

Protein IDs	Fasta headers
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R1GQK9;K2S0W9;A0A0D1Y0G4;A0A0G2GRL1;A0A063C3Q5;A0A0E9KSI8;A0A086T5E6;F4NSP0	>tr R1GQK9 R1GQK9_BOTPV Putative fatty acid synthase alpha subunit protein OS=Botryosphaeria parva (strain UCR-NP2) GN=UCRNP2_2699 PE=3 SV=1;>tr K2S0W9 K2S0W9_MACPH Beta-ketoacyl synthase OS=Macrophomina phaseolina (strain MS6) GN=MPH_02140 PE=3 SV=1;>tr A

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A0A068SER0;A0A068RM11;A0A077W6N4;A0A068RUC5;A0A077W9N3;A0A077WCD4;I1C6D0;A0A068S648;A0A077WJ41;I1CEZ4;A0A068RGP0;A0A0A1MYH3;A0A0C7AVV1;A0A0A1NXF7;S2K739;A0A0C9N7A5;S2JIT7	>tr A0A068SER0 A0A068SER0_9FUNG Cation-transporting ATPase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_11255.1 PE=3 SV=1;>tr A0A068RM11 A0A068RM11_9FUNG Ubiquitin-60s ribosomal protein I40 fusionprotein OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR

A0A0E9NGT7;A0A094D2P5;A0A0J0XKI2;J6F599;K1VXL5;A0A094EI87;A0A094GTC9;L8FPJ9;A0A094FBB1;A0A093Z7F6;A0A094AFS4;A0A094AKI7;A0A094HBU3;A0A094IH62;K2RFA0;A0A0D1XL42;G4TH72;A0A094BEH1;A0A094F3L7;S7QHB1;A0A094A3E7;R1GEX0;A0A0H2RIH5;A0A093ZTJ2;A0A068RHX9;A0A077WIP5;A0A077X1D6;F4PBY8;A0A068S968;W6MFK9;A0A0G2HDF1;I4YCA8;R9ANK7;A0A0C7BZ03;A0A0C7B726;A0A0C7C014;A0A0C7BZW0;A0A0A1NPL8;A0A0C7BYG2	>tr A0A0E9NGT7 A0A0E9NGT7_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_2795-t1 PE=3 SV=1;>tr A0A094D2P5 A0A094D2P5_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-4515 (FW-2607) GN=V496_05301 PE=3 SV=1;>tr A0A0
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A0A0B7N3T5;I1C2J8;A0A077WG75;A0A0C9MVH7;S2IYZ5;A0A068S2Y5;A0A0A1MI15;A0A0A1MWD6	>tr A0A0B7N3T5 A0A0B7N3T5_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_03822.1 scaffold 9853 PE=4 SV=1;>tr I1C2J8 I1C2J8_RHIO9 Uncharacterized protein OS=Rhizopus deleamar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO
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S2J7T9;G4TAG1	>tr S2J7T9 S2J7T9_MUCC1 Coatomer subunit alpha OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_07490 PE=4 SV=1;>tr G4TAG1 G4TAG1_PIRID Coatomer subunit alpha OS=Piriformospora indica (strain DSM 11827) GN=PIIN_02168 PE=4 SV=1
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F4NUS4	>tr F4NUS4 F4NUS4_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_15754 PE=3 SV=1
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S8ELR8;A0A077WP29	>tr S8ELR8 S8ELR8_FOMPI Uncharacterized protein OS=Fomitopsis pinicola (strain FP-58527) GN=FOMPIDRAFT_148672 PE=4 SV=1;>tr A0A077WP29 A0A077WP29_9FUNG Uncharacterized protein OS=Lichtheimia ramosa GN=LRAMOSA10505 PE=4 SV=1
A0A0E9NM83;J4U5P0;K1VHP0;A0A0B2UK16;W6MT35;A0A086J276;H8ZB34;I3EIJ6;I3ENE4;A0A086J274	>tr A0A0E9NM83 A0A0E9NM83_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_4932-t1 PE=3 SV=1;>tr J4U5P0 J4U5P0_TRIAS Vacuolar ATP synthase OS=Trichosporon asahii var. asahii (strain ATCC 90039 / CBS 2479 / JCM 2466 / KCTC 7840 / NC
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A0A068SFN8;A0A077WYY3	>tr A0A068SFN8 A0A068SFN8_9FUNG Calcium-transporting ATPase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_11865.1 PE=3 SV=1;>tr A0A077WYY3 A0A077WYY3_9FUNG Calcium-transporting ATPase OS=Lichtheimia ramosa GN=LRAMOSA05005 PE=3 SV=1
F4PAI0	>tr F4PAI0 F4PAI0_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_35901 PE=4 SV=1
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A0A077WDX7;A0A068RJ17;A0A0A1MJB4;A0A0C7B4L9;A0A0A1NNG7;A0A0H2RWD6;M2QWU9;R7SST5;K5V2S1;A0A0C9T8N4;B8PEP9;J4H5C6;W4JRG3;A0A060S428;G4TI90;A0A0D7B0G9;S7RH28;A0A0B7F7D5;A0A074SBA9;A0A0C3BPI3;X8IX54;A0A0C3PB57;S8F2S2;A0A067MHG0;I4YHS5;R9APG1;M5C830;A0A063BVA2;A0A0D2AKA8;S8DIY9;A0A0K6GB87;K4HXT9;A0A0C9NA37;S8DL36;L8WKL9	>tr A0A077WDX7 A0A077WDX7_9FUNG Putative ATP citrate (Pro-S)-lyase OS=Lichtheimia ramosa GN=LRAMOSA08153 PE=4 SV=1;>tr A0A068RJ17 A0A068RJ17_9FUNG Atp-citrate synthase subunit 1 (Atp-citrate (Pro-s)-lyase 1) OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCO

