apolipoprotein O
PF25479	1	1	1	1	1	1	3	RNA-binding protein vts1-like domain
PF02574	1	2	2	1	2	1	2	Homocysteine S-methyltransferase
PF26076	1	1	1	1	1	0	2	DDX60-like, winged helix domain
PF00849	0	0	0	1	1	2	2	RNA pseudouridylate synthase
PF13517	2	1	0	0	1	0	3	FG-GAP-like repeat
PF26794	0	0	0	1	2	0	1	LysM11 alpha/beta domain
PF10680	1	1	1	1	1	1	2	RNA polymerase I specific transcription initiation factor
PF02940	1	1	1	1	1	1	2	mRNA capping enzyme, beta chain
PF08491	0	0	2	1	1	1	2	Squalene epoxidase
PF13020	0	0	0	0	0	0	1	Protein NO VEIN, C-terminal
PF25423	1	1	1	1	1	0	2	Domain of unknown function (DUF7893)
PF03069	1	1	1	0	1	1	2	Acetamidase/Formamidase family
PF12634	1	1	1	1	1	1	2	Inheritance of peroxisomes protein 1
PF22493	1	1	1	1	1	1	2	NOP9-like PUF repeat domain
PF14629	1	1	1	1	1	1	2	Origin recognition complex (ORC) subunit 4 C-terminus
PF00953	1	1	1	1	1	1	2	Glycosyl transferase family 4
PF02597	1	2	2	1	1	1	3	ThiS family
PF15979	1	1	1	4	0	0	2	Glycosyl hydrolase family 115
PF17829	1	1	1	4	0	0	2	Glycosyl hydrolase family 115 C-terminal domain
PF24581	1	1	1	0	2	1	2	Domain of unknown function (DUF7608)
PF03147	1	1	1	1	1	1	2	Ferredoxin-fold anticodon binding domain
PF22534	1	1	1	1	1	1	2	Replication factor C subunit 3, C-terminal domain
PF06911	1	1	1	1	1	1	2	Senescence domain
PF07919	1	1	1	1	1	1	2	Gryzun, putative trafficking through Golgi
PF11817	1	1	1	1	1	1	2	Foie gras liver health family 1
PF12554	1	1	1	1	1	0	2	Mitotic-spindle organizing gamma-tubulin ring associated
PF08595	1	1	1	2	1	1	2	RXT2-like, N-terminal
PF12720	1	1	1	1	1	0	2	Protein of unknown function (DUF3807)
PF02560	1	2	2	2	2	2	2	Cyanate lyase C-terminal domain
PF02077	1	1	1	1	1	1	2	SURF4 family

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF28227	1	1	1	1	1	1	2	Large ribosomal subunit protein uL10m C-terminal domain
PF00591	1	1	1	1	1	1	2	Glycosyl transferase family, a/b domain
PF02885	0	1	1	1	1	0	2	Glycosyl transferase family, helical bundle domain
PF11720	1	1	1	1	1	1	2	Peptidase inhibitor I78 family
PF09382	1	1	1	1	2	1	1	RQC domain
PF04729	1	1	1	1	1	0	2	ASF1 like histone chaperone
PF10075	1	1	1	2	3	2	4	CSN8/PSMD8/EIF3K family
PF08596	1	1	1	1	1	1	2	Lethal giant larvae(Lgl) like, C-terminal
PF12460	1	1	1	1	1	2	1	RNAPII transcription regulator C-terminal
PF14500	1	1	1	1	1	0	1	Dos2-interacting transcription regulator of RNA-Pol-II
PF01599	1	0	0	1	1	1	1	Ribosomal protein S27a
PF13369	1	1	1	1	1	2	2	Transglutaminase-like superfamily
PF04437	1	1	1	1	1	1	1	RINT-1/TIP-1 family
PF25358	1	1	1	1	1	0	1	Fungal RdRP associated PH-like domain
PF04158	1	1	1	1	1	1	2	Sof1-like domain
PF18055	1	1	1	1	1	1	2	26S proteasome regulatory subunit RPN6 N-terminal domain
PF18503	1	1	1	1	1	1	2	26S proteasome subunit RPN6 C-terminal helix domain
PF12838	1	1	1	1	1	1	2	4Fe-4S dicluster domain
PF13187	1	1	1	1	1	1	2	4Fe-4S dicluster domain
PF16770	1	1	1	1	1	1	2	Regulator of Ty1 transposition protein 107 BRCT domain
PF13865	0	1	1	2	0	1	1	C-terminal duplication domain of Friend of PRMT1
PF06839	1	1	1	1	1	0	2	GRF zinc finger
PF04573	1	1	1	1	1	1	2	Signal peptidase subunit
PF01127	1	2	2	1	1	1	3	Succinate dehydrogenase/Fumarate reductase transmembrane subunit
PF00290	1	1	1	1	1	1	1	Tryptophan synthase alpha chain
PF23151	0	0	1	1	0	1	2	NuiA-like
PF05557	1	1	1	1	1	1	2	Mitotic checkpoint protein
PF01018	1	1	1	1	1	1	2	GTP1/OBG
PF08202	1	1	1	1	0	1	2	Mis12-Mtw1 protein family
PF14671	1	2	2	1	1	1	3	Dual specificity protein phosphatase, N-terminal half
PF22785	3	4	4	2	6	3	3	Polymorphic toxin system, DSP-PTPase phosphatase
PF24854	1	1	1	1	1	1	2	Domain of unknown function (DUF7728)
PF14578	1	1	1	1	1	1	2	Elongation factor Tu domain 4
PF20252	1	1	1	1	2	1	2	BIG2 C-terminal domain
PF08507	1	0	0	1	1	0	2	COPI associated protein
PF16912	4	5	5	6	4	3	4	Glucose dehydrogenase C-terminus
PF03937	1	1	1	1	1	1	2	Flavinator of succinate dehydrogenase
PF08213	1	1	1	1	2	1	2	Mitochondrial mRNA-processing protein COX24, C-terminal
PF02229	1	1	1	1	1	1	2	Transcriptional Coactivator p15 (PC4)
PF10253	1	1	1	1	1	1	2	Mitotic checkpoint regulator, MAD2B-interacting
PF08492	1	1	1	1	1	1	2	SRP72 RNA-binding domain
PF17004	1	1	1	1	1	1	2	Putative TPR-like repeat
PF26128	1	2	1	2	1	1	2	Gabija anti-defense 2 family protein
PF03371	1	1	1	1	1	1	2	PRP38 family
PF12922	1	1	1	1	1	1	1	non-SMC mitotic condensation complex subunit 1, N-term
PF03847	1	1	1	1	1	1	2	Transcription initiation factor TFIID subunit A
PF06883	1	1	1	1	1	1	2	RNA polymerase I, Rpa2 specific domain
PF19303	1	1	1	1	1	1	2	Anticodon binding domain of methionyl tRNA ligase
PF09811	3	2	2	2	4	2	3	Essential protein Yae1, N terminal
PF04098	1	1	1	2	1	3	2	Rad52/22 family double-strand break repair protein
PF08079	1	1	1	1	1	1	2	Ribosomal L30 N-terminal domain
PF03081	1	1	1	1	1	1	2	Exo70 exocyst complex subunit C-terminal
PF20669	1	1	1	1	1	1	2	Exocyst complex component Exo70 N-terminal
PF10502	1	1	1	2	1	2	2	Signal peptidase, peptidase S26
PF04511	2	2	2	2	2	2	4	Der1-like family
PF16653	1	1	1	1	1	1	2	Saccharopine dehydrogenase C-terminal domain
PF07061	1	1	1	0	2	1	2	Swi5
PF11654	1	1	1	0	1	0	2	Non-classical export protein 1
PF02991	1	1	1	1	1	1	2	Autophagy protein Atg8 ubiquitin like
PF04110	1	1	1	2	2	3	4	Ubiquitin-like autophagy protein Apg12
PF07093	1	1	1	1	1	1	2	SGT1 protein
PF06140	0	1	1	0	0	0	1	Interferon-induced 6-16 family
PF10392	1	1	1	1	1	1	3	Conserved oligomeric Golgi complex subunit 5, N-terminal
PF20649	1	1	1	1	1	1	3	Conserved oligomeric Golgi complex subunit 5, C-terminal
PF00224	1	1	1	2	1	1	2	Pyruvate kinase, barrel domain
PF02887	1	1	1	2	1	1	2	Pyruvate kinase, alpha/beta domain
PF08520	1	2	2	1	1	1	2	Mitofissin
PF10341	0	0	0	0	2	0	2	Shelterin complex subunit, TPP1/ACD
PF07774	1	1	1	1	1	1	2	ER membrane protein complex subunit 1, second beta-propeller
PF03547	2	2	2	1	2	2	4	Membrane transport protein
PF03635	1	1	1	1	1	1	2	Vacuolar protein sorting-associated protein 35
PF08738	1	0	0	1	2	0	2	Gon7 family
PF01803	1	2	2	1	2	2	2	LIM-domain binding protein
PF25482	1	1	1	0	1	1	2	Domain of unknown function (DUF7905)
PF04718	1	1	1	1	1	1	2	Mitochondrial ATP synthase g subunit
PF07915	2	2	2	2	2	1	4	Glucosidase II beta subunit-like protein
PF08292	1	1	1	1	1	1	2	RNA polymerase III subunit Rpc25
PF10453	1	1	1	1	2	1	2	FMR1-interacting protein 1 (NUFIP1)
PF08982	2	2	2	2	2	1	2	Acetylaranotin biosynthesis cluster protein L
PF12658	0	1	1	1	1	1	2	Telomere capping, CST complex subunit
PF05004	1	1	1	1	1	2	2	Interferon-related developmental regulator (IFRD)
PF09127	1	2	2	2	1	1	2	Leukotriene A4 hydrolase, C-terminal
PF01025	1	1	1	1	1	1	2	GrpE
PF12231	1	1	1	1	1	0	2	Rap1-interacting factor 1 N terminal
PF13691	1	2	2	1	1	1	2	tRNase Z endonuclease
PF07510	1	1	1	1	1	0	2	GmrSD restriction endonucleases, C-terminal domain
PF28386	0	0	0	0	1	1	1	BfoA family C-terminal domain
PF10175	0	0	0	0	0	0	1	M-phase phosphoprotein 6
PF13136	1	1	1	1	1	1	2	Protein of unknown function (DUF3984)
PF00130	2	2	2	2	3	2	4	Phorbol esters/diacylglycerol binding domain (C1 domain)
PF00649	1	1	1	2	1	1	1	Copper fist DNA binding domain
PF01784	2	1	1	1	1	2	2	Duf34/NIF3 (NGG1p interacting factor 3)
PF11093	0	0	1	1	1	0	2	Mitochondrial export protein Som1
PF10406	1	2	2	2	2	1	2	Transcription factor TFIID complex subunit 8 C-term
PF23664	1	1	1	1	2	1	2	Nucleoporin pom152-like, immunoglobulin-like domain
PF24097	1	1	1	1	1	0	2	Nucleoporin POM152, N-terminal transmembrane domain
PF24312	1	1	1	1	2	1	2	Nucleoporin POM152, Ig-like domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF24519	1	1	1	1	2	0	2	Nucleoporin pom152-like, first immunoglobulin-like domain
PF24527	1	1	1	1	2	1	2	Nucleoporin pom152-like, ninth immunoglobulin-like domain
PF22685	1	2	2	2	1	1	2	Gal80p, C-terminal domain
PF08549	1	1	1	1	1	2	2	SWI/SNF and RSC complexes subunit Ssr4 N-terminal
PF20497	1	1	1	1	1	2	2	SWI/SNF and RSC complexes subunit Ssr4 C-terminal
PF07081	2	1	1	1	2	2	1	Protein of unknown function (DUF1349)
PF10104	1	1	1	1	2	1	1	Di-sulfide bridge nucleocytoplasmic transport domain
PF25277	1	1	1	1	0	0	1	Domain of unknown function (DUF7871)
PF02296	1	1	1	1	1	1	2	Alpha adaptin AP2, C-terminal domain
PF18011	1	1	1	2	1	1	2	C-terminal domain found in long catalases
PF13180	0	0	0	0	0	1	2	PDZ domain
PF18265	1	2	2	1	1	1	2	Nas2 N_terminal domain
PF08737	1	1	1	1	1	1	2	Rgp1
PF13299	1	1	1	1	1	1	2	Cleavage and polyadenylation factor 2 C-terminal
PF14304	0	1	1	1	1	1	2	Transcription termination and cleavage factor C-terminal
PF14327	1	1	1	1	1	1	2	Hinge domain of cleavage stimulation factor subunit 2
PF03801	1	1	1	1	1	1	2	HEC/Ndc80p family
PF03006	2	2	2	4	3	1	4	Haemolysin-III related
PF23242	1	1	1	0	2	1	2	TRIP13-like, AAA+ ATPase lid C-terminal domain
PF23563	1	1	1	0	2	0	2	TRIP13 N-terminal domain
PF16978	1	1	1	1	1	1	1	SAPK-interacting protein 1 (Sin1), middle CRIM domain
PF16979	1	1	1	1	1	1	1	SAPK-interacting protein 1 (Sin1), Pleckstrin-homology
PF01992	1	1	1	1	1	1	2	ATP synthase (C/AC39) subunit
PF12063	1	1	1	1	1	1	1	Atg1-like, MIT domain 1
PF11894	1	1	1	1	1	0	2	Nuclear pore complex scaffold, nucleoporins 186/192/205
PF11640	1	1	1	2	1	0	2	Telomere-length maintenance and DNA damage repair
PF09282	1	1	1	1	1	1	2	Mago binding
PF02207	2	2	2	2	2	1	4	Putative zinc finger in N-recognin (UBR box)
PF02617	1	1	1	1	1	1	2	ATP-dependent Clp protease adaptor protein ClpS
PF18995	1	1	1	1	1	0	2	Proteolysis_6 C-terminal
PF22960	1	1	1	1	1	1	2	E3 ubiquitin-protein ligase UBR1-like, winged-helix domain
PF05856	1	1	1	1	1	1	2	ARP2/3 complex 20 kDa subunit (ARPC4)
PF28440	1	1	1	1	1	1	2	Domain of unknown function (DUF8399)
PF28442	1	1	1	1	1	1	2	Domain of unknown function (DUF8400)
PF06221	1	1	1	1	1	1	2	Putative zinc finger motif, C2HC5-type
PF08510	1	1	1	1	1	1	2	PIG-P
PF01200	1	1	1	1	1	1	1	Ribosomal protein S28e
PF16543	1	1	1	2	1	1	2	DRG Family Regulatory Proteins, Tma46
PF10215	1	1	1	1	0	1	2	Oligosaccaryltransferase
PF10366	0	0	0	1	1	1	2	Vacuolar sorting protein 39 domain 1
PF10367	0	0	0	1	1	1	2	Vacuolar sorting protein 39 C-terminal zinc finger domain
PF02982	1	1	1	0	2	1	4	Scytalone dehydratase
PF11559	0	1	1	1	2	1	2	Afadin- and alpha -actinin-Binding
PF12436	1	1	1	1	2	1	2	ICP0-binding domain of Ubiquitin-specific protease 7
PF14533	1	1	1	1	2	1	2	Ubiquitin-specific protease C-terminal
PF22486	2	1	1	1	2	0	2	MATH domain
PF08622	0	0	0	1	1	1	2	Svf1-like N-terminal lipocalin domain
PF17187	0	0	0	1	1	1	2	Svf1-like C-terminal lipocalin-like domain
PF05891	1	1	1	1	2	1	2	AdoMet dependent proline di-methyltransferase
PF25304	0	0	1	0	1	1	2	eIF2D winged helix domain
PF26291	0	0	1	0	1	1	2	eIF2D, SWIB domain
PF09363	1	1	1	1	1	1	2	XFP C-terminal domain
PF12589	1	1	1	1	1	1	2	Methyltransferase involved in Williams-Beuren syndrome
PF04148	1	1	1	1	2	1	4	Transmembrane adaptor Erv26
PF21203	2	1	1	0	1	1	2	ER membrane protein complex subunit 10
PF18151	1	1	1	1	1	1	2	Domain of unknown function (DUF5601)
PF08584	1	1	1	1	1	1	2	Ribonuclease P 40kDa (Rpp40) subunit
PF20770	1	1	1	1	1	1	2	PAN2 N-terminal
PF06916	1	1	1	2	2	1	2	FAM210A/B-like domain
PF14938	1	1	1	1	1	0	2	Soluble NSF attachment protein, SNAP
PF02686	1	1	1	1	1	0	2	Glu-tRNAGln amidotransferase C subunit
PF20977	1	1	1	1	1	0	2	Glutamyl-tRNA(Gln) amidotransferase subunit F
PF20978	1	1	1	1	1	0	2	Glutamyl-tRNA amidotransferase complex subunit Gta3
PF03007	0	0	0	3	1	0	1	Wax ester synthase/diacylglycerol acyltransferase catalytic domain
PF07247	2	2	2	5	1	0	2	Alcohol acetyltransferase
PF01946	1	1	1	1	1	1	4	Thi4 family
PF06087	1	1	1	2	1	1	2	Tyrosyl-DNA phosphodiesterase
PF05291	1	1	1	1	1	1	2	Bystin
PF08568	1	1	1	1	2	1	1	Uncharacterised protein family, YAP/Alf4/glomulin
PF18323	1	1	1	1	1	1	1	Cop9 signalosome subunit 5 C-terminal domain
PF04140	1	1	1	2	1	1	2	Isoprenylcysteine carboxyl methyltransferase (ICMT) family
PF04669	1	1	1	1	1	0	2	PBDC1 protein
PF01597	1	1	1	2	1	2	2	Glycine cleavage H-protein
PF01250	2	1	1	1	1	2	2	Ribosomal protein S6
PF08302	1	1	1	1	1	1	2	Fungal tRNA ligase phosphodiesterase domain
PF10261	0	1	1	2	1	1	2	Fat storage-inducing transmembrane protein
PF14615	1	1	1	1	1	1	2	Ribosome-assembly protein 3
PF16797	1	1	1	1	1	1	2	Fungal kinase associated-1 domain
PF07757	0	0	0	1	0	0	2	Predicted AdoMet-dependent methyltransferase
PF28462	1	1	1	1	1	1	2	TRM44-like, N-terminal bet v1-like domain
PF24321	1	1	1	1	1	1	1	Domain of unknown function (DUF7493)
PF02137	1	1	1	1	1	2	2	Adenosine-deaminase (editase) domain
PF11605	1	1	1	1	1	1	2	Vacuolar protein sorting protein 36 Vps36
PF16988	1	1	1	1	1	1	2	Vacuolar protein sorting 36 NZF-N zinc-finger domain
PF01195	1	1	1	1	2	1	2	Peptidyl-tRNA hydrolase
PF04142	1	2	2	1	1	1	2	Nucleotide-sugar transporter
PF08355	1	1	1	1	1	1	2	EF hand associated
PF08356	1	1	1	1	1	1	2	EF hand associated
PF08547	3	4	4	1	3	2	4	Complex I intermediate-associated protein 30 (CIA30)
PF04137	1	1	1	1	1	1	2	Endoplasmic Reticulum Oxidoreductin 1 (ERO1)
PF04241	1	1	1	0	1	1	2	Protein of unknown function (DUF423)
PF12816	1	1	1	2	1	1	2	Vps8 central TPR
PF23410	1	1	1	2	1	1	2	Vps8 beta-propeller
PF23413	0	1	1	0	0	0	1	Vps8 RING zinc finger, fungal
PF25066	1	1	1	2	1	1	2	VPS8-like, TPR-like repeats
PF12572	1	1	1	1	1	1	2	Protein of unknown function (DUF3752)
PF25147	0	0	0	2	1	1	2	Ribophorin_II, C-terminal domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF01658	1	1	1	1	1	1	2	Myo-inositol-1-phosphate synthase
PF07994	1	1	1	1	1	1	2	Myo-inositol-1-phosphate synthase
PF01916	1	1	1	1	1	1	2	Deoxyhypusine synthase
PF02493	1	1	1	0	1	2	2	MORN repeat
PF12619	1	1	1	1	1	2	3	Mini-chromosome maintenance protein 2
PF13831	2	2	2	4	1	2	3	PHD-finger
PF27758	0	0	0	1	1	1	2	Plasma membrane fusion protein PRM1
PF18098	1	1	1	1	1	1	3	26S proteasome regulatory subunit RPN5 C-terminal domain
PF12328	1	1	2	1	2	1	2	Rpp20 subunit of nuclear RNase MRP and P
PF21282	1	1	1	0	1	1	2	APC1 beta sandwich domain
PF21492	2	1	2	1	1	1	2	Ribosomal protein L31p, N-terminal
PF01419	2	2	2	4	2	1	1	Jacalin-like lectin domain
PF09818	1	1	1	0	1	2	2	P-loop domain
PF20446	1	1	1	0	1	1	2	ATPase of the ABC class N-terminal
PF21117	1	1	1	0	1	2	2	MRB1590 C-terminal domain
PF08658	1	1	1	1	1	1	2	Rad54 N terminal
PF08733	1	1	1	1	1	1	2	PalH/RIM21
PF03556	1	1	1	1	2	1	2	Cullin binding
PF09138	1	1	1	2	1	0	2	Urm1 (Ubiquitin related modifier)
PF04959	1	1	1	0	2	1	3	Arsenite-resistance protein 2
PF12066	1	1	1	1	2	1	3	SERRATE/Ars2, N-terminal domain
PF27660	1	1	1	1	1	1	2	Style cell-cycle inhibitor 1-like helix hairpin domain
PF22890	0	0	0	1	1	1	2	EMC2 TPR-like repeat domain
PF06624	1	1	1	1	1	1	2	Ribosome associated membrane protein RAMP4
PF25421	1	1	1	1	1	2	2	Domain of unknown function (DUF7891)
PF00475	1	1	1	1	2	1	1	Imidazoleglycerol-phosphate dehydratase
PF08880	1	1	1	1	1	1	2	QLQ
PF14619	1	1	1	1	1	1	2	Snf2-ATP coupling, chromatin remodelling complex
PF24320	1	1	1	2	1	6	2	Domain of unknown function (DUF7492)
PF10310	1	1	1	1	1	1	2	Family of unknown function (DUF5427)
PF17778	1	1	1	1	1	1	2	Beta-lactamase associated winged helix domain
PF01231	3	3	3	4	3	2	2	Indoleamine 2,3-dioxygenase
PF10280	1	1	1	1	2	1	2	Mediator complex protein
PF18380	1	1	1	1	2	0	2	Holliday junction resolvase Gen1 C-terminal domain
PF22799	4	3	3	1	6	3	4	Cell wall mannoprotein PIR1-like, C-terminal domain
PF01406	2	2	2	1	1	1	2	tRNA synthetases class I (C) catalytic domain
PF27986	1	1	1	2	3	0	2	Effector TSP1
PF13001	1	1	1	1	1	1	1	Proteasome component ECM29, N-terminal
PF23731	1	1	1	1	1	1	1	ECM29, C-terminal ARM-like repeats
PF08385	1	1	1	1	2	0	2	Dynein heavy chain, N-terminal region 1
PF08393	1	1	1	1	2	1	2	Dynein heavy chain, N-terminal region 2
PF02271	1	1	1	1	2	1	2	Ubiquinol-cytochrome C reductase complex 14kD subunit
PF02929	2	2	2	3	1	0	1	Beta galactosidase small chain
PF16353	2	2	2	3	1	0	1	Beta-galactosidase, domain 4
PF11767	1	1	1	1	2	1	1	Histone lysine methyltransferase SET associated
PF01281	1	1	1	0	1	1	4	Ribosomal protein L9, N-terminal domain
PF27885	1	1	1	1	2	1	2	NuzM, N-terminal domain
PF27886	1	1	1	1	2	1	2	NuzM C-terminal domain
PF12230	1	1	1	1	1	1	2	Pre-mRNA splicing factor PRP21 like protein
PF01991	0	1	1	1	1	2	2	ATP synthase (E/31 kDa) subunit
PF01940	1	1	1	1	1	1	2	Integral membrane protein DUF92
PF19271	1	1	1	0	3	0	2	Nis1 family
PF09785	1	1	1	1	1	1	2	Prp31 C terminal domain
PF15811	1	1	1	1	1	0	1	Small VCP/p97-interacting protein
PF09384	1	1	1	1	1	1	2	UTP15 C terminal
PF12423	1	1	1	1	1	1	1	Kinesin protein 1B
PF12473	1	1	1	1	1	1	1	Kinesin protein
PF16183	1	1	1	1	1	1	1	Kinesin-associated
PF25133	1	1	1	1	2	0	2	TYW2 N-terminal domain
PF12455	1	1	1	1	1	0	2	Dynein associated protein
PF26666	1	1	1	1	1	1	2	Domain of unknown function (DUF8221)
PF00935	1	1	1	1	1	1	2	Ribosomal protein L44
PF12824	1	1	1	1	0	1	2	Mitochondrial ribosomal protein subunit L20
PF05995	1	2	2	1	1	0	3	Cysteine dioxygenase type I
PF25481	3	1	1	1	1	1	2	Nucleoprotein TPR-like domain
PF02186	1	1	1	1	1	0	2	TFIIE beta subunit core domain
PF18121	1	1	1	1	1	0	2	TFA2 Winged helix domain 2
PF09173	1	1	1	1	1	1	2	Initiation factor eIF2 gamma, C terminal
PF03332	2	2	2	1	1	1	2	Eukaryotic phosphomannomutase
PF08282	2	1	1	0	1	0	2	haloacid dehalogenase-like hydrolase
PF10247	1	1	1	1	1	0	2	Reactive mitochondrial oxygen species modulator 1
PF23445	4	3	3	2	4	3	5	Winged Helix-turn-helix domain
PF03199	1	1	1	1	4	1	4	Eukaryotic glutathione synthase
PF03917	1	1	1	1	4	1	4	Eukaryotic glutathione synthase, ATP binding domain
PF00939	1	1	1	1	1	1	2	Sodium:sulfate symporter transmembrane region
PF13259	0	0	0	1	1	1	2	Gag1-like, clamp domain
PF05190	3	5	5	4	4	4	3	MutS family domain IV
PF27469	1	1	1	1	1	1	2	ATP synthase epsilon chain C-terminal domain
PF08628	2	2	2	2	2	2	1	Sorting nexin C terminal
PF19282	1	1	1	1	2	1	1	Exportin-T
PF14801	1	0	0	0	0	0	2	TrmI-like N-terminal
PF21800	1	1	1	1	1	1	2	KRR1 small subunit processome component, second KH domain
PF10384	1	1	1	1	2	1	2	Centromere protein Scm3
PF04111	1	1	1	1	1	1	2	Apg6 BARA domain
PF17675	1	1	1	1	1	1	2	Apg6 coiled-coil region
PF06159	1	1	1	1	1	1	2	Trafficking protein particle complex subunit 13, N-terminal
PF23647	1	1	1	1	1	1	2	Trafficking protein particle complex subunit 13, middle domain
PF10303	0	1	1	1	1	2	2	Protein of unknown function (DUF2408)
PF07817	1	1	1	1	1	0	2	GLE1-like protein
PF00576	1	1	1	1	2	1	2	HIUase/Transthyretin family
PF06963	1	1	2	1	2	0	2	Ferroportin1 (FPN1)
PF08313	1	1	1	1	1	1	2	SCA7, zinc-binding domain
PF21547	1	1	1	1	1	0	2	TELO2-interacting protein 1
PF24173	1	1	1	1	1	0	2	TTI1 N-terminal TPR domain
PF24181	1	1	1	1	1	0	2	TTI1 C-terminal TPR domain
PF01177	2	2	2	3	2	1	6	Asp/Glu/Hydantoin racemase
PF17645	1	1	1	0	2	0	2	Arylmalonate decarboxylase

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF07426	1	1	1	1	2	1	1	Dynactin subunit p22
PF14521	4	4	4	2	4	0	1	Lysine-specific metallo-endopeptidase
PF06957	1	1	1	1	1	1	2	Coatomer (COPI) alpha subunit C-terminus
PF05251	0	1	1	2	1	1	2	Oligosaccharyltransferase subunit 5
PF02144	0	1	1	1	1	1	2	Repair protein Rad1/Rec1/Rad17
PF01783	1	1	1	1	1	1	2	Ribosomal L32p protein family
PF12973	0	1	1	2	0	0	2	ChrR Cupin-like domain
PF00834	1	1	1	1	1	1	2	Ribulose-phosphate 3 epimerase family
PF16396	0	0	0	0	1	0	2	Domain of unknown function (DUF5005)
PF02805	1	1	1	1	0	1	1	Metal binding domain of Ada
PF23670	0	0	0	0	1	0	1	PIGBOS1-like
PF10163	1	1	1	0	2	0	2	Transcription factor e(y)2
PF26434	1	1	1	1	1	1	2	YAG7 dimerisation domain
PF09751	1	1	1	1	1	1	2	Nuclear protein Es2
PF00827	1	1	1	1	1	1	1	Ribosomal L15
PF00855	1	1	1	1	1	1	1	PWWP domain
PF01502	0	1	1	1	1	1	2	Phosphoribosyl-AMP cyclohydrolase
PF01503	0	1	1	1	1	1	2	Phosphoribosyl-ATP pyrophosphohydrolase
PF02615	1	2	2	2	1	0	2	Malate/L-lactate dehydrogenase
PF05129	1	1	1	1	1	1	2	Transcription elongation factor Elf1 like
PF12471	1	1	1	1	1	1	2	GTP cyclohydrolase N terminal
PF04457	1	1	1	0	1	1	2	MJ1316 RNA cyclic group end recognition domain
PF25485	2	2	2	0	3	1	3	Domain of unknown function (DUF7908)
PF02364	1	1	1	1	1	1	1	1,3-beta-glucan synthase component
PF14288	1	1	1	1	1	0	1	1,3-beta-glucan synthase subunit FKS1, domain-1
PF23605	1	1	1	1	1	0	1	1,3-beta-glucan synthase component FKS1, second domain
PF06427	1	1	1	1	1	1	2	UDP-glucose:Glycoprotein Glucosyltransferase
PF18403	1	1	1	1	1	1	2	Thioredoxin-like domain
PF18404	1	1	1	1	1	1	2	Glucosyltransferase 24
PF08641	1	1	1	1	1	1	2	Kinetochore protein Mis14 like
PF02911	1	1	1	0	1	0	1	Formyl transferase, C-terminal domain
PF01300	1	1	1	1	2	0	2	Telomere recombination
PF03481	1	1	1	1	2	0	2	Threonylcarbamoyl-AMP synthase, C-terminal domain
PF01470	1	1	1	2	2	1	3	Pyroglutamyl peptidase
PF01725	1	1	1	1	1	1	2	Ham1 family
PF25391	1	1	1	1	1	1	1	G protein beta WD-40 repeat protein
PF05839	1	1	1	1	1	1	2	Apc13p protein
PF20238	3	3	2	3	3	4	1	Copper acquisition factor BIM1-like
PF02109	1	1	1	1	1	1	2	DAD family
PF03647	1	1	1	2	1	1	3	Transmembrane proteins 14C
PF00719	2	2	2	2	1	1	2	Inorganic pyrophosphatase
PF09462	1	1	1	1	1	0	2	Mus7/MMS22 family
PF20750	1	1	1	1	1	1	2	Poly(A) polymerase nucleotidyltransferase domain
PF12051	1	1	1	0	1	2	1	Protein of unknown function (DUF3533)
PF23585	1	1	1	1	1	1	2	Domain of unknown function (DUF7137)
PF24563	1	1	1	1	2	1	2	Mug60/KHD4 KH type I domain
PF06337	1	1	1	2	1	1	2	DUSP domain
PF12074	1	1	1	1	1	1	1	Generalcontrol nonderepressible 1 (Gcn1) N-terminal
PF24916	1	1	1	1	1	1	1	Fungal GCN1-like, HEAT repeats
PF24993	1	1	1	1	1	0	1	Stalled ribosome sensor GCN1 N-terminal
PF26715	1	1	1	1	1	1	1	Stalled ribosome sensor GCN1, HEAT repeats
PF01851	2	2	2	2	2	2	4	Proteasome/cyclosome repeat
PF18004	1	1	1	1	1	1	2	26S proteasome regulatory subunit RPN2 C-terminal domain
PF14732	1	1	1	1	1	1	1	Ubiquitin/SUMO-activating enzyme ubiquitin-like domain
PF19036	1	1	1	1	2	1	1	First Longin domain of FUZ, MON1 and HPS1
PF19037	1	1	1	1	2	1	1	Second Longin domain of FUZ, MON1 and HPS1
PF04118	1	1	1	1	1	0	1	Dopey, N-terminal
PF24597	1	1	1	1	1	0	1	DOP1 middle TPR domain