A0A086TKL6;S8FHS0;A0A094F5H4;A0A063BVP3;A0A086TFE4;J4U7F7;L8X4Q9;A0A093XQ82;A0A094BS00;A0A094G0P4;G4TJ80;A0A0H2S453;A0A0J0XZG4;K5VUY0;S7QAJ9;A0A0C3B7T6;M2R2U5;A0A0D7BL04;J4I919;A0A094F3M7;A0A094G5G1;A0A0C3PHU8;F4NXD2;A0A0C3L7X4;A0A0G2G1W8;K2QXQ5;R1GLV0;R7S036;W4K0U0;A0A074SC89;A0A094ANG3;A0A0A1UKR0;A0A0B7FVU8;A0A0K6GHQ5;R9ARB8;A0A0D2A5B0;A0A094EFR8;A0A0B7MNV2;L8G0F2;I4YGH1;A0A0C9MI16;S2KJU7;A0A067N4V2;A0A094IX43;A0A0G2FMX1;A0A0B7NI11;A0A0C9MZB6;D6R7B5;I1C196;S2JTP7;A0A0A1NN97;A0A077WFM5;A0A068RIQ7;A0A077WBC4;M5BXX7;W6MSQ5;A0A0C3CYA8;A0A0E9NBB5;A0A068RZY4;A0A0E9KLH6;K1VUK6;A0A0C7BVR5;A0A093XFR1;A0A060SSX8;A0A0A1N1T3	>tr A0A086TKL6 A0A086TKL6_9FUNG Pyruvate carboxylase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11701 PE=4 SV=1
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A0A0B7MNY4;A0A0C7BLH3;S2JVU7;I1BTE0;F4P737;F4NWL5;A0A0C7CGG5;A0A0A1NRZ4	>tr A0A0B7MNY4 A0A0B7MNY4_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_00857.1 scaffold 1159 PE=3 SV=1;>tr A0A0C7BLH3 A0A0C7BLH3_9FUNG Putative P-type II C ATPase OS=Rhizopus microsporus GN=RMATCC62417_07760 PE=3 SV=1;>tr S2JVU7 S2JVU7_
A0A068SBE6;A0A077WGW5	>tr A0A068SBE6 A0A068SBE6_9FUNG Calcium-transporting ATPase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_10117.1 PE=3 SV=1;>tr A0A077WGW5 A0A077WGW5_9FUNG Calcium-transporting ATPase OS=Lichtheimia ramosa GN=LRAMOSA08425 PE=3 SV=1
A0A0H2SU79	>tr A0A0H2SU79 A0A0H2SU79_9HOMO ANTH-domain-containing protein OS=Schizopora paradoxa GN=SCHPADRAFT_816594 PE=4 SV=1
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A0A0E9NCP8	>tr A0A0E9NCP8 A0A0E9NCP8_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_1678-t1 PE=3 SV=1
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A0A077X4L5;A0A068RKV7;A0A077WAH9;A0A0A1N429;A0A0A1NEN4;A0A0C7BD88;I1C5C5;I1BH83;A0A076L6G6	>tr A0A077X4L5 A0A077X4L5_9FUNG Uncharacterized protein OS=Lichtheimia ramosa GN=LRAMOSA06418 PE=4 SV=1;>tr A0A068RKV7 A0A068RKV7_9FUNG Nad dependent glutamate OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_01310.1 PE=4 SV=1;>tr A0A077WAH9 A0A077WAH9_9FUNG
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Q876Z7	>tr Q876Z7 Q876Z7_9FUNG Alpha-glucosidase OS=Mortierella alliacea GN=agdA PE=2 SV=1
A0A0B7NND5;A0A0C9M592;S2JPY8;A0A0A1NH42;A0A0A1PKI3;A0A0C7B9G5;A0A0A1MRJ7;A0A0C7B9X4	>tr A0A0B7NND5 A0A0B7NND5_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_10700.1 scaffold 41683 PE=4 SV=1;>tr A0A0C9M592 A0A0C9M592_9FUNG Thiamin diphosphate-binding protein OS=Mucor ambiguus GN=MAM1_0070c04138 PE=4 SV=1;>tr S2JPY8 S2JPY8
A0A086TL56	>tr A0A086TL56 A0A086TL56_9FUNG Uncharacterized protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_12075 PE=4 SV=1
F4PEG6	>tr F4PEG6 F4PEG6_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDERAFT_14866 PE=4 SV=1

A0A094FL48;A0A094IX57;A0A094EXN9;A0A0C3DIL0;A0A0G2EWU9;A0A093Y214;A0A093YJ33;A0A093Z7S1;A0A093ZMR6;A0A094BAU6;A0A094CDX4;A0A094E1Z8;A0A094EBP7;A0A094F912;A0A094GUG7;L8FW72;A0A063BUS4;A0A086T0D9;A0A0G2H5P5;K2SPL4	>tr A0A094FL48 A0A094FL48_9PEZI Coatomer subunit beta OS=Pseudogymnoascus pannorum VKM F-4518 (FW-2643) GN=V500_05714 PE=4 SV=1;>tr A0A094IX57 A0A094IX57_9PEZI Coatomer subunit beta OS=Pseudogymnoascus pannorum VKM F-4520 (FW-2644) GN=V502_00727 PE=4 SV=1;
A0A0B7FWM5;M5BZG6	>tr A0A0B7FWM5 A0A0B7FWM5_THACB Uncharacterized protein OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=clfA PE=4 SV=1;>tr M5BZG6 M5BZG6_THACB Uncharacterized protein OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=BN14_06087
Q2PYR5	>tr Q2PYR5 Q2PYR5_9FUNG DNA-directed RNA polymerase (Fragment) OS=Mortierella verticillata GN=RPB1 PE=3 SV=1
A0A0E9NKL0;A0A0C2X5T8;L8XAN8;W4KJS6;A0A067MR21;A0A074RZC3;A0A0B7FRZ3;A0A0K6FV00;X8J6A4;A0A066WAQ8;A0A0C3QN57;M5BHW5;A0A0A1MU22;I4YAJ3;R9AKN9;A0A098VSY3;A0A0D1YD55;F4P7I4;A0A0C7B9M3;A0A0A1NR71;A0A0C9LPR7;A0A0C9M8F6;A0A094A699;A0A0C9MPN1;A0A0B7N7L4;A0A0C9MC31;A0A077X0A3;A0A0A1P8A7	>tr A0A0E9NKL0 A0A0E9NKL0_9ASCO ATP synthase subunit beta OS=Saitoella complicata NRRL Y-17804 GN=G7K_4071-t1 PE=3 SV=1;>tr A0A0C2X5T8 A0A0C2X5T8_9HOMO ATP synthase subunit beta OS=Serendipita vermifera MAFF 305830 GN=M408DRAFT_19768 PE=3 SV=1;>tr L8XAN8 L
G4TVY4;A0A0H2RIW5;A0A0C3A967;A0A0C3QDW2	>tr G4TVY4 G4TVY4_PIRID Related to chitin Synthase 4 OS=Piriformospora indica (strain DSM 11827) GN=PIIN_09460 PE=4 SV=1;>tr A0A0H2RIW5 A0A0H2RIW5_9HOMO Glycosyltransferase family 2 protein OS=Schizopora paradoxa GN=SCHPADRAFT_830539 PE=4 SV=1;>tr A0A0C3A9
A0A086TLI0;A0A0K6FP10;J4G102	>tr A0A086TLI0 A0A086TLI0_9FUNG Ubiquitin-activating enzyme E1 OS=Mortierella verticillata NRRL 6337 GN=MVEG_11333 PE=3 SV=1
M2RPJ5;W4KFM7;S8EFE0	>tr M2RPJ5 M2RPJ5_CERS8 Uncharacterized protein OS=Ceriporiopsis subvermispota (strain B) GN=CERSUDRAFT_111385 PE=4 SV=1;>tr W4KFM7 W4KFM7_9HOMO Uncharacterized protein OS=Heterobasidion irregulare TC 32-1 GN=HETIRDRAFT_34260 PE=4 SV=1;>tr S8EFE0 S8EFE0_FO

<p>A0A0B7MY32;A0A0C9N484;S2K1V3;A0A0C7BEQ7;A0A0K6FQ90;A0A067M5A6;A0A0C3AUW2;G4TJJ1;A0A0C3L5Z8;A0A0H2R714;I1C8U8;A0A074S3B0;A0A068RRL5;A0A077WFG0;A0A0B7FQR8;F4P171;A0A066VL66;M5C688;I1CHP3;L8WZP1;R9AKV1;W4K928;I4YDB7;S8EQK6;R1GGL8;A0A0C3RVN4;M2PTE5;S7Q3F4;A0A0J0XN23;A0A0D7B435;A0A0G2E3H9;A0A0D1XG76;K5VXI6;K2RT45;Q7Z985;A0A0A1NW61;A0A094B1E9;A0A094BDZ9;A0A094F3I5;A0A094GT83;A0A094F628;A0A093Y9Y3;A0A094F9N3;A0A093YS64;A0A094CAE7;A0A094DNU5;A0A094HD64;A0A086TBN0;A0A093ZNZ4;A0A094A4R8;A0A094CZG7;L8FNP5;A0A0C3HHQ5;A0A0C7BFL8;J4H3N3;A0A0G2GFR9;A0A060SGV0;X8IXZ9;A0A0A1NIV8</p>	<p>>tr A0A0B7MY32 A0A0B7MY32_9FUNG Microtubule-associated protein OS=Parasitella parasitica GN=PARPA_01143.1 scaffold 1359 PE=3 SV=1;>tr A0A0C9N484 A0A0C9N484_9FUNG V-type ATPase OS=Mucor ambiguus GN=MAM1_0264d08915 PE=3 SV=1;>tr S2K1V3 S2K1V3_MUCC1 V-type pr</p>
<p>A0A0D1XBK3;A0A086T3T2;A0A0G2E8J9;A0A0C3GW52;A0A093X2T6;A0A093YE08;A0A093YTN6;A0A093Z9C8;A0A093ZZX2;A0A094BEA2;A0A094BZB7;A0A094CY69;A0A094ELE9;A0A094FK83;A0A094HTS1;A0A094HVD6;A0A094I9W9;L8GAX3;A0A0E9KU11;A0A0E9NIC8;A0A0G2F142;K2QUF0;R1G615;A0A063C6L7;F4NWZ7;A0A0C9MQM7;A0A0B7NQS1;S2JJK9;A0A068RQI2;A0A077WE56;A0A0C7BNF6;I1BTE5;A0A094FVA0;A0A0A1N0W6;A0A098VSN3;A0A0C7CP34;A0A0A1P554</p>	<p>>tr A0A0D1XBK3 A0A0D1XBK3_9PEZI Uncharacterized protein OS=Verruconis gallopava GN=PV09_08748 PE=4 SV=1;>tr A0A086T3T2 A0A086T3T2_ACRCH 26S proteasome regulatory subunit rpn-like protein OS=Acremonium chrysogenum ATCC 11550 GN=ACRE_052040 PE=4 SV=1;>tr A0A</p>
<p>A0A086TL05;A0A0B7NRD5;S2JSQ5;A0A077X413;A0A068RY43;A0A0C9MRS9;S2J376;A0A0A1NQ98;A0A0C7BFZ2;I1C1M1;A0A0C7BVI8</p>	<p>>tr A0A086TL05 A0A086TL05_9FUNG Calcium-transporting ATPase OS=Mortierella verticillata NRRL 6337 GN=MVEG_12024 PE=3 SV=1;>tr A0A0B7NRD5 A0A0B7NRD5_9FUNG Calcium-transporting ATPase OS=Parasitella parasitica GN=PARPA_12173.1 scaffold 44939 PE=3 SV=1;>tr S2</p>