PF24598	1	1	1	1	1	1	1	DOP1 C-terminal
PF07535	0	0	0	1	2	2	2	DBF zinc finger
PF02548	0	0	0	1	2	2	2	Ketopantoate hydroxymethyltransferase
PF14204	1	1	1	1	1	1	1	Ribosomal L18 C-terminal region
PF10307	1	1	1	1	2	1	2	HAD domain family 1 in Swiss Army Knife RNA repair proteins
PF02811	1	1	1	1	1	1	2	PHP domain
PF06041	1	1	1	2	1	1	2	Bacterial protein of unknown function (DUF924)
PF01907	1	1	1	1	1	1	2	Ribosomal protein L37e
PF10056	2	2	2	2	3	1	1	Uncharacterized conserved protein (DUF2293)
PF13019	1	1	1	1	1	1	2	Yeast Splicing regulator sde2, N-terminal ubiquitin domain
PF22782	1	1	1	1	1	1	2	Splicing regulator SDE2, SDE2 domain
PF09351	3	3	3	3	1	0	2	Domain of unknown function (DUF1993)
PF08610	1	2	2	1	1	2	2	Peroxisomal membrane protein (Pex16)
PF20175	1	1	1	2	2	0	2	Tra1 HEAT repeat central region
PF13671	4	2	2	6	8	4	4	AAA domain
PF12735	1	1	1	1	1	2	2	TRAPP trafficking subunit Trs65 IgD3
PF09202	1	1	1	1	1	1	2	Rio2, N-terminal
PF17781	1	1	1	1	1	1	2	RPN1 N-terminal domain
PF18051	1	1	1	1	1	1	2	26S proteasome non-ATPase regulatory subunit RPN1 C-terminal
PF12766	1	1	1	1	2	1	1	Pyridoxamine 5'-phosphate oxidase
PF01474	1	1	1	1	1	1	2	Class-II DAHP synthetase family
PF25823	1	1	1	1	1	1	2	Ams2/SPT21 N-terminal domain
PF02734	4	3	3	5	4	1	4	DAK2 domain
PF10022	1	1	1	2	1	0	2	Uncharacterized protein conserved in bacteria (DUF2264)
PF20938	1	1	1	2	1	0	2	DUF2264 C-terminal domain
PF07855	1	1	1	1	2	1	2	Autophagy-related protein 101
PF08553	1	1	1	1	1	1	2	VID27 C-terminal WD40-like domain
PF17747	1	1	1	1	1	1	2	VID27 PH-like domain
PF17748	1	1	1	1	1	1	2	VID27 N-terminal region
PF01116	3	4	4	6	3	2	3	Fructose-bisphosphate aldolase class-II
PF23580	1	1	1	1	1	1	2	XIAP-associated factor 1-like, N-terminal zinc finger
PF24503	1	1	1	1	1	1	2	Domain of unknown function (DUF7590)
PF04104	1	1	1	1	1	1	2	Eukaryotic and archaeal DNA primase, large subunit C-terminal domain
PF26466	1	1	1	1	1	1	2	Eukaryotic and archaeal DNA primase, large subunit N-terminal domain
PF03845	1	0	0	0	0	0	1	Spore germination protein
PF01634	3	3	3	1	1	3	2	ATP phosphoribosyltransferase
PF08029	3	3	3	1	1	2	2	HisG, C-terminal domain
PF16842	1	2	2	1	1	1	2	Occluded RNA-recognition motif
PF08642	2	1	1	1	2	1	1	Histone deacetylation protein Rxt3

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF12330	1	1	1	1	1	1	2	Haspin like kinase domain
PF01564	1	1	1	2	2	2	3	Spermine/spermidine synthase domain
PF28362	0	1	1	1	0	1	2	NcaA C-terminal domain
PF05794	2	2	2	2	2	2	1	T-complex protein 11
PF12716	1	1	1	1	1	1	2	Nuclear pore assembly and biogenesis
PF10173	1	2	2	1	1	1	2	Mitochondrial K+-H+ exchange-related
PF25506	1	1	1	0	1	1	2	MTC6 partial TIM-barrel domain
PF01185	1	0	0	0	0	0	1	Fungal hydrophobin
PF06657	1	1	1	1	1	2	2	Centrosome microtubule-binding domain of Cep57
PF14197	1	0	0	1	1	2	2	Centrosome localisation domain of PPC89
PF00645	1	1	1	1	2	1	2	Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region
PF08695	1	1	2	1	1	1	2	Cytochrome oxidase complex assembly protein 1
PF10354	1	1	1	0	1	1	1	rRNA (uridine-N3-)-methyltransferase BTM5-like
PF12923	1	1	1	1	1	1	2	Ribosomal RNA-processing protein 7 (RRP7) C-terminal domain
PF17799	1	1	1	1	1	1	2	Rrp7 RRM-like N-terminal domain
PF03561	1	2	2	0	1	1	2	Allantoicase repeat
PF01843	2	2	2	2	2	2	2	DIL domain
PF25790	1	1	1	1	1	1	1	BCD1 domain
PF02141	2	2	2	2	4	2	2	DENN (AEX-3) domain
PF03456	2	2	2	2	4	2	2	uDENN domain
PF07955	1	1	1	1	1	1	2	Protein of unknown function (DUF1687)
PF03155	1	1	1	1	2	0	2	ALG6, ALG8 glycosyltransferase family
PF10537	1	1	1	1	1	1	1	ATP-utilising chromatin assembly and remodelling N-terminal
PF04847	1	1	1	1	2	1	2	Calcipressin
PF00479	1	1	1	1	1	1	2	Glucose-6-phosphate dehydrogenase, NAD binding domain
PF02781	1	1	1	1	1	1	2	Glucose-6-phosphate dehydrogenase, C-terminal domain
PF02540	0	0	0	1	1	2	2	NAD synthase
PF06732	0	0	0	1	1	1	2	Pescadillo N-terminus
PF18592	1	1	1	1	1	1	2	Tho1/MOS11 C-terminal domain
PF06179	1	1	1	1	1	1	2	Surfeit locus protein 5 subunit 22 of Mediator complex
PF08655	1	1	1	1	1	1	2	DASH complex subunit Ask1
PF25447	1	1	1	2	3	1	1	ZNF598 RING finger domain
PF01154	1	1	1	1	1	1	1	Hydroxymethylglutaryl-coenzyme A synthase N terminal
PF08540	1	1	2	1	1	1	1	Hydroxymethylglutaryl-coenzyme A synthase C terminal
PF25130	1	1	2	1	2	1	1	Domain of unknown function (DUF7820)
PF27033	0	1	1	1	0	0	1	Domain of unknown function (DUF8340)
PF25026	1	2	2	1	1	1	2	Asd-4-like domain
PF24054	1	1	1	1	1	1	2	Domain of unknown function (DUF7357)
PF01087	1	2	1	1	1	1	1	Galactose-1-phosphate uridyl transferase, N-terminal domain
PF02744	1	2	1	1	1	1	2	Galactose-1-phosphate uridyl transferase, C-terminal domain
PF00360	1	1	1	1	1	1	3	Phytochrome region
PF21188	1	2	2	1	1	1	2	Pre-mRNA-splicing helicase BRR2 plug domain
PF01229	0	0	0	0	0	0	1	Glycosyl hydrolases family 39
PF00183	1	1	1	1	1	1	1	Hsp90 protein
PF04031	1	2	2	1	1	1	3	Las1-like
PF03879	1	1	1	1	1	1	1	Cgr1 family
PF03224	1	1	1	1	1	2	2	V-ATPase subunit H
PF11698	1	1	1	1	1	1	2	V-ATPase subunit H
PF01501	4	2	2	3	2	4	3	Glycosyl transferase family 8
PF01106	1	1	1	2	1	0	2	NifU-like domain
PF08712	1	1	1	2	1	1	2	Scaffold protein Nfu/NifU N terminal
PF08644	1	1	1	1	1	1	2	FACT complex subunit (SPT16/CDC68)
PF21091	1	1	1	1	1	1	2	FACT complex subunit SPT16, C-terminal domain
PF24824	1	1	1	1	1	1	2	FACT complex subunit SPT16 PH-like domain
PF05187	0	0	0	1	1	1	2	Electron transfer flavoprotein-ubiquinone oxidoreductase, 4Fe-4S
PF13932	1	1	1	1	1	1	1	tRNA modifying enzyme MnmG/GidA C-terminal helical bundle
PF13656	3	3	4	2	2	2	2	RNA polymerase Rpb3/Rpb11 dimerisation domain
PF08580	1	1	1	1	2	1	2	Yeast cortical protein KAR9
PF10042	0	0	0	0	0	0	2	Uncharacterized conserved protein (DUF2278)
PF25351	1	1	1	1	1	1	2	BUD3 C-terminal PH domain
PF02487	1	2	2	3	1	1	2	CLN3 protein
PF04990	1	1	1	1	1	1	2	RNA polymerase Rpb1, domain 7
PF04992	1	1	1	1	1	1	1	RNA polymerase Rpb1, domain 6
PF05001	1	1	1	1	1	0	2	RNA polymerase Rpb1 C-terminal repeat
PF00736	4	2	2	1	1	1	2	EF-1 guanine nucleotide exchange domain
PF10270	1	1	1	1	2	1	2	Membrane magnesium transporter
PF27035	2	1	1	1	2	1	1	MutS5 N-terminal domain
PF26001	1	1	1	1	2	2	2	Peroxin 8 protein-like, N-terminal domain
PF27740	1	1	1	1	1	0	2	PEX8 helical domain
PF10190	1	1	1	1	1	1	2	Transmembrane protein 170A/B-like
PF24245	1	1	1	1	1	1	2	INO80 complex subunit F
PF09135	1	1	1	1	1	1	2	Alb1
PF03935	2	2	2	0	3	1	2	Beta-glucan synthesis-associated protein SKN1/KRE6/Sbg1
PF25701	1	1	1	1	2	1	1	YTH1-like RRM domain
PF20636	1	1	1	1	0	1	2	Survival Motor Neuron, Gemin2-binding domain
PF08648	1	1	1	1	1	2	2	U4/U6.U5 small nuclear ribonucleoproteins
PF17911	1	1	1	1	2	1	1	Ski2 N-terminal region
PF01351	1	1	1	1	1	1	2	Ribonuclease HII
PF02926	1	2	2	1	1	1	1	THUMP domain
PF14031	2	1	1	3	1	1	1	Putative serine dehydratase domain
PF01872	1	1	1	2	1	1	2	RibD C-terminal domain
PF00246	4	5	5	7	2	1	1	Zinc carboxypeptidase
PF01776	1	1	1	1	1	1	2	Ribosomal L22e protein family
PF08591	1	1	1	1	1	1	2	Ribonucleotide reductase inhibitor
PF09358	1	1	1	1	1	2	2	Ubiquitin fold domain
PF10585	1	1	1	1	1	2	2	Ubiquitin-activating enzyme, SCCH domain
PF06071	2	2	2	1	1	0	1	Protein of unknown function (DUF933)
PF01210	3	2	1	1	1	1	2	NAD-dependent glycerol-3-phosphate dehydrogenase N-terminus
PF07479	1	1	1	1	1	1	2	NAD-dependent glycerol-3-phosphate dehydrogenase C-terminus
PF24535	1	1	1	1	2	1	3	Domain of unknown function (DUF7598)
PF14572	3	3	3	3	3	4	4	Phosphoribosyl synthetase-associated domain
PF00186	1	1	1	1	2	1	1	Dihydrofolate reductase
PF03399	2	3	4	3	2	1	2	SAC3/GANP family
PF02257	3	2	2	2	2	0	2	RFX DNA-binding domain
PF25340	3	2	2	2	2	1	3	RFX BCD domain
PF07491	1	2	2	1	1	1	2	Protein phosphatase inhibitor
PF00035	2	1	2	1	2	1	2	Double-stranded RNA binding motif

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF26980	0	1	1	1	1	1	2	Dicer-like protein 2, dsRNA binding domain
PF16282	1	1	1	1	3	1	3	SANT/Myb-like domain of DAMP1
PF09814	1	1	1	1	2	1	2	HECT-like Ubiquitin-conjugating enzyme (E2)-binding
PF08771	1	1	1	1	1	1	2	FKBP12-rapamycin binding domain
PF00278	1	1	1	1	1	1	2	Pyridoxal-dependent decarboxylase, C-terminal sheet domain
PF01293	1	1	1	1	2	1	1	Phosphoenolpyruvate carboxykinase
PF02566	1	1	1	0	4	1	4	OsmC-like protein
PF05160	1	1	1	1	1	0	2	DSS1/SEM1 family
PF00162	1	1	1	1	1	0	2	Phosphoglycerate kinase
PF05631	0	0	0	0	1	0	2	Sugar-tranasporters, 12 TM
PF03661	1	1	1	1	1	1	1	Transmembrane protein 33/Nucleoporin POM33
PF23774	2	2	2	1	1	2	1	GEMI5 TPR domain
PF03908	1	1	1	1	1	1	2	Sec20
PF06093	1	1	1	1	1	1	2	Spt4/RpoE2 zinc finger
PF08321	1	1	1	1	1	1	1	PPP5 TPR repeat region
PF10378	1	2	2	1	2	1	2	Putative RRM domain
PF10567	1	2	2	1	2	1	2	RNA-recognition motif
PF06419	1	1	1	1	1	0	2	Conserved oligomeric complex COG6, N-terminal
PF11712	1	1	1	1	1	1	1	Endoplasmic reticulum-based factor for assembly of V-ATPase
PF24345	2	2	2	1	1	1	1	EVH1 domain-like
PF16987	1	1	1	0	2	0	1	KIX domain
PF11754	1	1	1	1	1	1	2	Velvet factor
PF16190	1	1	1	1	1	2	2	Ubiquitin-activating enzyme E1 FCCH domain
PF16191	1	1	1	1	1	2	2	Ubiquitin-activating enzyme E1 four-helix bundle
PF22934	0	1	1	0	1	0	2	Spartan-like zinc binding domain
PF04506	1	1	1	1	1	1	2	Rft protein
PF13440	0	0	0	0	0	1	2	Polysaccharide biosynthesis protein
PF15496	1	1	0	0	1	0	2	Domain of unknown function (DUF4646)
PF05181	1	1	1	1	1	1	2	XPA protein C-terminus
PF00881	1	1	1	2	2	1	2	Nitroreductase family
PF03848	0	1	1	0	2	0	1	Tellurite resistance protein TehB
PF15410	1	1	1	3	3	1	2	Pleckstrin homology domain
PF11001	1	1	1	2	1	1	1	YDR124W-like, helical bundle domain
PF12896	1	1	1	1	1	0	2	Anaphase-promoting complex, cyclosome, subunit 4
PF28359	0	0	0	1	1	1	1	Cullin-associated NEDD8-dissociated protein 1 N-terminal part
PF03073	1	1	1	1	1	2	1	TspO/MBR family
PF08161	1	1	1	1	1	2	2	Ribosomal RNA-processing protein 12, HEAT repeats
PF25772	1	1	1	1	1	1	2	RRP12-like, N-terminal HEAT repeats
PF08645	2	1	1	1	2	1	1	Polynucleotide kinase 3 phosphatase
PF23627	1	1	1	1	2	1	2	WDR26 Lis-homology motif
PF06479	1	1	1	1	1	1	2	Ribonuclease 2-5A
PF08718	1	1	1	1	1	1	2	Glycolipid transfer protein (GLTP)
PF06602	1	1	1	1	1	1	2	Myotubularin-like phosphatase domain
PF08208	1	1	1	1	1	0	2	DNA-directed RNA polymerase I subunit RPA34.5
PF14079	0	0	0	0	0	0	2	Domain of unknown function (DUF4260)
PF12814	2	2	2	2	3	2	1	Meiotic cell cortex C-terminal pleckstrin homology
PF12745	1	1	1	1	2	2	1	Anticodon binding domain of tRNAs
PF22617	1	2	2	2	1	1	1	Homocitrate synthase post-HMGL domain-like
PF12726	1	1	1	1	1	1	2	SEN1 N terminal
PF11787	1	1	1	1	1	1	2	Aft1 HRR domain
PF12157	2	2	2	2	1	1	1	Protein of unknown function (DUF3591)
PF25430	1	1	1	1	2	1	2	DDX23-like domain
PF03079	1	1	1	1	1	1	1	ARD/ARD' family
PF03455	1	1	1	1	2	0	1	dDENN domain
PF24580	1	1	1	1	1	0	1	Domain of unknown function (DUF7607)
PF06738	2	1	1	2	2	1	2	Putative threonine/serine exporter
PF28334	1	1	1	1	2	1	1	pH-response transcription factor pacC/RIM101 helical domain
PF20415	1	1	1	1	1	1	1	Family of unknown function (DUF6699)