A0A0D7B3T8	>tr A0A0D7B3T8 A0A0D7B3T8_9HOMO Uncharacterized protein OS=Cylindrobasidium torrendii FP15055 ss-10 GN=CYLTODRAFT_412766 PE=4 SV=1
I1BJB5;A0A0C9MG20;A0A0B7MWM7;I1C225;S2K9T4;A0A0A1NS76;A0A0C7BMA7;A0A0A1NZS2;A0A0C7CBA1	>tr I1BJB5 I1BJB5_RHIO9 Hsp7-like protein OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_00999 PE=3 SV=1;>tr A0A0C9MG20 A0A0C9MG20_9FUNG Heat shock protein OS=Mucor ambiguus GN=MAM1_0281c09192 PE=3 SV=1;>tr A0A0B7MW
A0A0C9M950;A0A0B7MVE0;A0A0A1N5I6;A0A0C7BSD0;I1BRG8;I1CBW1;S2JP68;A0A0C7BP19;A0A0A1NMJ9;A0A0C7CLG2;J5SJ22;K1VKV0;R1G1T9;A0A068RU12;A0A0E9NDU0;A0A0G2GKZ1;K2RU13;A0A0B7NV59;A0A0C9MME5;S2J2R5;F4P4B0;A0A077X4Z6;A0A0E9KN83;A0A086TB44;A0A063C6S6;A0A0G2GEV6;A0A0C3S5Z8;K5VRR7;A0A0A1P4Y1	>tr A0A0C9M950 A0A0C9M950_9FUNG Malate synthase OS=Mucor ambiguus GN=MAM1_0142d06426 PE=3 SV=1;>tr A0A0B7MVE0 A0A0B7MVE0_9FUNG Malate synthase OS=Parasitella parasitica GN=PARPA_03654.1 scaffold 9273 PE=3 SV=1;>tr A0A0A1N5I6 A0A0A1N5I6_9FUNG Malate synthas
A0A0C9N7N3;A0A0C7CMT3;S2K3K1;A0A0B7MMD2;A0A0B7MN93;A0A0C3D4G3;I1BZ86;A0A0D1Y0D4;S2J6D1;I1CP20;A0A0A1N3V7;A0A0A1N8P8;A0A0A1P4K4;A0A0C7B0D6;I1BU72;A0A0B7NKC6;A0A0C9MSX0;S2K3Z1;A0A0J1BAA6;W4KIL5;A0A068RXN4;A0A077WH87;A0A0A1NRW1;A0A0A1NRW5;A0A0C7BHW0;I1CSD9;A0A0C9MWV0	>tr A0A0C9N7N3 A0A0C9N7N3_9FUNG 60S ribosomal protein I7-like protein OS=Mucor ambiguus GN=MAM1_0384c10208 PE=3 SV=1;>tr A0A0C7CMT3 A0A0C7CMT3_9FUNG Putative 50S ribosomal protein L7e OS=Rhizopus microsporus GN=RMATCC62417_18293 PE=3 SV=1;>tr S2K3K1 S2K3K1
A0A0E9NDU2;A0A094E621;A0A094IEP1;A0A094G343;A0A093YVD2;A0A094H6J7;A0A093X9X8;A0A093Y9Y4;A0A094DQF0;A0A094E570;A0A094EHG4;A0A094ETM7;A0A063BQ69;A0A0D2ASM7;A0A0C3GA26;A0A0G2DQZ7;L8FYS6;R1EDE3;A0A0C9MCN2;S2JWD4;A0A0E9KR01;A0A086T7D0;L8X9E5;A0A074S2K6;X8JF27;A0A0H2RKU0;A0A0C3AVD4;A0A0B7FU49;A0A0K6FV40;S7QFD6;A0A0C3QWW2;R9AGK6;A0A060SKH5;J4IBF7;A0A067MYW4;M2QMN5;W4KKP7;S8DZW3;A0A0D7BMW1;I1C4I7;A0A0C3S1P0;K5UZH1;K2RQ38;A0A0A1NBY8;A0A0C7BNH0;A0A0C9MDJ2;S2JSB2;A0A068S5R5;A0A077WX77;I1CPJ4;A0A077X4J8;A0A068S5Z5;A0A066WKE5;A0A0A1NVN6;M5C086	>tr A0A0E9NDU2 A0A0E9NDU2_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_2202-t1 PE=3 SV=1;>tr A0A094E621 A0A094E621_9PEZI Eukaryotic translation initiation factor 3 subunit I OS=Pseudogymnoascus pannorum VKM F-103 GN=V499_05920
A0A0E9NMR5;A0A0C7BPE1;A0A0A1MK79;A0A0A1P546	>tr A0A0E9NMR5 A0A0E9NMR5_9ASCO Alpha-1,4 glucan phosphorylase OS=Saitoella complicata NRRL Y-17804 GN=G7K_5204-t1 PE=3 SV=1;>tr A0A0C7BPE1 A0A0C7BPE1_9FUNG Alpha-1,4 glucan phosphorylase OS=Rhizopus microsporus GN=RMATCC62417_08022 PE=3 SV=1;>tr A0A0A1MK7
A0A0E9NFY1;A0A068RNQ1;A0A077WC58;A0A077WSH5;S2JX63;A0A0A1MSY9;A0A0A1PCQ2;A0A0B7MR78;A0A0C9MW47;I1BMC2;I1BSW4;I1CBF0;S2JXD8;A0A0B7NMD8;A0A068RJM0	>tr A0A0E9NFY1 A0A0E9NFY1_9ASCO 40S ribosomal protein S12 OS=Saitoella complicata NRRL Y-17804 GN=G7K_2492-t1 PE=3 SV=1;>tr A0A068RNQ1 A0A068RNQ1_9FUNG 40S ribosomal protein S12 OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_03177.1 PE=3 SV=1;>tr A0A077W