PF01095	3	4	4	1	5	0	1	Pectinesterase
PF25353	1	1	1	1	1	0	1	Second PH domain in LRR-containing protein
PF22999	1	1	1	1	1	1	2	LTN1 family HEAT repeat region
PF23009	1	1	1	1	1	1	2	Ubiquitin conjugating domain-like
PF09431	1	1	1	2	1	0	1	SPIN90/Ldb17, leucine-rich domain
PF01174	1	1	1	1	1	2	1	SNO glutamine amidotransferase family
PF15365	1	1	1	1	1	1	1	Proline-rich nuclear receptor coactivator motif
PF02935	1	1	1	1	1	1	4	Cytochrome c oxidase subunit VIIc
PF12862	1	1	1	1	1	1	1	Anaphase-promoting complex subunit 5
PF00387	4	3	3	4	6	2	1	Phosphatidylinositol-specific phospholipase C, Y domain
PF06645	1	1	1	1	1	1	1	Microsomal signal peptidase 12 kDa subunit (SPC12)
PF07064	1	1	1	1	1	1	2	RIC1 C-terminal alpha solenoid region
PF25440	1	1	1	1	1	1	2	RIC1 second beta propeller domain
PF00233	1	1	1	1	2	1	1	3'5'-cyclic nucleotide phosphodiesterase
PF09324	1	1	1	1	2	1	2	Mon2/Sec7/BIG1-like, HDS
PF27239	0	1	1	1	1	1	1	Dihydrofolate synthetase, C-terminal domain
PF09340	1	2	2	1	1	1	1	Histone acetyltransferase subunit NuA4
PF08193	1	1	1	1	1	1	1	INO80 complex subunit Ies4
PF08578	1	1	1	1	1	1	1	Protein of unknown function (DUF1765)
PF12138	3	4	4	1	0	2	1	Spherulation-specific family 4
PF13385	1	1	1	2	1	0	1	Concanavalin A-like lectin/glucanases superfamily
PF23295	1	1	1	1	1	1	1	Armadillo-like repeats
PF17866	0	1	1	1	0	1	2	AAA lid domain
PF04084	1	1	1	1	1	1	2	Origin recognition complex subunit 2 RecA-like domain
PF24882	1	1	1	1	1	1	2	ORC2 WHD
PF08543	1	1	1	1	1	1	3	Phosphomethylpyrimidine kinase
PF08101	1	1	1	1	1	1	1	Meiotically up-regulated protein Msb1/Mug8 domain
PF04263	1	1	1	1	2	1	2	Thiamin pyrophosphokinase, catalytic domain
PF04265	1	1	1	1	2	1	2	Thiamin pyrophosphokinase, vitamin B1 binding domain
PF25140	1	1	1	1	2	1	1	GPI inositol-deacylase transmembrane domain
PF17283	0	0	0	1	1	0	2	SprT-like zinc ribbon domain
PF10259	0	0	1	2	1	2	2	Rogdi leucine zipper containing protein
PF04667	1	1	1	1	2	1	1	cAMP-regulated phosphoprotein/endosulfine conserved region
PF12850	1	3	3	3	2	1	1	Calcineurin-like phosphoesterase superfamily domain
PF10330	1	1	1	1	1	1	1	Putative Sin3 binding protein
PF12929	1	1	1	1	2	1	2	Stretch-activated Ca2+-permeable channel component
PF16922	1	1	1	1	1	1	2	DNA replication complex GINS protein SLD5 C-terminus
PF08638	1	2	2	1	1	1	1	Mediator complex subunit MED14
PF13396	1	1	1	0	1	0	2	Phospholipase_D-nuclease N-terminal

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF00001	0	1	1	2	1	0	2	7 transmembrane receptor (rhodopsin family)
PF23518	3	2	2	1	2	1	2	WW domain
PF23878	1	1	1	1	1	1	2	ELP1 TPR domain
PF23925	1	1	1	1	1	1	2	ELP1 alpha-solenoid
PF14847	1	2	2	1	1	1	1	Ras-binding domain of Byr2
PF03153	1	1	1	0	1	1	2	Transcription factor IIA, alpha/beta subunit
PF09996	2	1	1	0	3	1	2	Uncharacterized protein conserved in bacteria (DUF2237)
PF14429	1	1	1	2	1	0	1	C2 domain in Dock180 and Zizimin proteins
PF23554	1	1	1	2	1	0	1	Dedicator of cytokinesis (DOCK) TPR region
PF01883	1	0	0	0	2	1	1	Iron-sulfur cluster assembly protein
PF14701	1	0	0	2	1	1	2	Glycogen debranching enzyme, glucanotransferase domain
PF14702	1	0	0	2	1	1	2	Central domain of human glycogen debranching enzyme
PF08623	0	0	0	1	1	1	2	TATA-binding protein interacting (TIP20)
PF25782	0	0	0	1	1	1	2	CAND1-like, TPR repeats
PF05808	0	0	0	0	1	0	1	Podoplanin
PF07749	0	0	0	1	1	1	1	Endoplasmic reticulum protein ERp29, C-terminal domain
PF04622	1	1	1	0	1	0	3	ERG2 and Sigma1 receptor like protein
PF01757	1	3	3	7	8	2	1	Acyltransferase domain
PF22998	0	0	0	2	1	1	2	LYC1 GNAT-like C-terminal domain
PF14613	2	1	1	1	1	2	2	HAM1-like, C-terminal domain
PF19343	2	1	1	1	1	1	1	HAM1-like, N-terminal domain
PF13465	0	0	0	0	0	0	1	Zinc-finger double domain
PF12754	1	1	1	1	1	1	2	Get5, N-terminal domain
PF17183	1	1	1	1	1	1	2	Get5, C-terminal domain
PF07967	0	0	0	1	1	1	2	NuBaID N-terminal domain (aka zf-C3HC)
PF08600	0	0	0	1	1	1	2	NuBaID, C-terminal domain
PF11781	1	1	1	0	1	1	1	Zinc-finger of RNA-polymerase I-specific TFIIB, Rrn7
PF20644	1	1	1	1	1	1	1	Rrn7/TAF1B, N-terminal cyclin domain
PF00567	1	1	1	1	1	1	1	Tudor domain
PF06003	0	0	0	0	0	0	1	Survival motor neuron protein (SMN), Tudor domain
PF01454	1	1	1	1	1	1	1	MAGE homology domain
PF07189	1	1	1	1	1	1	1	Splicing factor 3B subunit 10 (SF3b10)
PF12053	0	0	0	0	0	0	1	N-terminal of Par3 and HAL proteins
PF08953	1	1	1	1	1	1	3	Domain of unknown function (DUF1899)
PF00209	1	2	2	0	5	0	1	Sodium:neurotransmitter symporter family
PF05907	1	1	1	1	1	2	3	CXXC motif containing zinc binding protein, eukaryotic
PF02138	1	1	1	1	1	2	1	Beige/BEACH domain
PF23325	1	1	1	3	1	2	1	GBF1-like, tetratrico peptide repeat region
PF05345	1	1	1	1	1	1	2	Putative Ig domain
PF13360	1	3	2	2	2	1	1	Outer membrane protein assembly factor BamB
PF25293	1	1	1	1	1	0	1	EMC1 N-terminal beta-propeller domain
PF03894	1	1	1	1	1	1	1	D-xylulose 5-phosphate/D-fructose 6-phosphate phosphoketolase
PF09364	1	1	1	1	1	1	1	XFP N-terminal domain
PF08284	1	1	1	0	2	1	1	Retroviral aspartyl protease
PF23914	0	0	0	0	0	0	2	Cytochrome c-type biogenesis protein H TPR domain
PF12775	1	1	1	1	2	0	1	P-loop containing dynein motor region
PF12780	1	1	1	1	2	0	1	P-loop containing dynein motor region D4
PF22597	1	1	1	1	2	0	1	Dynein heavy chain, ATPase lid domain
PF25416	1	1	1	1	1	1	1	GRHL1-like, C-terminal domain
PF13474	0	0	0	0	1	1	1	SnoaL-like domain
PF05141	1	0	0	1	2	1	1	Pyoverdine/dityrosine biosynthesis protein
PF00586	1	1	1	1	1	1	1	AIR synthase related protein, N-terminal domain
PF04121	1	1	1	1	1	1	1	Nuclear pore protein 84 / 107
PF23576	1	1	1	1	1	1	1	Helicase SEN1 beta-barrel domain
PF20520	1	1	1	1	1	1	3	V0 complex accessory subunit Ac45/VOA1 transmembrane domain
PF27676	1	1	1	1	1	0	3	BIG1 N-terminal domain
PF04931	1	1	1	1	1	1	1	DNA polymerase phi
PF17284	1	1	1	1	1	1	1	Spermidine synthase tetramerisation domain
PF04516	1	1	1	1	1	1	1	CP2 transcription factor
PF04769	1	1	0	0	1	1	1	Mating-type protein MAT alpha 1 HMG-box
PF23147	1	1	1	1	3	1	2	NAD-dependent glutamate dehydrogenase, N-terminal domain
PF23152	1	1	1	1	3	0	2	NAD-specific glutamate dehydrogenase, second domain
PF13015	1	1	1	1	1	0	2	Glucosidase II beta subunit-like protein
PF13936	0	1	1	0	0	0	1	Helix-turn-helix domain
PF00631	0	1	1	1	1	1	1	GGL domain
PF27809	1	1	1	1	1	1	1	Ino eighty subunit 1 N-terminal domain
PF06012	1	1	1	1	2	1	1	Domain of Unknown Function (DUF908)
PF09495	1	1	1	1	1	1	1	Protein of unknown function (DUF2462)
PF03221	4	3	4	5	3	3	2	Tc5 transposase DNA-binding domain
PF22250	1	1	1	1	1	0	2	Vacuolar membrane protease, C-terminal domain
PF25422	1	1	1	1	1	0	1	Domain of unknown function (DUF7892)
PF24855	2	1	1	1	1	1	1	Domain of unknown function (DUF7729)
PF01876	1	1	1	1	1	1	1	RNase P subunit p30
PF00538	1	1	1	1	1	1	1	linker histone H1 and H5 family
PF02517	1	1	1	1	2	1	1	Type II CAAX prenyl endopeptidase Rce1-like
PF04892	0	0	0	1	2	1	2	VanZ like family
PF10241	1	1	1	1	1	1	1	Uncharacterized conserved protein
PF04114	1	1	1	1	1	1	1	Gaa1-like, GPI transamidase component
PF02375	2	2	2	2	4	1	1	jmjN domain
PF06027	2	2	2	2	1	1	1	Solute carrier family 35
PF12044	1	1	1	2	3	1	1	Putative peptidase family
PF23381	1	4	3	3	1	0	1	IFT122 first beta-propeller
PF01120	1	3	3	1	2	0	1	Alpha-L-fucosidase
PF03932	0	0	0	1	2	0	1	CutC family
PF25141	1	1	1	1	2	1	1	GPI inositol-deacylase beta-sandwich domain
PF20510	1	1	1	2	3	1	1	Homogentisate 1,2-dioxygenase N-terminal
PF03208	1	2	2	1	1	1	2	PRA1 family protein
PF24669	0	0	0	0	0	0	1	Ddi2 HDD domain
PF12222	0	0	0	2	2	1	1	Peptide N-acetyl-beta-D-glucosaminyl asparaginase amidase A
PF01285	1	1	1	1	1	0	1	TEA/ATTS domain
PF02200	1	1	1	2	1	1	1	STE like transcription factor
PF24967	0	0	0	0	1	0	1	TR130 NTS domain
PF04926	1	1	1	1	1	1	1	Poly(A) polymerase predicted RNA binding domain
PF04928	1	1	1	1	1	0	1	Poly(A) polymerase central domain
PF02817	2	3	3	5	1	2	1	e3 binding domain
PF11865	1	1	1	1	1	1	1	Serine/threonine-protein kinase mTOR domain
PF16300	1	1	1	1	1	1	1	Type of WD40 repeat

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF11710	1	1	1	1	2	1	2	G protein-coupled glucose receptor regulating Gpa2
PF14599	1	1	1	1	2	0	1	Zinc-ribbon
PF08167	1	1	1	1	2	0	1	rRNA processing/ribosome biogenesis
PF02928	1	1	1	1	2	1	2	C5HC2 zinc finger
PF20653	1	1	1	1	1	1	1	Conserved Oligomeric Golgi complex subunit 6, C-terminal
PF12054	1	1	1	1	1	1	1	Domain of unknown function (DUF3535)
PF01015	1	1	1	1	1	1	1	Ribosomal S3Ae family
PF13886	1	1	1	1	2	0	1	TM7S3/TM198-like domain
PF27739	1	1	1	1	2	2	1	PEX8 C-terminal domain
PF27812	1	1	1	1	2	2	1	PEX8 central TPR-like domain
PF02076	1	1	1	1	1	0	1	Pheromone A receptor
PF07106	1	1	1	0	1	0	1	TBPIP/Hop2 winged helix domain
PF06742	2	3	3	0	2	0	1	Protein of unknown function (DUF1214)
PF13398	0	0	0	1	0	0	1	Peptidase M50B-like
PF09748	1	1	1	1	1	1	1	Transcription factor subunit Med10 of Mediator complex
PF04882	1	1	1	1	2	1	1	Peroxin-3
PF15613	1	1	1	1	1	1	1	Williams-Beuren syndrome DDT (WSD), D-TOX E motif
PF21235	1	1	1	2	1	1	1	E3 ubiquitin-protein ligase ARIH1, UBA-like domain
PF21392	1	0	0	0	0	1	0	Ubiquinone biosynthesis protein COQ9, N-terminal domain
PF13805	2	2	2	2	2	2	0	Eisosome component PIL1
PF08429	1	1	1	1	2	1	0	PLU-1-like protein
PF25178	0	0	0	0	0	1	0	WDR41
PF17846	1	2	2	3	1	1	0	Xrn1 helical domain
PF01247	1	1	1	1	1	1	0	Ribosomal protein L35Ae
PF16866	1	1	1	1	1	1	0	PHD-finger
PF21127	1	1	1	1	1	1	0	ATG1-like, MIT domain 2
PF03893	0	1	1	0	0	1	0	Lipase 3 N-terminal region
PF03256	1	1	1	1	1	1	0	Anaphase-promoting complex, subunit 10 (APC10)
PF05783	0	0	0	1	0	1	0	Dynein light intermediate chain (DLIC)
PF08581	1	1	1	1	1	1	0	Tup N-terminal
PF01134	1	1	1	1	1	1	0	Glucose inhibited division protein A
PF21680	1	1	1	1	1	1	0	tRNA modifying enzyme MnmG/GidA C-terminal helical domain
PF10451	0	0	0	0	0	1	0	Telomere regulation protein Stn1
PF04840	1	1	1	1	1	1	0	Vps16, C-terminal region
PF14611	0	0	0	1	0	1	0	SLS1 protein first KH domain
PF05502	0	1	1	1	1	1	0	Dynactin p62 family
PF21098	0	0	0	0	0	1	0	MTMR6-9, GRAM domain
PF02784	1	1	1	1	1	1	0	Pyridoxal-dependent decarboxylase, pyridoxal binding domain
PF10455	1	1	1	2	1	1	0	Bin/amphiphysin/Rvs domain for vesicular trafficking
PF27810	1	1	1	1	2	1	0	MSB2 C-terminal domain
PF24959	0	0	0	0	0	1	0	FHOD1/3 FH3 domain
PF03501	1	1	1	1	1	1	0	Plectin/S10 domain
PF13092	0	0	0	1	0	1	0	Centromere protein L
PF01381	0	0	0	1	0	1	0	Helix-turn-helix
PF01204	2	2	2	3	1	2	0	Trehalase
PF07492	1	1	1	2	1	1	0	Neutral trehalase Ca2+ binding domain
PF23043	0	0	0	0	0	1	0	UBE2O, SH3-B domain
PF13002	1	1	1	3	1	1	0	Arrestin_N terminal like
PF23943	0	0	0	0	0	1	0	PUS7L N-terminal domain
PF10013	0	0	0	0	1	1	0	Uncharacterized protein conserved in bacteria (DUF2256)
PF06522	0	0	0	1	2	1	0	NADH-ubiquinone reductase complex 1 MLRQ subunit
PF06090	0	0	0	1	0	1	0	Inositol-pentakisphosphate 2-kinase
PF05470	0	1	1	1	1	1	0	Eukaryotic translation initiation factor 3 subunit 8 N-terminus
PF23274	1	1	1	1	1	3	0	Domain of unknown function (DUF7077)