F4NW20;W6MWC4;A0A068S0H4;A0A0B7NF58;A0A0C9M8K2;S2J EJ8;A0A067N2K4;I1C323;A0A077WRI6;R9AP02;A0A0B7FXW0;G4 TN57;A0A0C3BGY4;W4K4N7;S8E422;A0A060SL88;A0A0A1NMG7; A0A0C7BJE4;M2QKB9;J0WWP9;A0A074S708;A0A0C3RXH6;K5W 5G5;I4YID4;L8WRC3;X8JK97;J4ICG5;A0A066VJ20;A0A0A1N4G8; A0A0K6GCZ9	>tr F4NW20 F4NW20_BATDJ Putative uncharacterized protein OS=Batrachyochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_32863 PE=3 SV=1;>tr W6MWC4 W6MWC4_9ASCO Uncharacterized protein OS=Kuraishia capsulata CBS 1993 GN=KUCA_T00003177001 PE=3 S
A0A068SCV7	>tr A0A068SCV7 A0A068SCV7_9FUNG Uncharacterized protein OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_09893.1 PE=4 SV=1
J4HZZ4;K5WJ21;A0A060S2W5;A0A067MIY1;A0A0C3P408;A0A0D 7BR29;A0A0H2SF60;B8PIG2;M2RQE1;R7SYN5;S7QJ18;W4KFF8; A0A0C2XWA6;S8FN91;A0A0C3Q731;A0A074STA1;X8JST7;I4YIZ1 ;W6MK41;G4U3C8;A0A0E9NQD9;A0A0B7FNI4;R9AG98;K1VJZ3;A 0A077WAX4;A0A0K6GEB1;J6EV92;A0A066W8W5;M5BJN6	>tr J4HZZ4 J4HZZ4_9APHY Uncharacterized protein OS=Fibroporia radiculosa GN=FIBRA_06995 PE=3 SV=1;>tr K5WJ21 K5WJ21_PHACS Uncharacterized protein OS=Phanerochaete carnososa (strain HHB- 10118-sp) GN=PHACADRAFT_205564 PE=3 SV=1;>tr A0A060S2W5 A0A060S2W5_PYCCI
Q9Y5B0	>tr Q9Y5B0 Q9Y5B0 · CTDP1_HUMAN=Homo sapiens (Human) GN=CTDP1 PE=4 SV=1
A0A077WSG0	>tr A0A077WSG0 A0A077WSG0_9FUNG Uncharacterized protein OS=Lichtheimia ramosa GN=LRAMOS11022 PE=4 SV=1
F4P7A7;A0A0B7N4M9;A0A0C9MEG7;S2K574;I1BZ33;A0A0C7BQE 7;A0A0C7CKL8	>tr F4P7A7 F4P7A7_BATDJ Plasma membrane ATPase OS=Batrachyochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_17188 PE=3 SV=1;>tr A0A0B7N4M9 A0A0B7N4M9_9FUNG Plasma membrane ATPase OS=Parasitella parasitica GN=PARPA_07323.1 scaffold 27460 PE=3
A0A0C9N0L6;I1CQJ2;A0A0A1NPA5;A0A0B7N823;S2JD73;A0A0A1 NPM9;A0A0C7B9Z9;A0A0C9MQC1;S2K3N8;A0A0C7BAC5	>tr A0A0C9N0L6 A0A0C9N0L6_9FUNG ATP-dependent metalloproteinase Hfl OS=Mucor ambiguus GN=MAM1_0268c08979 PE=3 SV=1;>tr I1CQJ2 I1CQJ2_RHIO9 Uncharacterized protein OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_15433
A0A0H2RSH9	>tr A0A0H2RSH9 A0A0H2RSH9_9HOMO Uncharacterized protein OS=Schizopora paradoxa GN=SCHPADRAFT_293610 PE=4 SV=1
G9M7Z9	>tr G9M7Z9 G9M7Z9_9FUNG DNA-directed RNA polymerase (Fragment) OS=Olpidium bornovanus GN=RPB2 PE=3 SV=1
J7RG29;A0A0C3BKE0;G4TAR2;A0A074S7H8;A0A0B7FDH1;X8JTI 9;A0A060ST12;A0A067LXY6;A0A0D7BT53;A0A0H2SSN7;S8EFK8; A0A0C3MDA1;I1CLA5;L8WXR2;A0A0J0XF02;A0A0B7NA28;A0A0K 6FN93;A0A0C3S255;A0A0E9NC05;F4P8G5;A0A077WVC1;A0A0A 1NWK7;A0A0C7BT09;A0A0C9N4E8;I1BN79;K5VFA9;M2QYW2;S2 J5Q6;S7QL63;A0A066VT40;W4KKT4;A0A098VSC3;M5CDF7;M5C DG8;A0A0A1MZW7	>tr J7RG29 J7RG29_9APHY Uncharacterized protein OS=Fibroporia radiculosa GN=FIBRA_00056 PE=3 SV=1;>tr A0A0C3BKE0 A0A0C3BKE0_9HOMO Proteasome subunit alpha type OS=Serendipita vermifera MAFF 305830 GN=M408DRAFT_327068 PE=3 SV=1;>tr G4TAR2 G4TAR2_PIRID Prote

L8WVP5;J6EYV2;K1VFP4;A0A0D7BTJ3;A0A0H2REC5;A0A060SJ72;W4KHJ0;A0A0B7FRI8;J4IAR8;A0A0J0XHX5;K5V9D0;A0A074RN42;A0A0A1UJJ8;A0A066VNR3;A0A0K6FZP6;A0A0C3SCX4;M5CFQ6;B8PPF3;A0A067LXF0;S7QJ36	>tr L8WVP5 L8WVP5_THACA Uncharacterized protein OS=Thanatephorus cucumeris (strain AG1-IA) GN=AG1IA_05096 PE=4 SV=1;>tr J6EYV2 J6EYV2_TRIAS Iron-sulfur cluster assembly-related protein OS=Trichosporon asahii var. asahii (strain ATCC 90039 / CBS 2479 / JCM
A0A0B7MXV1	>tr A0A0B7MXV1 A0A0B7MXV1_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_01067.1 scaffold 1359 PE=3 SV=1
A0A098VMQ6;A0A067M237;F4NY70	>tr A0A098VMQ6 A0A098VMQ6_9MICR ATP-dependent Clp protease ATP-binding subunit ClpB OS=Mitosporidium daphniae GN=DI09_8p330 PE=4 SV=1;>tr A0A067M237 A0A067M237_9HOMO Uncharacterized protein OS=Botryobasidium botryosum FD-172 SS1 GN=BOTBODRAFT_149840 PE=3 S
A0A094DPP3;A0A094ETV5;A0A094H507;A0A093Z8Z4;A0A094EE X6;A0A093XQ02;A0A094GQF3;A0A094BXC4;A0A094CD73;A0A0G2EBR6;A0A093ZQA6;A0A0D1XW82;I6NKP4;L8FY69;A0A094GCM0;A0A0C3GZY4;A0A063C0B9;A0A086THB2;A0A093X8V0	>tr A0A094DPP3 A0A094DPP3_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-4515 (FW-2607) GN=V496_05016 PE=4 SV=1;>tr A0A094ETV5 A0A094ETV5_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-4518 (FW-2643) GN=V500_10748 PE=4 S
A0A0K6G9X5;A0A066VRV3;J4G9G6;A0A074S1D3;S8ECE6;A0A0D7BAF2;I4YDU0;R9ACU3	>tr A0A0K6G9X5 A0A0K6G9X5_9HOMO 40S ribosomal protein S8 OS=Rhizoctonia solani GN=RSOLAG22IIIB_05891 PE=3 SV=1;>tr A0A066VRV3 A0A066VRV3_9HOMO 40S ribosomal protein S8 (Fragment) OS=Rhizoctonia solani AG-8 WAC10335 GN=RSAG8_05489 PE=3 SV=1;>tr J4G9G6 J4G9G
A0A086TKM4;A0A0B7N5N8;A0A0C9LV45;S2K4E3	>tr A0A086TKM4 A0A086TKM4_9FUNG Plasma membrane ATPase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11894 PE=3 SV=1
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A0A086TKU6	>tr A0A086TKU6 A0A086TKU6_9FUNG Eukaryotic translation initiation factor 3 subunit C OS=Mortierella verticillata NRRL 6337 GN=NIP1 PE=3 SV=1
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H0ZKV9	>tr H0ZKV9 H0ZKV9_TAEGU Ubiquitin carboxyl-terminal hydrolase OS=Taeniopygia guttata (Zebra finch) (Poephila guttata) GN=TNFAIP3 PE=4 SV=1
I1BVK0;A0A0A1P571;A0A0C7BKK9;A0A0A1NB70;A0A0C7C078	>tr I1BVK0 I1BVK0_RHIO9 Uncharacterized protein OS=Rhizopus deleamar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_04935 PE=4 SV=1;>tr A0A0A1P571 A0A0A1P571_9FUNG Putative N-acetyl-gamma-glutamyl-phosphate reductase OS=Rhizopus microsp
A0A0K6FWU3;L8WIB7;M5C3I2;A0A074S3E2;A0A0A1UJF8;A0A066W3A6;A0A0B7G0L7;R9AKB4;I4Y633;W4JZD7;A0A060S8Y5;S7Q860;A0A0C3QAJ5;A0A0C2WZV1;A0A0B7G0Q9	>tr A0A0K6FWU3 A0A0K6FWU3_9HOMO Transitional endoplasmic reticulum ATPase OS=Rhizoctonia solani GN=RSOLAG22IIIB_04316 PE=3 SV=1;>tr L8WIB7 L8WIB7_THACA Cell division cycle protein 48 OS=Thanatephorus cucumeris (strain AG1-IA) GN=AG1IA_09499 PE=3 SV=1;>tr M
A0A068RNX5;A0A077WCV8;A0A0E9NK06;A0A063C4E8;A0A098VRQ4;A0A0G2DZL6;A0A0G2G549;A0A093Y5N3;A0A093Y7D9;A0A093ZGB8;A0A094AA59;A0A094BFR3;A0A094BLF0;A0A094C872;A0A094CA35;A0A094CL57;A0A094EQ43;A0A094EYH6;A0A094FZ07;A0A094H0S5;A0A094HEY9;A0A0D2AX77;S8FSC3;A0A0C3HPG7;K2RPG8;L8FXH0;R1GFY9;A0A086SVW9;A0A0C3PBI7;K5WJX5;A0A0E9KN38;A0A0B2UN17;J9DBX9;W6MXZ3;A0A0H2QVZ9;A0A0A1NBT2	>tr A0A068RNX5 A0A068RNX5_9FUNG Aaa atpase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_03252.1 PE=3 SV=1;>tr A0A077WCV8 A0A077WCV8_9FUNG Putative Cell division cycle protein 48 OS=Lichtheimia ramosa GN=LRAMOS07448 PE=3 SV=1;>tr A0A0E9NK06 A0A0E9NK06_

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G4TFJ6;A0A0C9M832;A0A0B7N6V2;A0A0C7B887;I1C410;I1CHG1;S2JRB2;A0A067M8R6;A0A0H2S4Y3;A0A0H2RNA8;A0A0H2R2B9;A0A0A1N9Q0;R7SG39	>tr G4TFJ6 G4TFJ6_PIRID Probable CDC48-Microsomal protein of CDC48/PAS1/SEC18 family of ATPases OS=Piriformospora indica (strain DSM 11827) GN=PIIN_04051 PE=3 SV=1;>tr A0A0C9M832 A0A0C9M832_9FUNG Valosin-containing protein OS=Mucor ambiguus GN=MAM1_0123d05
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A0A0C9MND7;S2K2L6	>tr A0A0C9MND7 A0A0C9MND7_9FUNG Glutamine synthetase OS=Mucor ambiguus GN=MAM1_0042c02963 PE=3 SV=1;>tr S2K2L6 S2K2L6_MUCC1 Uncharacterized protein OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_06772 PE=3 SV=1
J4G9K1;S8E830;M2RPI7	>tr J4G9K1 J4G9K1_9APHY Eukaryotic translation initiation factor 3 subunit B OS=Fibroporia radiculosa GN=PRT1 PE=3 SV=1;>tr S8E830 S8E830_FOMPI Eukaryotic translation initiation factor 3 subunit B OS=Fomitopsis pinicola (strain FP-58527) GN=PRT1 PE=3 SV=1;
A0A086TKR4;A0A0E9N9M0;A0A0E9N9W8;A0A077WGS9;A0A0A1MUX9;A0A0A1NV14;A0A0B7MYE9;A0A068S130;A0A077WE13;A0A0C9MEX2;S2K027;I1BYA0;A0A0D1YIY2;A0A0A1N553;A0A0C7B531;A0A0C9MTK7;S2IXF1;F4NSP6;A0A0B7N7J6;I1CAT7;A0A0C7C8Q1;A0A0C7C9P0	>tr A0A086TKR4 A0A086TKR4_9FUNG Aconitate hydratase, mitochondrial OS=Mortierella verticillata NRRL 6337 GN=MVEG_11934 PE=3 SV=1
A0A063BYM3;A0A068S356;REV__A0A068S356;A0A0E9KUC2	>tr A0A063BYM3 A0A063BYM3_9HYPO NIMA-like protein kinase OS=Ustilaginoidea virens GN=UV8b_5147 PE=4 SV=1;>tr A0A068S356 A0A068S356_9FUNG Protein fam63a OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_07355.1 PE=4 SV=1;>tr A0A068S356 A0A068S356_9FUNG Prote

A0A0D7BMS5	>tr A0A0D7BMS5 A0A0D7BMS5_9HOMO SART-1 protein OS=Cylindrobasidium torrendii FP15055 ss-10 GN=CYLTODRAFT_418741 PE=4 SV=1
W6MRC6	>tr W6MRC6 W6MRC6_9ASCO Uncharacterized protein OS=Kuraishia capsulata CBS 1993 GN=KUCA_T00004903001 PE=4 SV=1
A0A086TL10	>tr A0A086TL10 A0A086TL10_9FUNG Uncharacterized protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_12029 PE=4 SV=1
A0A0A1MXN8;A0A0A1MGY5;A0A0C7AX49;A0A0C7C6X1;A0A0C7C621	>tr A0A0A1MXN8 A0A0A1MXN8_9FUNG Putative NADPH--cytochrome P450 reductase OS=Rhizopus microsporus GN=RMCBS344292_06062 PE=4 SV=1;>tr A0A0A1MGY5 A0A0A1MGY5_9FUNG NADPH--cytochrome P450 reductase OS=Rhizopus microsporus GN=RMCBS344292_00052 PE=3 SV=1;>tr A0A
A0A067MY86;A0A0D7B003;A0A0B7G3Y2;A0A086SUF6;G4TCP5;A0A0C3LAW3;A0A0C3PRM1;K5WJM7;A0A0K6FP65;A0A068S6A0;A0A077X4C3;A0A0H2S178;P55251;W4KGQ5;A0A0C3PT10;S7QJ49;A0A0C2WGV4;A0A074SCU3;X8JRC4;L8X8H1;A0A066W9Q2;M5BJV5	>tr A0A067MY86 A0A067MY86_9HOMO 3-isopropylmalate dehydratase OS=Botryobasidium botryosum FD-172 SS1 GN=BOTBODRAFT_50784 PE=3 SV=1;>tr A0A0D7B003 A0A0D7B003_9HOMO 3-isopropylmalate dehydratase OS=Cylindrobasidium torrendii FP15055 ss-10 GN=CYLTODRAFT_38224
W6MR58	>tr W6MR58 W6MR58_9ASCO Uncharacterized protein OS=Kuraishia capsulata CBS 1993 GN=KUCA_T00004828001 PE=4 SV=1
A0A086TL98	>tr A0A086TL98 A0A086TL98_9FUNG Propionyl-CoA carboxylase alpha chain OS=Mortierella verticillata NRRL 6337 GN=MVEG_11252 PE=4 SV=1
A0A086TKP7	>tr A0A086TKP7 A0A086TKP7_9FUNG ATP-binding cassette, subfamily D (ALD), member 2 OS=Mortierella verticillata NRRL 6337 GN=MVEG_11917 PE=3 SV=1
A0A086TKN0	>tr A0A086TKN0 A0A086TKN0_9FUNG Methylmalonyl-CoA mutase, mitochondrial OS=Mortierella verticillata NRRL 6337 GN=MVEG_11900 PE=4 SV=1
Q2I5T0	>tr Q2I5T0 Q2I5T0_9FUNG DNA-directed RNA polymerase (Fragment) OS=Mortierella verticillata GN=RPB2 PE=3 SV=1
A0A086TKK6	>tr A0A086TKK6 A0A086TKK6_9FUNG Uncharacterized protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_11692 PE=4 SV=1
G4TXU6	>tr G4TXU6 G4TXU6_PIRID Uncharacterized protein OS=Piriformospora indica (strain DSM 11827) GN=PIIN_10139 PE=4 SV=1
A0A077WT34	>tr A0A077WT34 A0A077WT34_9FUNG Acyl-coenzyme A oxidase OS=Lichtheimia ramosa GN=LRAMOSA03090 PE=3 SV=1
F4P5N3	>tr F4P5N3 F4P5N3_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_33377 PE=3 SV=1