PF01833	0	0	1	1	1	1	0	IPT/TIG domain
PF25603	0	0	1	0	0	1	0	SPT23/MGA2 DNA-binding domain
PF22624	1	1	1	2	1	1	0	4'-phosphopantetheinyl transferase, N-terminal
PF10021	2	2	2	1	1	3	0	Microbial-type PARG, catalytic domain
PF05063	1	1	1	1	1	1	0	MT-A70
PF09598	0	1	1	1	1	1	0	Stm1
PF11526	0	0	0	1	0	2	0	Pef11, Clp1-interaction domain
PF08446	1	1	1	1	1	1	0	PAS fold
PF21399	1	1	1	0	0	1	0	Telomerase reverse transcriptase, C-terminal extension
PF05139	0	0	0	0	0	1	0	Erythromycin esterase
PF26280	0	0	0	1	0	1	0	Trs120/TRAPPC9, second Ig-like domain
PF26282	0	0	0	1	0	1	0	Trs120/TRAPPC9, third Ig-like domain
PF26283	1	1	1	1	0	1	0	Trs120/TRAPPC9, fourth Ig-like domain
PF11864	0	0	0	1	0	1	0	Domain of unknown function (DUF3384)
PF08601	1	1	1	0	1	1	0	Transcription factor PAP1
PF10033	2	1	1	1	1	1	0	Autophagy-related protein 13
PF22952	1	1	1	1	2	1	0	Eukaryotic type KH-domain (KH-domain type I)
PF09805	1	1	1	1	1	1	0	Nucleolar protein 12 (25kDa)
PF05303	0	1	1	0	1	1	0	GSKIP domain
PF01067	1	1	1	0	1	2	0	Calpain large subunit, domain III
PF02551	0	0	0	0	0	1	0	Acyl-CoA thioesterase
PF25381	1	1	1	1	2	2	0	Fungal PH-like domain
PF24513	1	1	1	1	0	1	0	Domain of unknown function (DUF7593)
PF24521	0	0	0	1	0	1	0	KRIT1 ankyrin-repeats domain
PF16275	1	1	1	3	1	1	0	Splicing factor 1 helix-hairpin domain
PF26916	0	0	0	1	0	1	0	Domain of unknown function (DUF8275)
PF08631	1	1	1	2	1	1	0	Meiosis protein SPO22/ZIP4 like
PF13094	0	0	0	1	0	1	0	CENP-Q, a CENPA-CAD centromere complex subunit
PF07217	3	3	3	2	2	3	0	Heterokaryon incompatibility protein Het-C
PF07958	2	2	2	2	1	1	0	Protein of unknown function (DUF1688)
PF03537	1	2	2	2	1	5	0	Glycoside-hydrolase family GH114
PF02417	0	0	0	1	0	1	0	Chromate transporter
PF06218	1	1	1	1	1	1	0	Nitrogen permease regulator 2
PF09110	1	1	1	1	1	1	0	HAND
PF09111	1	1	1	1	1	1	0	SLIDE
PF10497	1	1	1	1	1	1	0	Zinc-finger domain of monoamine-oxidase A repressor R1
PF10315	0	0	0	0	0	1	0	Altered inheritance of mitochondria protein 19
PF03131	2	3	3	1	1	1	0	bZIP Maf transcription factor
PF21162	0	0	0	1	1	1	0	ETF-QO, ubiquinone-binding
PF11416	2	2	1	1	1	1	0	Syntaxin-5 N-terminal, Sly1p-binding domain
PF14633	1	1	1	1	1	1	0	SH2 domain
PF21710	1	1	1	1	1	1	0	Spt6, S1/OB domain
PF09056	1	1	1	2	0	1	0	Prokaryotic phospholipase A2

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF13243	1	1	1	2	1	1	0	Squalene-hopene cyclase C-terminal domain
PF23217	1	0	0	0	0	1	0	Domain of unknown function (DUF7066)
PF12770	0	0	0	0	0	1	0	CHAT domain
PF11489	1	1	1	1	1	1	0	Altered inheritance of mitochondria protein 21
PF25097	1	1	1	0	1	1	0	Cnot1 ARM repeat
PF14699	1	0	0	2	1	1	0	N-terminal domain from the human glycogen debranching enzyme
PF09341	1	1	1	1	1	2	0	Transcription factor Pcc1
PF05238	0	0	0	1	0	1	0	Kinetochore protein CHL4 like
PF22741	0	0	0	0	1	1	0	DSP-PTPase phosphatase fused to NAD+ Kinase
PF00612	4	4	4	2	3	2	0	IQ calmodulin-binding motif
PF08303	1	1	1	1	1	1	0	tRNA ligase kinase domain
PF09511	1	1	1	1	1	1	0	RNA ligase
PF06745	0	1	1	0	1	2	0	KaiC
PF06423	1	1	1	1	1	1	0	GWT1
PF23284	1	1	1	1	1	1	0	Transcription elongation factor SPT5, second KOW domain
PF12014	1	1	1	1	1	1	0	Cyclin D1 binding domain
PF16558	2	1	1	2	1	1	0	Amino-terminal Zinc-binding domain of ubiquitin ligase E3A
PF15413	0	0	0	1	0	3	0	Pleckstrin homology domain
PF26087	1	1	1	2	2	1	0	Domain of unknown function (DUF8032)
PF01981	1	1	1	1	0	1	0	Peptidyl-tRNA hydrolase PTH2
PF10165	1	1	1	1	1	1	0	Guanine nucleotide exchange factor synembryn
PF18859	0	0	0	1	1	1	0	Actinobacteria/chloroflexi VLRF1 release factor
PF13347	0	0	0	2	2	2	0	MFS/sugar transport protein
PF07005	1	1	1	3	2	1	0	Sugar-binding N-terminal domain
PF22591	1	1	1	1	1	1	0	eIF3a, PCI domain, TPR-like region
PF13945	2	2	2	1	2	1	0	Salt tolerance down-regulator
PF20571	0	0	0	0	0	1	0	Domain of unknown function (DUF6780)
PF05532	0	0	0	1	0	1	0	CsbD-like
PF09794	1	1	1	1	1	1	0	Transport protein Avl9
PF20645	1	1	1	1	1	1	0	Rrn7/TAF1B, C-terminal cyclin domain
PF10496	1	0	0	1	1	1	0	SNARE-complex protein Syntaxin-18 N-terminus
PF03951	1	1	1	1	1	1	0	Glutamine synthetase, beta-Grasp domain
PF12921	1	1	1	1	1	1	0	Mitochondrial ATPase expression
PF00900	1	1	1	1	1	1	0	Ribosomal family S4e
PF08071	1	1	1	1	1	1	0	RS4NT (NUC023) domain
PF09243	1	1	1	1	1	1	0	Mitochondrial small ribosomal subunit Rsm22
PF10495	1	1	1	1	1	1	0	Pericentrin-AKAP-450 domain of centrosomal targeting protein
PF04194	1	1	1	1	1	1	0	Programmed cell death protein 2, C-terminal putative domain
PF04494	1	2	2	1	1	1	0	WD40 associated region in TFIID subunit, NTD2 domain
PF03721	1	1	1	2	7	2	0	UDP-glucose/GDP-mannose dehydrogenase family, NAD binding domain
PF10528	0	0	0	1	2	2	0	GLEYA domain
PF08612	0	0	0	0	0	1	0	TATA-binding related factor (TRF) of subunit 20 of Mediator complex
PF12776	0	0	0	1	0	2	0	Myb/SANT-like DNA-binding domain
PF13232	0	0	0	0	0	1	0	Complex1_LYR-like
PF07738	1	1	1	1	2	2	0	Sad1 / UNC-like C-terminal
PF01259	1	1	1	1	1	1	0	SAICAR synthetase
PF08637	1	1	1	1	1	1	0	ATP synthase regulation protein NCA2
PF27562	1	1	1	1	1	1	0	APC1 fourth domain
PF03718	0	0	0	1	0	1	0	Glycosyl hydrolase family 49
PF17433	0	0	0	1	0	1	0	Glycosyl hydrolase family 49 N-terminal Ig-like domain
PF18783	0	0	0	1	0	1	0	Isopullulanase beta-solenoid repeat
PF18841	0	0	0	1	0	1	0	Beta solenoid repeat from Dextranase
PF10304	0	0	0	1	0	1	0	Required for nuclear transport of RNA pol II C-terminus 2
PF10363	0	0	0	1	0	1	0	Required for nuclear transport of RNA pol II C-terminus 1
PF11785	1	1	1	1	1	1	0	Aft1 osmotic stress response (OSM) domain
PF11786	1	1	1	1	1	1	0	Aft1 HRA domain
PF01471	0	0	0	0	0	1	0	Putative peptidoglycan binding domain
PF10232	1	1	1	1	2	1	0	Mediator of RNA polymerase II transcription complex subunit 8
PF17144	1	1	1	1	1	1	0	Ribosomal large subunit proteins 60S L5, and 50S L18
PF09273	0	0	0	0	0	1	0	Rubisco LSMT substrate-binding
PF28387	0	0	0	0	0	1	0	BfoA N-terminal domain
PF07926	1	1	1	1	1	1	0	TPR/MLP1/MLP2-like protein
PF25785	2	1	1	1	1	1	0	Nucleoprotein TPR-like domain
PF18916	0	0	0	1	0	1	0	Lycopene cyclase
PF05769	0	0	0	0	0	2	0	SIKE family
PF08433	1	1	1	2	2	1	0	Chromatin associated protein KTI12
PF00316	2	2	2	2	1	1	0	Fructose-1-6-bisphosphatase, N-terminal domain
PF18913	2	2	2	2	1	1	0	Fructose-1-6-bisphosphatase, C-terminal domain
PF09288	0	0	0	1	1	1	0	Fungal ubiquitin-associated domain
PF28296	1	1	1	1	2	1	0	Maintenance of telomere capping protein 4 N-terminal domain
PF10587	1	1	1	1	1	1	0	Eukaryotic elongation factor 1 beta central acidic region
PF13880	1	1	1	0	0	1	0	ESCO1/2 acetyl-transferase
PF01283	1	1	1	1	1	1	0	Ribosomal protein S26e
PF18345	1	2	2	0	0	3	0	Zinc finger domain
PF13541	1	1	1	1	1	1	0	Subunit ChlI of Mg-chelatase
PF08672	0	0	0	1	0	1	0	Anaphase promoting complex (APC) subunit 2
PF01183	1	0	0	2	2	1	0	Glycosyl hydrolases family 25
PF12411	1	1	1	1	1	2	0	Choline sulfatase enzyme C terminal
PF10155	0	0	0	0	0	1	0	CCR4-NOT transcription complex subunit 11
PF27642	0	0	0	0	0	1	0	Uncharacterized protein C23H4.16c N-terminal domain
PF00707	0	0	0	1	0	1	0	Translation initiation factor IF-3, C-terminal domain
PF03235	0	0	0	0	0	1	0	GmrSD restriction endonuclease, N-terminal domain
PF03259	1	1	1	1	0	1	0	Roadblock/LC7 domain
PF01092	1	1	1	1	1	1	0	Ribosomal protein S6e
PF10224	0	1	1	1	2	1	0	Short coiled-coil protein
PF24160	1	1	1	0	0	1	0	Root UVB sensitive protein, C-terminal
PF24694	0	0	0	1	0	1	0	PITM 1-3, LNS2 domain
PF12765	0	1	2	1	3	1	0	HEAT repeat associated with sister chromatid cohesion
PF10361	0	0	0	1	0	1	0	Protein of unknown function (DUF2434)
PF25080	2	1	1	2	2	1	0	RING zinc finger-like domain
PF10346	2	1	1	2	0	2	0	Conidiation protein 6
PF06859	1	1	1	0	0	1	0	Bicoid-interacting protein 3 (Bin3)
PF08285	1	1	1	1	1	1	0	Dolichol-phosphate mannosyltransferase subunit 3 (DPM3)
PF23258	1	1	1	1	2	1	0	Domain of unknown function (DUF7072)
PF09421	1	1	1	1	1	1	0	Frequency clock protein
PF00670	1	2	1	1	1	1	0	S-adenosyl-L-homocysteine hydrolase, NAD binding domain
PF14658	1	1	1	1	1	1	0	EF-hand domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF12761	1	1	1	1	1	1	0	Actin cytoskeleton-regulatory complex protein END3
PF24340	2	2	2	1	1	1	0	DBL homology domain (DH-domain)
PF24344	2	2	2	1	1	1	0	PH domain
PF12998	1	2	2	1	1	1	0	Inhibitor of growth proteins N-terminal histone-binding
PF13598	0	0	0	1	0	1	0	Domain of unknown function (DUF4139)
PF13600	0	0	0	1	0	1	0	N-terminal domain of unknown function (DUF4140)
PF08267	1	1	1	1	1	1	0	Cobalamin-independent synthase, N-terminal domain
PF04143	1	0	0	2	0	1	0	Sulphur transport
PF00325	0	0	0	0	0	1	0	Bacterial regulatory proteins, crp family
PF01655	1	1	1	1	1	1	0	Ribosomal protein L32
PF15519	1	1	1	1	1	1	0	linker between RRM2 and RRM3 domains in RBM39 protein
PF25326	1	1	1	1	1	1	0	SRB8 ARM-like domain
PF14595	0	0	0	0	0	1	0	Thioredoxin
PF19304	1	1	1	1	2	1	0	D-3-phosphoglycerate dehydrogenase intervening domain
PF02254	0	0	0	0	0	1	0	TrkA-N domain
PF13934	0	0	0	1	0	1	0	Nuclear pore complex assembly
PF11704	0	0	0	1	0	1	0	Vesicle coat protein involved in Golgi to plasma membrane transport
PF12705	0	0	0	1	0	1	0	PD-(D/E)XK nuclease superfamily
PF20206	1	1	1	2	2	1	0	Tra1 HEAT repeat ring region
PF28224	1	0	0	1	1	1	0	Nucleolar protein 6 C-terminal domain
PF25762	1	2	2	1	1	1	0	HAUS augmin-like complex subunit 1
PF01930	0	0	0	1	0	1	0	Domain of unknown function DUF83
PF21123	0	0	0	1	0	1	0	Dna2 Rift barrel domain
PF08297	0	0	0	1	0	1	0	U3 snoRNA associated
PF02861	0	0	0	1	0	1	0	Clp repeat (R) N-terminal domain
PF23936	1	1	1	1	1	1	0	ELP1 three-helix bundle
PF13741	0	0	0	1	0	1	0	Mitochondrial ribosomal protein S25
PF07543	0	0	0	1	0	1	0	Protein trafficking PGA2
PF12660	1	1	1	1	1	1	0	Putative zinc-finger of transcription factor IIIC complex
PF02927	0	0	0	0	0	1	0	Cellulase N-terminal ig-like domain
PF00759	0	0	0	0	0	1	0	Glycosyl hydrolase family 9
PF14844	1	1	1	1	1	2	0	PH domain associated with Beige/BEACH
PF12013	0	3	3	2	3	6	0	Orsellinic acid/F9775 biosynthesis cluster protein D
PF10291	1	1	1	1	1	1	0	Muniscin C-terminal mu homology domain
PF22699	1	0	0	0	2	1	0	GEM-interacting protein-like, FCH domain
PF18089	0	0	0	0	0	1	0	DAPG hydrolase PhiG domain
PF04152	1	1	1	1	2	1	0	Mre11 DNA-binding presumed domain
PF27979	0	1	1	2	2	1	0	CON7 transcription factor helical domain
PF22892	1	1	1	1	1	1	0	MRPL44 dsRNA-binding domain
PF18391	0	0	0	0	0	1	0	CHIP N-terminal tetratricopeptide repeat domain
PF11338	0	0	0	1	1	1	0	Protein of unknown function (DUF3140)
PF06747	2	3	3	1	2	2	0	CHCH domain
PF01447	1	0	0	1	0	1	0	Thermolysin metallopeptidase, catalytic domain
PF02868	1	0	0	1	0	1	0	Thermolysin metallopeptidase, alpha-helical domain
PF00297	1	1	1	1	3	1	0	Ribosomal protein L3
PF25545	0	0	0	3	0	2	0	Domain of unknown function (DUF7924)
PF20246	1	2	3	1	1	2	0	Family of unknown function (DUF6601)
PF25115	2	3	3	0	0	5	0	Agd3 deacetylase domain
PF25116	2	3	3	0	0	1	0	Agd3 CBM87
PF25117	2	3	3	0	0	5	0	Agd3 C-terminal domain
PF03360	0	0	0	0	0	1	0	Glycosyltransferase family 43
PF22352	3	2	2	0	0	2	0	K319L-like, PKD domain
PF13867	1	1	1	1	0	1	0	Sin3 binding region of histone deacetylase complex subunit SAP30
PF24714	0	0	0	0	0	3	0	TORTIFOLIA1 N-terminal
PF14598	1	1	1	0	0	1	0	PAS domain
PF14529	0	1	1	0	6	2	0	Endonuclease-reverse transcriptase
PF05870	1	1	1	0	1	1	0	Phenolic acid decarboxylase (PAD)
PF22036	0	0	0	0	0	1	0	MoaF-like
PF17897	0	0	0	0	0	1	0	Vanadium chloroperoxidase N-terminal domain
PF22778	1	0	0	0	0	1	0	VCPO second helical-bundle domain
PF23202	1	1	1	2	3	2	0	ZNF598 PAH domain
PF23230	1	1	1	2	3	2	0	C2H2-type zinc finger
PF20516	0	2	3	0	2	5	0	PD-(D/E)XK nuclease superfamily
PF09496	0	0	0	1	0	1	0	Cenp-O kinetochore centromere component
PF22354	4	4	4	2	2	1	0	Hydrophobin
PF04172	0	0	0	3	0	1	0	LrgB-like family
PF08611	0	0	0	1	0	1	0	Fungal protein of unknown function (DUF1774)
PF09350	1	1	1	1	1	1	0	DnaJ homologue, subfamily C, member 28, conserved domain
PF07741	0	1	1	1	1	2	0	Brf1-like TBP-binding domain
PF16657	1	2	2	0	0	1	0	Maltogenic Amylase, C-terminal domain
PF00468	0	0	0	1	0	1	0	Ribosomal protein L34
PF17046	0	0	0	0	0	2	0	SesB domain on fungal death-pathway protein
PF10306	1	1	1	1	1	1	0	Hypothetical protein FLILHELTA
PF10390	0	0	0	0	0	1	0	RNA polymerase II elongation factor ELL
PF04471	1	1	1	1	1	1	0	Restriction endonuclease
PF09759	1	1	1	1	1	1	0	Spinocerebellar ataxia type 10 protein domain
PF12047	0	0	0	0	0	1	0	Cytosine specific DNA methyltransferase replication foci domain
PF00210	0	0	0	0	0	1	0	Ferritin-like domain
PF20635	0	0	0	1	0	1	0	Survival Motor Neuron, YG-box
PF11916	1	1	2	1	1	1	0	Vacuolar protein 14 C-terminal Fig4p binding
PF23010	1	1	1	1	2	1	0	PHLPP protein RA domain
PF13848	1	1	1	1	1	1	0	Thioredoxin-like domain
PF11700	5	3	3	1	4	1	0	Vacuole effluxer Atg22 like
PF20248	0	0	0	0	0	1	0	Family of unknown function (DUF6603)
PF03587	2	2	2	2	2	1	0	EMG1/NEP1 methyltransferase
PF05871	1	1	1	1	2	1	0	ESCRT-II complex subunit
PF19314	0	0	0	0	0	1	0	Family of unknown function (DUF5917)
PF26571	0	0	0	1	0	1	0	VldE, C-terminal domain
PF05834	0	0	0	0	0	1	0	Lycopene cyclase protein
PF09072	1	1	1	1	1	1	0	Translation machinery associated TMA7
PF01749	1	1	1	1	1	1	0	Importin beta binding domain
PF16186	1	1	1	1	1	1	0	Atypical Arm repeat
PF28351	0	0	0	1	2	1	0	CLZ1 N-terminal domain
PF24492	1	1	1	1	2	2	0	Proteasome adapter and scaffold protein ECM29, HEAT-repeat domain
PF07250	2	2	2	1	2	1	0	Glyoxal oxidase N-terminus
PF04252	1	1	1	2	1	1	0	Protein arginine N-methyltransferase SFM1-like
PF14773	1	0	0	1	1	1	0	Helicase-associated putative binding domain, C-terminal

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF25806	1	0	0	1	1	1	0	ERCC6L2-like, ribbon-helix-helix domain
PF23561	0	0	0	0	0	1	0	C2H2 zinc finger
PF15406	1	1	1	1	1	2	0	Pleckstrin homology domain
PF05462	0	1	1	2	0	1	0	Slime mold cyclic AMP receptor
PF04760	0	0	0	1	1	1	0	Translation initiation factor IF-2, N-terminal region
PF03707	1	1	1	1	1	1	0	Bacterial signalling protein N terminal repeat
PF04218	2	1	1	3	1	1	0	CENP-B N-terminal DNA-binding domain
PF16294	0	0	0	0	0	1	0	RNSP1-SAP18 binding (RSB) motif
PF01918	1	0	0	0	3	1	0	Alba
PF14864	0	0	0	0	1	1	0	Alkyl sulfatase C-terminal
PF05365	1	1	1	1	1	1	0	Cytochrome b-c1 complex subunit 9
PF13524	1	0	0	0	1	1	0	Glycosyl transferase-like
PF06025	1	1	1	1	2	1	0	Domain of Unknown Function (DUF913)
PF23865	1	0	0	2	3	1	0	Domain of unknown function (DUF7223)
PF23354	1	1	1	1	0	1	0	NUP160/120 middle TPR
PF02100	1	1	1	1	1	1	0	Ornithine decarboxylase antizyme
PF12454	1	1	1	0	1	1	0	GPI-anchored cell wall organization protein
PF08326	2	2	2	1	1	1	0	Acetyl-CoA carboxylase, central region
PF21385	2	2	2	1	1	1	0	Acetyl-CoA carboxylase, BT domain
PF28431	0	0	0	0	0	1	0	Domain of unknown function (DUF8392)
PF01741	0	0	0	1	0	1	0	Large-conductance mechanosensitive channel, MscL
PF28329	2	2	2	2	1	2	0	Zinc finger transcription factor ace1 N-terminal domain
PF28347	2	2	2	2	1	2	0	ACE1 small beta sheet domain
PF13917	1	1	1	1	0	1	0	Zinc knuckle
PF12030	0	0	0	1	0	1	0	Domain of unknown function (DUF3517)
PF14518	0	1	1	1	0	2	0	Iron-containing redox enzyme
PF00221	1	1	1	1	1	1	0	Aromatic amino acid lyase
PF19977	0	0	0	0	0	1	0	xRRM domain
PF08221	1	1	1	1	1	1	0	RNA polymerase III subunit RPC82 helix-turn-helix domain
PF02791	1	1	1	1	1	1	0	DDT domain
PF27653	0	0	0	1	0	1	0	Spore killer 2 N-terminal domain
PF09587	0	0	0	0	2	1	0	Bacterial capsule synthesis protein PGA_cap
PF08732	1	1	1	1	2	1	0	HIM1
PF11196	0	0	0	0	0	1	0	Protein of unknown function DUF2834
PF03813	1	1	1	1	1	1	0	Nrap protein domain 1
PF10961	0	0	0	0	0	1	0	Selenoprotein SelK_SelG
PF23011	0	0	0	1	0	1	0	Histone-lysine N-methyltransferase NSD-like, PHD zinc finger 1
PF03643	1	1	1	1	1	1	0	Vacuolar protein sorting-associated protein 26
PF10591	0	0	0	0	0	2	0	Secreted protein acidic and rich in cysteine Ca binding region
PF03781	1	2	2	1	1	1	0	Sulfatase-modifying factor enzyme 1-like domain
PF12867	1	2	2	1	1	1	0	DinB superfamily
PF07983	2	1	1	1	2	1	0	X8 domain
PF25156	0	0	0	2	2	1	0	PNGase_A C-terminal domain
PF19445	1	0	0	1	0	1	0	C-terminal region of eIF3h
PF01568	0	0	0	0	1	1	0	Molydopterin dinucleotide binding domain
PF08630	0	0	0	1	2	2	0	Dfp1/Him1, central region
PF22437	0	0	0	1	2	2	0	BRCT domain
PF02594	0	0	0	1	0	1	0	Uncharacterised ACR, YggU family COG1872
PF08785	0	1	0	1	1	1	0	Ku C terminal domain like
PF21071	1	1	1	0	2	1	0	LARP1 HEAT repeat region
PF20354	1	2	2	1	1	1	0	Family of unknown function (DUF6649)
PF24818	0	0	0	1	1	1	0	TRF2/HOY1 PH-like domain
PF07249	3	2	2	1	1	1	0	Cerato-platanin
PF07052	0	2	2	1	0	1	0	Hepatocellular carcinoma-associated antigen 59
PF12520	1	0	0	0	0	1	0	Protein of unknown function (DUF3723)
PF02655	0	0	0	3	1	1	0	ATP-grasp domain
PF10343	0	0	0	1	0	1	0	Queuosine salvage protein
PF12359	1	1	1	0	2	1	0	Protein of unknown function (DUF3645)
PF14273	0	0	0	1	0	1	0	Domain of unknown function (DUF4360)
PF03184	2	2	5	0	0	1	0	DDE superfamily endonuclease
PF26970	0	0	0	1	0	1	0	Ubiquitin-like domain
PF25396	1	1	1	2	1	1	0	ZNFX1 domain
PF05933	0	0	0	0	0	1	0	Fungal ATP synthase protein 8 (A6L)
PF19327	1	1	1	1	2	1	0	Ap4A phosphorylase N-terminal domain
PF12774	1	1	1	1	2	1	0	Hydrolytic ATP binding site of dynein motor region
PF22254	1	0	0	1	0	1	0	Tfa2 E-tether
PF07720	0	0	0	0	0	3	0	Tetratricopeptide repeat
PF19287	0	0	0	0	0	1	0	Family of unknown function (DUF5910)
PF24534	0	2	1	3	6	1	0	PCA1 HMA heavy metal-associated domain
PF06355	0	0	0	0	0	1	0	Aegerolysin
PF04434	0	0	0	1	0	1	0	SWIM zinc finger
PF27039	0	1	1	0	0	1	0	ZBED1 RNase-like helical domain
PF12777	1	1	1	1	2	1	0	Microtubule-binding stalk of dynein motor
PF14826	1	1	1	1	1	1	0	FACT complex subunit SPT16 N-terminal lobe domain
PF09447	0	0	0	1	0	1	0	Cnl2/NKP2 family protein
PF01170	1	1	1	0	1	1	0	RMKL-like, methyltransferase domain
PF07961	1	1	1	1	0	0	0	MBA1-like protein
PF02128	1	1	1	2	0	0	0	Fungalysin metallopeptidase (M36)
PF07504	1	1	1	2	0	0	0	Fungalysin/Thermolysin Propeptide Motif
PF26641	1	1	1	0	1	0	0	Domain of unknown function (DUF8213)
PF05630	1	2	2	8	2	0	0	Necrosis inducing protein (NPP1)
PF02838	2	1	1	2	1	0	0	Glycosyl hydrolase family 20, domain 2
PF11034	2	1	1	2	1	0	0	Glucose-repressible protein Grg1
PF00544	9	8	7	5	2	0	0	Pectate lyase
PF13367	1	1	1	0	1	0	0	PrsW family intramembrane metalloprotease
PF23617	1	0	0	1	0	0	0	EF-hand
PF02102	4	4	4	2	3	0	0	Deuterolysin metalloprotease (M35) family
PF05433	1	1	1	0	2	0	0	Glycine zipper 2TM domain
PF17237	1	0	0	1	0	0	0	ERMES regulator 1
PF14609	1	1	1	1	1	0	0	Gamma-Tubulin ring complex non-core subunit mod21, N-terminal
PF20685	1	1	1	1	1	0	0	Gamma-Tubulin ring complex non-core subunit mod21, C-terminal
PF12903	1	0	0	0	0	0	0	Protein of unknown function (DUF3830)
PF12657	1	1	1	1	1	0	0	Transcription factor IIIC subunit delta bet-propeller domain
PF17851	6	5	5	3	1	0	0	Beta xylosidase C-terminal Concanavalin A-like domain
PF03900	1	2	2	2	0	0	0	Porphobilinogen deaminase, C-terminal domain
PF12831	2	2	2	4	0	0	0	FAD dependent oxidoreductase
PF02178	4	1	1	3	0	0	0	AT hook motif

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF16155	1	2	2	0	2	0	0	4-hydroxylaminobenzoate lyase
PF21761	1	0	0	0	0	0	0	NADPH-dependent reductive aminase-like, C-terminal domain
PF16172	1	1	1	2	1	0	0	DOCK N-terminus
PF01391	2	0	1	0	2	0	0	Collagen triple helix repeat (20 copies)
PF14663	1	1	1	1	1	0	0	Rapamycin-insensitive companion of mTOR RasGEF_N domain
PF14668	1	1	1	1	1	0	0	Rapamycin-insensitive companion of mTOR, domain 5
PF05048	1	1	1	0	0	0	0	Periplasmic copper-binding protein (NosD)
PF13229	5	4	5	2	0	0	0	Right handed beta helix region
PF14616	1	1	1	1	1	0	0	Transcription regulator Rua1, C-terminal
PF22251	1	1	1	1	1	0	0	Vacuolar membrane protease, transmembrane domain
PF14033	2	3	3	1	1	0	0	Protein of unknown function (DUF4246)
PF10067	5	4	3	2	0	0	0	Predicted membrane protein (DUF2306)
PF17852	1	1	1	1	2	0	0	Dynein heavy chain AAA lid domain
PF09227	2	1	1	0	0	0	0	Bubble protein
PF12015	1	1	1	0	0	0	0	Bud3, N-terminal
PF03211	6	3	3	4	1	0	0	Pectate lyase
PF06766	2	2	2	3	6	0	0	Fungal hydrophobin
PF00195	1	1	1	2	0	0	0	Chalcone and stilbene synthases, N-terminal domain
PF02797	1	1	0	2	0	0	0	Chalcone and stilbene synthases, C-terminal domain
PF08541	1	0	0	1	0	0	0	3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III C terminal
PF06110	1	1	1	0	0	0	0	Thioredoxin domain-containing protein 17-like, thioredoxin domain
PF02423	4	0	0	2	1	0	0	Ornithine cyclodeaminase/mu-crystallin family
PF23036	1	1	1	0	1	0	0	Trafficking protein particle complex subunit 10-like, N-terminal
PF05257	1	0	0	2	0	0	0	CHAP domain
PF05841	1	0	1	0	1	0	0	Apc15p protein
PF04428	1	1	1	1	1	0	0	Choline kinase N terminus
PF09733	1	1	1	1	0	0	0	VEFS-Box of polycomb protein
PF10333	1	1	1	0	1	0	0	GPI-Mannosyltransferase II co-activator
PF00685	1	1	1	1	0	0	0	Sulfotransferase domain
PF06863	3	3	3	0	2	0	0	Protein of unknown function (DUF1254)
PF03575	1	1	1	0	0	0	0	Peptidase family S51
PF04299	1	1	1	1	1	0	0	Putative FMN-binding domain
PF26204	1	2	2	1	0	0	0	Fungal Med14 domain
PF00375	1	1	1	1	0	0	0	Sodium:dicarboxylate symporter family
PF01731	2	2	2	1	2	0	0	Arylesterase
PF22842	1	1	1	1	0	0	0	Pel9A-like, right handed beta helix region
PF13482	1	0	0	0	1	0	0	RNase_H superfamily
PF12141	1	1	1	0	0	0	0	Beta-mannosyltransferases
PF04960	1	1	1	1	0	0	0	Glutaminase
PF07779	1	1	1	1	0	0	0	10 TM Acyl Transferase domain found in Cas1p
PF07938	1	0	0	0	0	0	0	Fungal fucose-specific lectin
PF02065	1	1	1	2	1	0	0	Melibiase
PF16874	1	1	1	1	1	0	0	Glycosyl hydrolase family 36 C-terminal domain
PF16875	1	1	1	2	1	0	0	Glycosyl hydrolase family 36 N-terminal domain
PF00497	1	0	0	0	0	0	0	Bacterial extracellular solute-binding proteins, family 3
PF23625	1	0	0	0	2	0	0	Ubiquitin interaction motif
PF08457	1	1	1	0	1	0	0	Sfi1 spindle body protein
PF14330	2	0	0	4	0	0	0	Domain of unknown function (DUF4387)