J6EYH7;A0A0E9KQ23;A0A0G2GWG3;A0A093YHX5;A0A093Z1Y7;A0A093ZNE8;A0A094BZP8;A0A094CG39;A0A094DUR2;L8G4R3;A0A0G2G5X6;K2RDR7;R1GFI2;A0A086T4N2;A0A094CA04;A0A094FDB3;A0A094FU68;A0A094H8C1;A0A094EIF0;A0A094GT47;A0A0D2APY6;A0A063BTL4;A0A077WQ80;A0A0C3CUH7;W4KM46;A0A068SA39;K1VRK0;A0A0A1NB24;A0A0A1NHG2;A0A0B7N264;A0A0C7CIA0;A0A0C9MW57;I1BW16;S2JTY9;F4P646;G4TI18;A0A0C3AXL4;A0A0D7BSN6;K2REW0;R1GPY5;A0A0J1BAB0;A0A0G2EU90;A0A0C7AZJ8;A0A0C7CGR2;A0A074S5G4;M5BN85;L8X781;A0A0E9NLS9;R7S797;A0A0C3QBU0;R7S793;A0A060STC0;R9AFU0;R7SA46;K5W7V5;A0A0K6FPY3;S7RTG4;X8JD90;A0A0B7F2E1;I4YIS7;A0A067LUR0;A0A0H2RFI0;A0A0C3S9A8;J4GBZ0;M2QM14;W6MF87;I1CCT3;S8G197;A0A066V786	>tr J6EYH7 J6EYH7_TRIAS Tryptophan synthase OS=Trichosporon asahii var. asahii (strain ATCC 90039 / CBS 2479 / JCM 2466 / KCTC 7840 / NCYC 2677 / UAMH 7654) GN=A1Q1_03208 PE=3 SV=1;>tr A0A0E9KQ23 A0A0E9KQ23_9HYPO Uncharacterized protein OS=Ustilagoidea v
A0A0L0DK15	>tr A0A0L0DK15 A0A0L0DK15_THETB Uncharacterized protein OS=Thecamonas trahens ATCC 50062 GN=AMSG_07736 PE=4 SV=1
A0A0L0DBJ6	>tr A0A0L0DBJ6 A0A0L0DBJ6_THETB Uncharacterized protein OS=Thecamonas trahens ATCC 50062 GN=AMSG_05981 PE=4 SV=1
F4PAH5;A0A098VZ08;A0A0B7NT48;A0A068SCE6;A0A077WP39;A0A0A1N5Q1;A0A0A1PAL5;A0A0B7NLE1;A0A0C7BS52;A0A0C9N064;I1C9B6;I1CIE3;S2J7G4	>tr F4PAH5 F4PAH5_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_17631 PE=3 SV=1
A0A0B7NPF5;S2KAM6;A0A068RFE5;A0A077WK92;I1CQ87;A0A0C7BF33;A0A0C9MMG7;A0A0C7C969	>tr A0A0B7NPF5 A0A0B7NPF5_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_11544.1 scaffold 44469 PE=3 SV=1;>tr S2KAM6 S2KAM6_MUCC1 ATP-binding cassette, subfamily D (ALD), member 3 OS=Mucor circinelloides f. circinelloides (strain 1006PhL)
J6F217;K1VPA9;F4NZ15;A0A098VLY0	>tr J6F217 J6F217_TRIAS Glutamine-fructose-6-phosphate transaminase (Isomerizing) OS=Trichosporon asahii var. asahii (strain ATCC 90039 / CBS 2479 / JCM 2466 / KCTC 7840 / NCYC 2677 / UAMH 7654) GN=A1Q1_07778 PE=4 SV=1;>tr K1VPA9 K1VPA9_TRIAC Glutamine-fru
A0A068S1Y6;A0A077WN23	>tr A0A068S1Y6 A0A068S1Y6_9FUNG Homoaconitase, mitochondrial OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_07448.1 PE=3 SV=1;>tr A0A077WN23 A0A077WN23_9FUNG Homoaconitase, mitochondrial OS=Lichtheimia ramosa GN=LRAMOS10136 PE=3 SV=1
Q55GV9	>tr Q55GV9 Q55GV9 · LIMCH_DICDI Uncharacterized protein OS=Dictyostelium discoideum (Social amoeba) GN=ChLim PE=4 SV=1
Q6E6C6	>tr Q6E6C6 Q6E6C6_ANTLO SEC18-like vesicular fusion protein (Fragment) OS=Antonospora locustae PE=3 SV=1
I1BRG5;A0A0A1P1D7;A0A0A1PEE6;A0A0C7CJ35	>tr I1BRG5 I1BRG5_RHIO9 Uncharacterized protein OS=Rhizopus deleamar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_03500 PE=3 SV=1;>tr A0A0A1P1D7 A0A0A1P1D7_9FUNG Putative Vacuolar sorting protein 1 OS=Rhizopus microsporus GN=RMCBS3442