PF21340	1	1	1	0	0	0	0	Cip1-like, core domain
PF13933	1	2	2	1	2	0	0	Putative peptidase family
PF01607	1	1	1	0	3	0	0	Chitin binding Peritrophin-A domain
PF07683	3	2	2	1	2	0	0	Cobalamin synthesis protein cobW C-terminal domain
PF08560	1	1	1	1	0	0	0	Protein of unknown function (DUF1757)
PF17674	1	1	1	1	1	0	0	HHH domain
PF12752	1	1	1	1	2	0	0	SUZ domain
PF08212	1	1	1	1	0	0	0	Lipocalin-like domain
PF09830	1	1	1	2	2	0	0	ATP adenylyltransferase C-terminal domain
PF18777	1	1	1	1	1	0	0	Chromosome region maintenance or exportin repeat
PF18784	1	1	1	1	1	0	0	CRM1 / Exportin repeat 2
PF25909	1	1	1	1	1	0	0	AHC1 C2H2 zinc-finger domain
PF04762	2	1	1	1	1	0	0	ELP1 first N-terminal beta-propeller
PF23797	2	1	1	1	1	0	0	ELP1 N-terminal second beta-propeller
PF03088	1	2	2	0	0	0	0	Strictosidine synthase
PF00848	2	3	3	4	2	0	0	Ring hydroxylating alpha subunit (catalytic domain)
PF16350	2	1	1	1	1	0	0	FAD dependent oxidoreductase central domain
PF22803	1	1	1	3	0	0	0	Glycan binding domain Y3
PF00832	1	1	1	0	1	0	0	Ribosomal L39 protein
PF26616	2	1	1	0	4	0	0	CorA-like transporters
PF02595	1	1	1	1	0	0	0	Glycerate kinase family
PF05704	1	1	1	2	3	0	0	Capsular polysaccharide synthesis protein
PF07221	1	0	0	0	0	0	0	N-acylglucosamine 2-epimerase (GlcNAc 2-epimerase)
PF00165	1	1	1	0	0	0	0	Bacterial regulatory helix-turn-helix proteins, AraC family
PF04749	1	1	1	2	2	0	0	PLAC8 family
PF16355	1	0	0	1	0	0	0	Domain of unknown function (DUF4982)
PF18565	1	0	0	1	0	0	0	Glycoside hydrolase family 2 C-terminal domain 5
PF13593	1	1	1	1	2	0	0	SBF-like CPA transporter family (DUF4137)
PF25006	2	2	2	1	2	0	0	Domain of unknown function (DUF7783)
PF25008	2	2	2	1	2	0	0	Domain of unknown function (DUF7784)
PF24666	1	0	0	0	0	0	0	Fungal C2H2 zinc finger
PF10344	1	1	1	0	1	0	0	Hobbit/FMP27/BTLP2 family
PF24626	2	0	0	0	2	0	0	Tf2-1-like, SH3 domain
PF10233	1	0	0	1	1	0	0	Uncharacterized conserved protein CG6151-P
PF01989	1	0	0	2	2	0	0	Aconitase X swivel domain
PF04412	1	0	0	2	2	0	0	Aconitase X first domain
PF28403	1	0	0	2	2	0	0	Aconitase X second domain
PF28406	1	0	0	2	2	0	0	Aconitase X third domain
PF02311	1	1	1	0	0	0	0	AraC-like ligand binding domain
PF22740	1	0	1	0	0	0	0	RapZ C-terminal domain
PF25598	1	1	1	0	0	0	0	Plant U-box protein ARM repeat region
PF05592	2	3	2	3	0	0	0	Bacterial alpha-L-rhamnosidase concanavalin-like domain
PF08531	2	3	2	3	0	0	0	Alpha-L-rhamnosidase N-terminal domain
PF25788	2	3	2	3	0	0	0	Rha78A-like, N-terminal immunoglobulin domain
PF13230	1	1	1	0	0	0	0	Glutamine amidotransferases class-II
PF19501	1	1	1	1	0	0	0	PcRGLX-like N-terminal RIFT barrel domain
PF21345	1	1	1	1	0	0	0	PcRGLX-like protein central beta sandwich domain
PF21346	1	1	1	1	0	0	0	PcRGLX-like protein C-terminal alpha/alpha toroid domain
PF05198	1	1	1	0	0	0	0	Translation initiation factor IF-3, N-terminal domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF20736	1	1	1	3	2	0	0	Beta-L-arabinofuranosidase, GH127 middle domain
PF20737	1	1	1	0	2	0	0	Glycoside hydrolase family 127 C-terminal domain
PF25904	1	1	1	1	1	0	0	Tmrp11 THUMP N-terminal domain
PF20162	1	1	1	1	1	0	0	Septation protein etd1
PF26607	1	0	0	1	0	0	0	PLL-like beta propeller
PF16865	1	0	0	0	0	0	0	Glutathione S-transferase, C-terminal domain
PF14542	1	1	1	0	0	0	0	GCN5-related N-acetyl-transferase
PF04305	1	1	1	0	0	0	0	Protein of unknown function (DUF455)
PF11051	2	1	2	2	2	0	0	Mannosyltransferase putative
PF03577	1	1	1	0	1	0	0	Peptidase family C69
PF03777	1	0	0	0	0	0	0	ChpA-C
PF12821	1	0	0	1	1	0	0	Threonine/Serine exporter, ThrE
PF14248	1	1	1	0	0	0	0	Domain of unknown function (DUF4345)
PF24827	2	1	1	0	0	0	0	Succinylglutamate desuccinylase/Aspartoacylase catalytic domain
PF23280	1	1	0	1	0	0	0	Fungal tetratrico peptide repeats
PF28223	1	1	1	2	2	0	0	CAP22
PF18402	1	1	1	1	1	0	0	Thioredoxin-like domain
PF13376	1	1	1	1	2	0	0	Bacteriocin-protection, YdeI or OmpD-Associated
PF28474	1	1	1	1	2	0	0	Domain of unknown function (DUF8412)
PF02449	1	2	2	0	0	0	0	Beta-galactosidase
PF08532	1	2	2	0	0	0	0	Beta-galactosidase trimerisation domain
PF05699	1	2	3	0	0	0	0	hAT family C-terminal dimerisation region
PF27671	1	1	1	0	1	0	0	YPL277C N-terminal domain
PF00444	1	1	1	1	0	0	0	Ribosomal protein L36
PF09962	1	1	1	1	1	0	0	Uncharacterized conserved protein (DUF2196)
PF01341	1	1	1	2	0	0	0	Glycosyl hydrolases family 6
PF02958	1	1	1	2	3	0	0	Ecdysteroid kinase-like family
PF12215	2	1	1	0	0	0	0	beta-glucosidase 2, glycosyl-hydrolase family 116 N-term
PF16670	1	1	1	1	1	0	0	Phosphoinositide phospholipase C, Ca2+-dependent
PF03313	1	1	1	1	0	0	0	Serine dehydratase alpha chain
PF03315	1	1	1	1	0	0	0	Serine dehydratase beta chain
PF23915	1	1	1	0	0	0	0	Alpha-amylase SusG C-terminal domain
PF12340	1	1	1	0	2	0	0	Protein of unknown function (DUF3638)
PF20255	1	1	1	0	2	0	0	Family of unknown function (DUF6606)
PF06249	1	1	1	1	2	0	0	Ethanolamine utilisation protein EutQ
PF07103	1	1	1	1	1	0	0	Protein of unknown function (DUF1365)
PF23614	1	1	1	1	1	0	0	Domain of unknown function (DUF7141)
PF03596	1	1	1	0	0	0	0	Cadmium resistance transporter
PF22773	1	1	1	0	0	0	0	Myosin-1, central acidic domain
PF26157	1	0	0	1	0	0	0	Endo-beta-1,2-glucanase SGL
PF04041	1	1	1	2	2	0	0	beta-1,4-mannooligosaccharide phosphorylase
PF18951	1	1	1	1	1	0	0	Family of unknown function (DUF5695)
PF22847	1	1	1	0	1	0	0	Arabinosidase BT_3657-like, N-terminal
PF19527	1	0	0	1	0	0	0	Family of unknown function (DUF6055)
PF16588	1	1	1	0	0	0	0	C2H2 zinc-finger
PF18647	1	4	5	0	1	0	0	Putative glycan binding domain
PF28342	1	1	1	0	1	0	0	Fungal ACT-like domain
PF12897	1	0	0	1	0	0	0	Aspartate amino-transferase
PF26640	1	1	1	0	0	0	0	Domain of unknown function (DUF8212)
PF18120	1	1	1	1	1	0	0	Domain of unknown function (DUF5597)
PF10297	1	0	0	1	0	0	0	Minimal binding motif of Hap4 for binding to Hap2/3/5
PF04927	1	1	1	2	0	0	0	Seed maturation protein
PF24895	1	1	1	0	0	0	0	Nonribosomal peptide synthetase sidD N-terminal
PF01121	1	1	1	1	2	0	0	Dephospho-CoA kinase
PF17996	1	1	1	0	0	0	0	Carbohydrate esterase 2 N-terminal
PF01906	0	0	0	1	0	0	0	Putative heavy-metal-binding
PF10014	0	0	0	2	0	0	0	2OG-Fe dioxygenase
PF28575	0	0	0	1	0	0	0	ZEB2-like helical domain
PF20493	0	1	1	1	0	0	0	Fungal WD-like
PF06414	0	0	0	2	2	0	0	Zeta toxin
PF08228	0	0	0	1	0	0	0	RNase P subunit Pop3
PF24483	0	0	0	1	0	0	0	Domain of unknown function (DUF7582)
PF05536	0	0	0	1	0	0	0	Neurochondrin
PF00959	0	0	0	3	2	0	0	Phage lysozyme
PF10288	0	1	1	1	0	0	0	Cytoplasmic tRNA 2-thiolation protein 2
PF15906	0	1	1	1	0	0	0	Zinc-finger of nitric oxide synthase-interacting protein
PF03736	0	0	0	1	0	0	0	EPTP domain
PF18538	0	0	0	1	0	0	0	Domain of unknown function (DUF5624)
PF21104	0	0	0	1	0	0	0	Glycosyl hydrolase family 78 alpha-rhamnosidase N-terminal domain
PF21858	0	1	1	3	4	0	0	Family of unknown function (DUF6914)
PF18308	0	0	0	1	0	0	0	N-terminal extension of GAT domain
PF15227	0	0	0	2	3	0	0	zinc finger of C3HC4-type, RING
PF21877	0	0	0	2	0	0	0	PH domain-like
PF05958	0	0	0	1	1	0	0	tRNA (Uracil-5-)-methyltransferase
PF22543	0	0	0	1	0	0	0	Soluble Rieske-type ferredoxin
PF28293	0	0	0	2	0	0	0	Biotrophy-associated secreted protein 2
PF12550	0	0	0	1	1	0	0	Transcriptional activator of glycolytic enzymes
PF12904	0	0	0	1	0	0	0	Putative collagen-binding domain of a collagenase
PF13204	0	0	0	1	0	0	0	Apiosidase-like, catalytic domain
PF16485	0	0	0	1	0	0	0	Protealysin propeptide
PF19373	0	0	0	1	2	0	0	Family of unknown function (DUF5948)
PF01755	0	0	0	3	1	0	0	Glycosyltransferase family 25 (LPS biosynthesis protein)
PF28209	0	0	0	2	0	0	0	Histidine triad hairpin domain
PF12457	0	0	0	1	0	0	0	Tuftelin interacting protein N terminal
PF10503	0	1	1	2	1	0	0	Esterase PHB depolymerase
PF09184	0	0	0	1	1	0	0	PPP4R2
PF28488	0	0	0	1	0	0	0	SPCC553.12c
PF23195	0	0	0	1	0	0	0	Ubiquilin-1-like domain
PF07063	0	0	0	3	0	0	0	2-oxoadipate dioxygenase/decarboxylase
PF28504	0	0	0	1	0	0	0	Gramillins biosynthetic cluster protein GRA5
PF09594	0	1	1	1	1	0	0	Glycosyltransferase family 87
PF14636	0	0	0	1	0	0	0	Folliculin-interacting protein N-terminus
PF08016	0	0	0	2	0	0	0	Polycystin cation channel
PF18107	0	0	0	1	0	0	0	Fission yeast centromere protein N-terminal domain
PF01977	0	2	1	2	0	0	0	3-octaprenyl-4-hydroxybenzoate carboxy-lyase Rift-related domain
PF20695	0	1	1	2	0	0	0	3-octaprenyl-4-hydroxybenzoate carboxy-lyase N-terminal domain
PF20696	0	2	1	2	0	0	0	3-octaprenyl-4-hydroxybenzoate carboxy-lyase C-terminal domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF06089	0	0	0	1	1	0	0	L-asparaginase II
PF03475	0	0	0	1	0	0	0	YiiM-like, 3-alpha helix domain
PF16579	0	0	0	1	0	0	0	Adenylate sensor of SNF1-like protein kinase
PF00017	0	0	0	1	0	0	0	SH2 domain
PF22677	0	0	0	1	0	0	0	Bleomycin resistance protein-like N-terminal
PF24470	0	0	0	1	0	0	0	Isochorismatase, thioredoxin-like
PF14610	0	0	0	1	0	0	0	Ykl077w/Psg1 (Pma1 Stabilization in Golgi)
PF18600	0	0	0	2	0	0	0	Fungal MCSS domain
PF18601	0	0	0	2	0	0	0	EZH2 N-terminal domain
PF25586	0	0	0	1	0	0	0	PAN3 CCCH zinc finger domain
PF12326	0	0	0	1	0	0	0	N-glycosylation protein
PF27672	0	0	0	1	0	0	0	CLU5d C-terminal domain
PF15965	0	0	0	1	0	0	0	TRAF-like zinc-finger
PF06330	0	0	0	2	0	0	0	Trichodiene synthase (TRI5)
PF18631	0	0	0	1	0	0	0	Cucumopine synthase C-terminal helical bundle domain
PF14871	0	0	0	1	0	0	0	Hypothetical glycosyl hydrolase 6
PF21678	0	0	0	1	0	0	0	Csf1 N-terminal region
PF00750	0	0	0	1	0	0	0	tRNA synthetases class I (R), catalytic domain
PF06920	0	0	0	2	0	0	0	DHR-2, Lobe A
PF02214	0	0	0	2	0	0	0	BTB/POZ domain
PF23414	0	1	2	1	0	0	0	Echinoderm microtubule-associated protein second beta-propeller
PF09807	0	0	0	1	0	0	0	Elongation complex protein 6
PF14099	0	0	0	1	0	0	0	Polysaccharide lyase
PF13672	0	1	1	1	1	0	0	Protein phosphatase 2C
PF28364	0	0	0	1	0	0	0	YOL029C N-terminal domain
PF28391	0	0	0	2	0	0	0	ARB_05566 N-terminal domain
PF03572	0	1	1	2	2	0	0	Peptidase family S41
PF06983	0	0	0	2	0	0	0	3-demethylubiquinone-9 3-methyltransferase
PF15588	0	0	0	1	0	0	0	Immunity protein 10
PF11327	0	0	0	1	0	0	0	Egh16-like virulence factor
PF24539	0	0	0	5	0	0	0	Domain of unknown function (DUF7600)
PF03747	0	0	0	2	0	0	0	ADP-ribosylglycohydrolase
PF16541	0	0	0	1	2	0	0	Alternaria alternata allergen 1
PF15891	0	0	0	1	0	0	0	Nucleoside 2-deoxyribosyltransferase like
PF06993	0	1	1	1	0	0	0	Protein of unknown function (DUF1304)
PF20183	0	0	0	2	0	0	0	Family of unknown function (DUF6546)
PF04577	0	1	1	2	0	0	0	Glycosyltransferase 61
PF28457	0	0	0	1	0	0	0	Probable beta-glucosidase btgE N-terminalo domain
PF02983	0	0	0	2	0	0	0	Alpha-lytic protease prodomain
PF09471	0	0	0	1	0	0	0	IgA Peptidase M64
PF15474	0	0	0	1	0	0	0	Meiotically up-regulated gene family
PF21087	0	1	0	1	0	0	0	Glycosyl hydrolase family 134
PF27599	0	0	0	3	4	0	0	CcsR C-terminal domain
PF05837	0	0	0	1	0	0	0	Centromere protein H (CENP-H)
PF15617	0	1	2	2	1	0	0	C-C_Bond_Lyase of the TIM-Barrel fold
PF02661	0	0	0	3	0	0	0	Fic/DOC family