A0A0B7N8F4;A0A0C9MY59;S2JJU6;A0A0C3AUA7;G4TJR9;A0A0J0XYJ8;A0A0D7BSY3;A0A0H2RTV2;R7SUI3;A0A0C3Q8D0;S7PWU8;S8F1D6;A0A068S5G0;J4I8K6;M2QET4;A0A060S8G2;K5X5A3;W4JWL3;A0A077WWX1;A0A068RU42;A0A077WLH2;A0A077X039;A0A0C7BHC7;I1BTL2;I1CNR6;K5WGJ3;A0A068SD15;A0A0A1N6H0	>tr A0A0B7N8F4 A0A0B7N8F4_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_05103.1 scaffold 16495 PE=4 SV=1;>tr A0A0C9MY59 A0A0C9MY59_9FUNG L-glutamine D-fructose 6-phosphate amidotransferase OS=Mucor ambiguus GN=MAM1_0212d08081 PE=4 SV=1;>t
A0A067N6N3;A0A094H6G0;A0A094B920;A0A094BBH0;A0A094DEW6;A0A093XNM3;A0A093YAN5;A0A093ZII6;A0A094A6A5;A0A094E196;A0A094F369;A0A094GTG0;A0A094H1V8;L8FZR3	>tr A0A067N6N3 A0A067N6N3_9HOMO Uncharacterized protein OS=Botryobasidium botryosum FD-172 SS1 GN=BOTBODRAFT_101931 PE=3 SV=1
A0A0D7B517;A0A0E9NEF0;A0A0C3NUD5;A0A060SAX8;A0A0C3MM95;A0A0H2S3T2;L8X638;A0A074S695;A0A0B7FTU3;A0A0C2XFH3;X8J741;K5VYL6;G4TAL0;S7QG80;R9A9R6;R7S7P6;I4Y6Q5;A0A0C3SDD7;J4H2Z6;S8EQ62;W6MQA0;A0A0J0XBS3;M2RHX6;J5T9P3;K1VQF8;A0A066WK74;A0A0K6FVF4;A0A0D7BG47;M5BIR7;M5BK00;A0A0A1N1I7;A0A0K6FUZ1	>tr A0A0D7B517 A0A0D7B517_9HOMO HSP90-domain-containing protein OS=Cylindrobasidium torrendii FP15055 ss-10 GN=CYLTODRAFT_57565 PE=3 SV=1;>tr A0A0E9NEF0 A0A0E9NEF0_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_2412-t1 PE=3 SV=1;
A0A0E9NAR8;A0A0K6FWH7;A0A0K6FNC1;A0A0D7BNB4;A0A0H2S4Q8;W4K2B1;S7Q8K7;A0A074RQQ0;A0A0C9SX40;X8JBQ3;A0A067MHA6;A0A0B7FKV5;A0A0D7B0L8;A0A0C3PR61;A0A066W6P0	>tr A0A0E9NAR8 A0A0E9NAR8_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_1184-t1 PE=3 SV=1
A0A0A1NKJ7;A0A0A1PFV2;A0A0B7N021;A0A0C7BC67;A0A0C7BYP8;A0A0C9MN47;I1CME7;S2JG76;A0A077WMI7;A0A0B7NGT6;A0A0C9MUQ8;F4NRT5;A0A0C7BYL0;A0A098VT28	>tr A0A0A1NKJ7 A0A0A1NKJ7_9FUNG Uncharacterized protein OS=Rhizopus microsporus GN=RMCBS344292_06520 PE=4 SV=1;>tr A0A0A1PFV2 A0A0A1PFV2_9FUNG Uncharacterized protein OS=Rhizopus microsporus GN=RMCBS344292_17020 PE=4 SV=1;>tr A0A0B7N021 A0A0B7N021_9FUNG Uncharacterized protein OS=Rhizopus microsporus GN=RMCBS344292_17020 PE=4 SV=1;>t

A0A0E9NDK2;A0A086SUH6;A0A0C3HTL6;A0A0G2GXM6;A0A0D2AI79;K2R9D2;R1GFI6;A0A063BVK3;A0A0G2E9E3;A0A068S6X2;A0A077WLR8;A0A0A1P2R1;A0A0B7NCZ9;A0A0C9M5W9;I1BHX6;S2K6Z3;F4NZZ6	>tr A0A0E9NDK2 A0A0E9NDK2_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_2122-t1 PE=3 SV=1;>tr A0A086SUH6 A0A086SUH6_ACRCH Proteasome subunit alpha type OS=Acremonium chrysogenum ATCC 11550 GN=ACRE_085420 PE=3 SV=1;>tr A0A0C3HTL6
L8X7E9;A0A067N1F3;A0A0H2SJ96;A0A060SKJ8;A0A074RXQ6;A0A0B7F5X5;A0A0C3S646;A0A0D7AVE1;A0A0K6FPI1;M2R2D4;S7QEI9;S8FXR3;W4KKN2;M5BLH8;X8JSS9;A0A066WD23;K5VW41;J4GQ97;W6MUU9;A0A0J0XFH5	>tr L8X7E9 L8X7E9_THACA Vacuolar ATP synthase catalytic subunit A OS=Thanatephorus cucumeris (strain AG1-IA) GN=AG1IA_00946 PE=3 SV=1;>tr A0A067N1F3 A0A067N1F3_9HOMO Uncharacterized protein OS=Botryobasidium botryosum FD-172 SS1 GN=BOTBODRAFT_154959 PE=3 S
A0A0E9N8N7;A0A0E9N964	>tr A0A0E9N8N7 A0A0E9N8N7_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_0496-t2 PE=3 SV=1;>tr A0A0E9N964 A0A0E9N964_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_0496-t1 PE=3 SV=1
A0A0B7NGY2;A0A0C9N1F1;S2J405	>tr A0A0B7NGY2 A0A0B7NGY2_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_08806.1 scaffold 34807 PE=3 SV=1;>tr A0A0C9N1F1 A0A0C9N1F1_9FUNG DEAD-domain-containing protein OS=Mucor ambiguus GN=MAM1_0290d09299 PE=3 SV=1;>tr S2J405 S2J405_MUCC
A0A0C9LTB9;S2KDV0;A0A0B7N4S6;A0A068SEA7;A0A0A1NYQ7;A0A0C7BQY9;A0A077WNP1;A0A0B7MRN5;I1C040;A0A0C9MXZ0;S2JT39;A0A0A1NDE1;A0A0A1NDJ7;A0A0C7BKU3;A0A0C7CCN9;A0A0A1NW87;A0A0C7BNM8;I1C9I8;A0A0C7C209;A0A098VS42;L8X2S4;A0A0J0XV55;S7PSN3;K5WDN5;A0A0C3SER9;Q01576;A0A060SYW1;R7S8F1;A0A0C9M6A5;A0A0C3Q169;A0A066V2N0;A0A067MBF0;A0A074RQC8;A0A0K6G404;K1W6C3;M5BY72;X8JCV5;G4TE95;S2JAY2;A0A0B7N8C4;A0A0C3AUC4;A0A0C3S4S1;R7SUN5;W4JV87;A0A0H2RAB1;A0A0A1NDF9;A0A0A1P9P7;A0A0C7B8I6;A0A0C9MV87;I4YGF9;K5VZR1;R9AX93;S2J684;A0A068SCE5;A0A077WEZ1;A0A077WQL4;A0A0B7NQQ4;I1C4Q0;M2PKF3;J4I8G5;S8FKL5;Q5GMQ4	>tr A0A0C9LTB9 A0A0C9LTB9_9FUNG Acetyl-coenzyme A synthetase OS=Mucor ambiguus GN=MAM1_0044c03055 PE=3 SV=1;>tr S2KDV0 S2KDV0_MUCC1 Acetyl-coenzyme A synthetase OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_02579 PE=3 SV=1;>tr A0
A0A074RXT1;A0A0K6GFP4;A0A0B7G059;M5BYK5;L8WIT1	>tr A0A074RXT1 A0A074RXT1_9HOMO Acyl-coenzyme A oxidase OS=Rhizoctonia solani T23E GN=V565_053500 PE=3 SV=1;>tr A0A0K6GFP4 A0A0K6GFP4_9HOMO Acyl-coenzyme A oxidase OS=Rhizoctonia solani GN=RSOLAG22IIIB_06628 PE=3 SV=1;>tr A0A0B7G059 A0A0B7G059_THACB
A0A0G2FQD7	>tr A0A0G2FQD7 A0A0G2FQD7_9PEZI Putative dnak-type molecular chaperone bipa OS=Diplodia seriata GN=UCDDS831_g08373 PE=3 SV=1
W6MM85;G4TLJ8;A0A0C3B4G4	>tr W6MM85 W6MM85_9ASCO Uncharacterized protein OS=Kuraishia capsulata CBS 1993 GN=KUCA_T00003658001 PE=3 SV=1;>tr G4TLJ8 G4TLJ8_PIRID Related to glucose-regulated protein 78 of hsp70 family OS=Piriformospora indica (strain DSM 11827) GN=PIIN_06126 PE=3 SV
W4KNF7;S7S0B1;J0DCI2;A0A0C3P282;S8G1W2;B8PHR3;A0A0D7BN55;J4HWB2;A0A067M7Q2;A0A0J1B8S2;R9AMX9;I4Y7N1;J5SJB3;K1WYH5	>tr W4KNF7 W4KNF7_9HOMO Uncharacterized protein OS=Heterobasidium irregulare TC 32-1 GN=HETIRDRAFT_431648 PE=3 SV=1;>tr S7S0B1 S7S0B1_GLOTA 40S ribosomal protein S3 OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=GLOTRDRAFT_102492 P
A0A086SYT5	>tr A0A086SYT5 A0A086SYT5_ACRCH 78 kDa glucose-regulated protein-like protein OS=Acremonium chrysogenum ATCC 11550 GN=ACRE_070010 PE=3 SV=1
A6XP71	>tr A6XP71 A6XP71_MORAP Malic enzyme OS=Mortierella alpina GN=mce2 PE=3 SV=1