PF01421	0	0	0	1	0	0	0	Reprolysin (M12B) family zinc metalloprotease
PF03193	0	0	0	1	0	0	0	RsgA GTPase
PF00829	0	0	0	1	0	0	0	Ribosomal prokaryotic L21 protein
PF21136	0	0	0	1	0	0	0	Crossover junction endonuclease MUS81-like, winged helix domain
PF01431	0	0	0	1	0	0	0	Peptidase family M13
PF05649	0	0	0	1	0	0	0	Peptidase family M13
PF18566	0	0	0	2	0	0	0	Linalool dehydratase/isomerase
PF28381	0	0	0	1	0	0	0	TRS130-like, immunoglobulin-like domain
PF07778	0	0	0	2	0	0	0	Mis6
PF11145	0	0	0	1	0	0	0	Transmembrane E3 ligase/DUF2921 transmembrane domain
PF02187	0	0	0	1	0	0	0	Growth-Arrest-Specific Protein 2 Domain
PF13173	0	0	0	1	0	0	0	AAA domain
PF18648	0	0	0	1	0	0	0	Tse2 ADP-ribosyltransferase toxin
PF16697	0	0	0	1	0	0	0	Inner membrane component of T3SS, cytoplasmic domain
PF04885	0	0	0	1	0	0	0	Stigma-specific STIG1-like protein family
PF23416	0	0	0	1	0	0	0	Domain of unknown function (DUF7107)
PF20398	0	0	0	1	0	0	0	Family of unknown function (DUF6691)
PF14021	0	0	0	1	0	0	0	Tuberculosis necrotizing toxin
PF27939	0	0	0	2	0	0	0	Domain of unknown function (DUF8363)
PF23238	0	0	0	2	0	0	0	Domain of unknown function (DUF7068)
PF25567	0	0	0	1	0	0	0	SYO1-like, TPR repeats
PF26728	0	0	0	1	0	0	0	FMNK-like N-terminal domain
PF14815	0	0	0	1	0	0	0	NUDIX domain
PF25312	0	0	0	2	0	0	0	Allergen Asp f 4-like domain
PF04261	0	0	0	1	0	0	0	Dyp-type peroxidase, N-terminal
PF20055	0	0	0	1	1	0	0	Family of unknown function (DUF6454)
PF14234	0	0	0	1	0	0	0	Domain of unknown function (DUF4336)
PF21621	0	0	0	1	0	0	0	Mannose-6-phosphate isomerase, cupin domain
PF11991	0	0	0	3	0	0	0	Tryptophan dimethylallyltransferase
PF06165	0	0	0	1	0	0	0	Glycosyl hydrolase 94, supersandwich domain
PF17167	0	0	0	1	0	0	0	Glycosyl hydrolase 94 superfamily, catalytic domain
PF26706	0	0	0	1	0	0	0	DOP1B-like, TPR repeats
PF20470	0	0	0	2	0	0	0	Helix-turn-helix domain
PF21099	0	0	0	2	0	0	0	DNA_pol_Q helicase like region helical domain
PF25453	0	0	0	2	0	0	0	Domain of unknown function (DUF7898)
PF10458	0	0	0	1	0	0	0	Valyl tRNA synthetase tRNA binding arm
PF22953	0	0	0	1	2	0	0	Polyketide synthase extender module SpnB, Rossmann fold domain
PF08392	0	0	0	1	0	0	0	FAE1/Type III polyketide synthase-like protein
PF08545	0	0	0	1	0	0	0	3-Oxoacyl-[acyl-carrier-protein (ACP)] synthase III
PF00077	0	0	0	2	0	0	0	Retroviral aspartyl protease
PF15477	0	0	0	1	0	0	0	Small acidic protein family
PF22521	0	0	0	1	0	0	0	Carbamoyltransferase, Kae1-like Domain, second subdomain
PF03492	0	1	1	1	0	0	0	SAM dependent carboxyl methyltransferase
PF03442	0	0	0	1	0	0	0	Carbohydrate binding domain X2
PF01547	0	0	0	1	0	0	0	Bacterial extracellular solute-binding protein
PF13343	0	2	2	1	1	0	0	Bacterial extracellular solute-binding protein
PF13531	0	0	0	1	0	0	0	Bacterial extracellular solute-binding protein
PF02875	0	1	1	1	0	0	0	Mur ligase, glutamate ligase domain
PF06042	0	0	0	1	0	0	0	Nucleotidyltransferase
PF17233	0	0	0	1	0	0	0	Family of unknown function (DUF5308)
PF03407	0	0	0	2	1	0	0	Nucleotide-diphospho-sugar transferase

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium cranfordii* (FJII-L10-SW-DR1)	*Cladosporium cranfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora burdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF18368	0	0	0	1	0	0	0	Exo-beta-D-glucosaminidase Ig-fold domain
PF13603	0	0	0	1	0	0	0	Leucyl-tRNA synthetase, editing domain
PF00917	0	0	0	1	0	0	0	MATH domain
PF07947	0	0	0	1	0	0	0	YhhN family
PF20994	0	0	0	1	0	0	0	CENPU protein
PF19270	0	0	0	1	0	0	0	F-box only protein C-terminal region
PF07575	0	2	2	1	1	0	0	Nup85 Nucleoporin
PF17872	0	0	0	1	0	0	0	AAA lid domain
PF08627	0	0	0	1	0	0	0	CRT-like, chloroquine-resistance transporter-like
PF01931	0	0	0	1	0	0	0	Protein of unknown function DUF84
PF01400	0	0	0	1	0	0	0	Astacin (Peptidase family M12A)
PF19279	0	0	0	1	0	0	0	YegS C-terminal NAD kinase beta sandwich-like domain
PF23388	0	0	0	2	0	0	0	Domain of unknown function (DUF7099)
PF23391	0	0	0	1	0	0	0	Domain of unknown function (DUF7100)
PF23392	0	0	0	1	0	0	0	Domain of unknown function (DUF7101)
PF10200	0	0	0	1	0	0	0	NADH:ubiquinone oxidoreductase, NDUFS5-15kDa
PF01762	0	0	0	1	0	0	0	Galactosyltransferase
PF14759	0	0	0	1	0	0	0	Reductase C-terminal
PF01943	0	0	0	1	0	0	0	Polysaccharide biosynthesis protein
PF13093	0	0	0	1	0	0	0	Kinetochore complex Fta4 of Sim4 subunit, or CENP-50
PF10445	0	0	0	1	0	0	0	Protein of unknown function (DUF2456)
PF14856	0	0	0	1	3	0	0	Pathogen effector; putative necrosis-inducing factor
PF02156	0	0	0	1	0	0	0	Glycosyl hydrolase family 26
PF16990	0	0	0	1	0	0	0	Carbohydrate binding module (family 35)
PF10009	0	0	0	1	0	0	0	Uncharacterized protein conserved in bacteria (DUF2252)
PF01422	0	0	0	2	0	0	0	NF-X1 type zinc finger
PF15892	0	0	0	1	0	0	0	BNR repeat-containing family member
PF14623	0	0	0	1	0	0	0	Hint-domain
PF14624	0	0	0	1	0	0	0	VWA / Hh protein intein-like
PF10181	0	0	0	1	0	0	0	GPI-GlcNAc transferase complex, PIG-H component
PF03732	0	0	0	1	0	0	0	Retrotransposon gag protein
PF19259	0	0	0	1	0	0	0	Ty3 transposon capsid-like protein
PF01094	0	1	1	0	0	0	0	Receptor family ligand binding region
PF13433	0	1	1	0	0	0	0	Periplasmic binding protein domain
PF13458	0	1	1	0	0	0	0	Periplasmic binding protein
PF22935	0	1	1	0	0	0	0	Large ribosomal subunit protein mL44, endonuclease domain
PF25411	0	1	1	0	5	0	0	Domain of unknown function (DUF7888)
PF21986	0	1	1	0	0	0	0	Allophanate hydrolase C-terminal domain
PF22658	0	1	1	0	0	0	0	YycE-like N-terminal domain
PF22659	0	1	0	0	0	0	0	YycE-like C-terminal domain
PF02434	0	1	1	0	0	0	0	Fringe-like
PF02384	0	1	1	0	0	0	0	N-6 DNA Methylase
PF25468	0	1	1	0	0	0	0	HEATR5A-like, HEAT repeats
PF05028	0	1	1	0	1	0	0	Poly (ADP-ribose) glycohydrolase (PARG), Macro domain fold
PF19055	0	1	1	0	0	0	0	ABC-2 type transporter
PF04107	0	1	1	0	0	0	0	Glutamate-cysteine ligase family 2(GCS2)
PF14877	0	1	1	0	0	0	0	Mitochondrial translation initiation factor
PF13289	0	1	1	0	0	0	0	SIR2-like domain
PF24584	0	1	1	0	0	0	0	CYK3 C-terminal Ig-like domain
PF16757	0	1	1	0	0	0	0	Alpha-L-fucosidase C-terminal domain
PF25038	0	1	1	0	0	0	0	Csf1 family C-terminal region
PF01225	0	1	1	0	0	0	0	Mur ligase family, catalytic domain
PF08245	0	1	1	0	0	0	0	Mur ligase middle domain
PF02525	0	1	1	0	1	0	0	Flavodoxin-like fold
PF04607	0	1	1	0	0	0	0	Region found in RelA / SpoT proteins
PF16334	0	1	1	0	2	0	0	Domain of unknown function (DUF4964)
PF04371	0	1	1	0	2	0	0	Porphyromonas-type peptidyl-arginine deiminase
PF13576	0	1	1	0	0	0	0	Pentapeptide repeats (9 copies)
PF04972	0	1	1	0	0	0	0	BON domain
PF28511	0	1	1	0	0	0	0	Domain of unknown function (DUF8420)
PF03243	0	1	1	0	0	0	0	Alkylmercury lyase
PF01041	0	1	1	0	0	0	0	DegT/DnrJ/EryC1/StrS aminotransferase family
PF08892	0	1	0	0	0	0	0	YqcI/YcgG family
PF22810	0	1	1	0	0	0	0	Lytic polysaccharide monooxygenase AA14
PF06821	0	1	1	0	0	0	0	Serine hydrolase
PF26421	0	0	1	0	0	0	0	Avidin-like protein
PF23798	0	0	1	0	0	0	0	SPT8 beta propeller
PF13358	0	0	1	0	0	0	0	DDE superfamily endonuclease
PF25597	0	0	0	0	2	0	0	Retroviral polymerase SH3-like domain
PF24813	0	0	0	0	1	0	0	Domain of unknown function (DUF7709)
PF09258	0	0	0	0	1	0	0	Glycosyl transferase family 64 domain
PF27892	0	0	0	0	1	0	0	Bud site selection protein RAX1, C-terminal domain
PF05821	0	0	0	0	1	0	0	NADH-ubiquinone oxidoreductase ASHI subunit (CI-ASHI or NDUFB8)
PF00754	0	0	0	0	2	0	0	F5/8 type C domain
PF22633	0	0	0	0	2	0	0	NedA-like, galactose-binding domain
PF15251	0	0	0	0	1	0	0	Telomere attrition and p53 response 1 protein-like
PF27605	0	0	0	0	1	0	0	ODF2 C-terminal coiled coil domain
PF13449	0	0	0	0	2	0	0	Esterase-like activity of phytase
PF22590	0	0	0	0	1	0	0	CRISPR-associated nuclease/helicase Cas3, C-terminal
PF25139	0	0	0	0	2	0	0	Secreted LysM effector LysM14, C-terminal domain
PF19951	0	0	0	0	2	0	0	Family of unknown function (DUF6413)
PF14552	0	0	0	0	1	0	0	Tautomerase enzyme
PF24758	0	0	0	0	1	0	0	FBD-associated F-box protein At5g56370, LRR repeats
PF11380	0	0	0	0	2	0	0	Stealth protein CR2, conserved region 2
PF17101	0	0	0	0	2	0	0	Stealth protein CR1, conserved region 1
PF17103	0	0	0	0	1	0	0	Stealth protein CR4, conserved region 4
PF13931	0	0	0	0	1	0	0	Kinesin-associated microtubule-binding
PF04774	0	0	0	0	1	0	0	Hyaluronan / mRNA binding family
PF21317	0	0	0	0	1	0	0	Beta-galactosidase, first all-beta domain
PF21467	0	0	0	0	1	0	0	Beta-galactosidase, galactose-binding domain
PF03644	0	0	0	0	2	0	0	Glycosyl hydrolase family 85
PF22693	0	0	0	0	2	0	0	Fungal MACPF-like domain
PF16367	0	0	0	0	1	0	0	RNA recognition motif
PF17863	0	0	0	0	1	0	0	AAA lid domain
PF04069	0	0	0	0	1	0	0	Substrate binding domain of ABC-type glycine betaine transport system
PF14588	0	0	0	0	1	0	0	YjgF/chorismate_mutase-like, putative endoribonuclease
PF25794	0	0	0	0	1	0	0	Sacsin domain

Pfam domain	*Cladosporium prattiae* (FJI-L7-BK-DG1)	*Cladosporium crawfordii* (FJII-L10-SW-DR1)	*Cladosporium crawfordii* (FKII-L3-CM-PAB1)	*Waltergamsia balasubramanianii (FKII-L8-BK-P5)*	*Phaeophleospora hurdickii* (FKII-L3-CM-PAB3)	*Spissiomyces californiae* (FJII-L1-SW-P2)	*Neocatenulostroma huberii* (FJI-L3-BK-P2)	Description
PF13359	0	0	0	0	2	0	0	DDE superfamily endonuclease
PF26138	0	0	0	0	2	0	0	Domain of unknown function (DUF8040)
PF05014	0	0	0	0	1	0	0	Nucleoside 2-deoxyribosyltransferase
PF03092	0	0	0	0	1	0	0	BT1 family
PF01216	0	0	0	0	1	0	0	Calsequestrin
PF18520	0	0	0	0	1	0	0	Spindle pole body component 110 C-terminal domain
PF24968	0	0	0	0	2	0	0	Domain of unknown function (DUF7770)
PF04879	0	0	0	0	1	0	0	Molybdopterin oxidoreductase Fe4S4 domain
PF26633	0	0	0	0	1	0	0	Domain of unknown function (DUF8206)
PF14863	0	0	0	0	1	0	0	Alkyl sulfatase dimerisation
PF17276	0	0	0	0	2	0	0	Family of unknown function (DUF5341)
PF02317	0	0	0	0	1	0	0	NAD/NADP octopine/nopaline dehydrogenase, alpha-helical domain
PF10979	0	0	0	0	2	0	0	Protein of unknown function (DUF2786)
PF23771	0	0	0	0	2	0	0	Domain of unknown function (DUF7168)
PF00274	0	0	0	0	1	0	0	Fructose-bisphosphate aldolase class-I
PF01464	0	0	0	0	2	0	0	Transglycosylase SLT domain
PF00471	0	0	0	0	1	0	0	Ribosomal protein L33
PF08263	0	0	0	0	1	0	0	Leucine rich repeat N-terminal domain
PF12740	0	0	0	0	1	0	0	PET hydrolase-like
PF21294	0	0	0	0	1	0	0	Polysaccharide lyase 14
PF05050	0	0	0	0	2	0	0	Methyltransferase FkbM domain
PF13527	0	0	0	0	2	0	0	Acetyltransferase (GNAT) domain
PF09837	0	0	0	0	1	0	0	Uncharacterized protein conserved in bacteria (DUF2064)
PF12345	0	0	0	0	2	0	0	Protein of unknown function (DUF3641)
PF06197	0	0	0	0	2	0	0	Protein of unknown function (DUF998)
PF03059	0	0	0	0	1	0	0	Nicotianamine synthase protein
PF11765	0	0	0	0	1	0	0	Hyphally regulated cell wall protein N-terminal
PF09766	0	0	0	0	2	0	0	Fms-interacting protein/Thoc5
PF17112	0	0	0	0	1	0	0	Mitochondrial import receptor subunit Tom6, fungal
PF06550	0	0	0	0	1	0	0	Signal-peptide peptidase, presenilin aspartyl protease
PF00665	0	0	0	0	1	0	0	Integrase core domain