A0A086TMJ4	>tr A0A086TMJ4 A0A086TMJ4_9FUNG Uncharacterized protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_11206 PE=4 SV=1
A0A086TJV3;A0A068S942;A0A077X174;A0A068RWG7;A0A077WLT6;A0A0C7AWZ9;I1C6C0;A0A0C9LX46;S2JJ12;A0A0B7NMG9;A0A0A1NMT6;A0A0A1MNK8;A0A0G2EGR4;A0A0D1XIB7;A0A0E9NGG8	>tr A0A086TJV3 A0A086TJV3_9FUNG Polyadenylate-binding protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_11868 PE=3 SV=1
A0A0C9MDS9;S2J7C3;A0A0B7N6U8;I1C685;I1CF23;A0A068SH58;A0A077WLJ6;A0A0A1NIY7;A0A0A1PGE3	>tr A0A0C9MDS9 A0A0C9MDS9_9FUNG 78 kDa glucose-regulated protein OS=Mucor ambiguus GN=MAM1_0093c04945 PE=3 SV=1;>tr S2J7C3 S2J7C3_MUCC1 Glucose-regulated protein OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_07196 PE=3 SV=1;>tr A
M5BLD6;A0A066V9T0;A0A0B7G3V0	>tr M5BLD6 M5BLD6_THACB Cysteine desulfurase OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=BN14_01565 PE=3 SV=1;>tr A0A066V9T0 A0A066V9T0_9HOMO Uncharacterized protein (Fragment) OS=Rhizoctonia solani AG-8 WAC10335 GN=RSAG8_10406 PE=3 SV=1
A0A0C9MY05;A0A0C9N482;G4TJX9;A0A0E9N9B5;J4I1W9;A0A0H2RTJ6;I4YJP1;A0A0B7MUL7;A0A066VLM9;A0A074RTQ2;A0A0A1N3S4;A0A0B7FAC4;A0A0J0XEY0;A0A0K6G076;J6ERD3;K1V8P1;S2JGR4;X8JQC8;A0A077W8H8;A0A093X261;A0A093YSF6;A0A094ACL3;A0A094CXQ2;A0A094D5N1;A0A094DJE6;A0A094EM80;A0A094FI28;A0A094FNK8;A0A094H3I2;A0A094IEC3;A0A0B7NI66;A0A0C3NXY4;A0A0C7BTA6;A0A0D1YKG6;A0A0E9KPR7;A0A0G2DXQ9;A0A0G2H026;K2QMU3;K5V0N2;L8G7G9;M2R655;R1EX08;S7QFN3;S8DNZ7;W4KHM2;A0A086SYQ2;A0A0C3GSI9;A0A0C7BQX4;A0A0D7AWZ2;I1BLK8;I1BZB0;S2J5G2;A0A063BQE3;A0A068RJJ6;A0A068RLQ4;A0A068S880;A0A077WR11;A0A077X0D2;A0A0A1P3I9;A0A0A1NSI3;A0A0C7C0J5;M5C121;R9APB7;A0A0C7BR25;W6MN93;A0A0C9MCL5;S2JPB1;A0A0B2ULP8;S2JTE9;F4NV58;A0A067MS29;A0A0C3MFI1;I1C589;I1CS55;A0A086J0C6;H8ZES1;J9D3H8;I3EEV7;I3EM72;A0A094AC89;A0A060S950;A0A098VU31;A0A0C7C7Q8;A0A0C2WVM3	>tr A0A0C9MY05 A0A0C9MY05_9FUNG Uncharacterized protein OS=Mucor ambiguus GN=MAM1_0207c08004 PE=4 SV=1;>tr A0A0C9N482 A0A0C9N482_9FUNG RAS-related protein Rab-11A OS=Mucor ambiguus GN=MAM1_0419c10422 PE=4 SV=1;>tr G4TJX9 G4TJX9_PIRID Probable GTP-binding p
A0A060SHG2;A0A086TIP5;A0A068RPV5;A0A093XJH9	>tr A0A060SHG2 A0A060SHG2_PYCCI Uncharacterized protein OS=Pycnoporus cinnabarinus GN=BN946_scf184915.g23 PE=3 SV=1;>tr A0A086TIP5 A0A086TIP5_9FUNG Uncharacterized protein OS=Podila verticillata NRRL 6337 GN=MVEG_12331 PE=3 SV=1
A0A067N2P5;W4KJD9	>tr A0A067N2P5 A0A067N2P5_9HOMO Uncharacterized protein OS=Botryobasidium botryosum FD-172 SS1 GN=BOTBODRAFT_128038 PE=3 SV=1;>tr W4KJD9 W4KJD9_9HOMO Uncharacterized protein OS=Heterobasidion irregulare TC 32-1 GN=HETIRDRAFT_407686 PE=3 SV=1
I1CPC3;A0A0C7CAR1;A0A0C7BG15;A0A0A1NHV5;A0A0C7BG62;A0A0C7CA42	>tr I1CPC3 I1CPC3_RHIO9 Hsp7-like protein OS=Rhizopus deleamar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_15014 PE=3 SV=1;>tr A0A0C7CAR1 A0A0C7CAR1_9FUNG Putative Heat shock 70 kDa protein OS=Rhizopus microsporus GN=RMATCC62417_1475

A0A068RH98;A0A077WKX3;W4KCY8;A0A067MVJ1;L8WQZ6;L8X575;A0A068RW83;A0A0B7G190;A0A0K6FSX1;A0A074SZZ0;X8JT R2;A0A077WVJ7;A0A0C3AXX1;R7SKC1;A0A0C3SFT7;S7QJ12;A0A0H2S769;G4TH29;M5CDL6;J4IBK8;A0A060S8S4;A0A094HT98;S8EHM6;A0A0B7NQ25;W6MGQ1;A0A0C9MLD5;M2R884;K5V9A6;J4IBH8;W4KFF6;A0A067MY36;A0A0C3QR77;A0A0C7BMX1;S2J8F1;A0A0B7FMZ4;L8X2J6;A0A0E9NB75;F4PD17;A0A0C3C7K1;A0A0K6GCE2;R1GBZ6;A0A0G2HFR7;A0A094FUJ4;L8FZG8;I1BSG2;S8DVU6;A0A0G2H1E8;A0A0D2AN53;A0A0H2RJQ4;A0A086T3I5;M2PCB0;A0A0D2BA45;K5X4Y9;A0A0D7BGQ7;S7Q3J2;R7SKV5;F4NSI0;A0A094GUB1;A0A0C3NZS9;A0A094CIS2;A0A093ZGU4;J4H2F4;K2RZB2;A0A0A1NVP1;A0A0A1PHA4;A0A0H2RSX5;A0A060SY59;R7S5R6;W6MMG4;A0A063C7N6;A0A0C7CEV0;A0A094A261	>tr A0A068RH98 A0A068RH98_9FUNG Atp-dependent rna helicase dbp2 OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_00842.1 PE=3 SV=1;>tr A0A077WKX3 A0A077WKX3_9FUNG Uncharacterized protein OS=Lichtheimia ramosa GN=LRAMOS01959 PE=3 SV=1;>tr W4KCY8 W4KCY8_9HO
G4T8Z4	>tr G4T8Z4 G4T8Z4_PIRID Related to HSP70 heat shock protein 70 (Hsp70) OS=Piriformospora indica (strain DSM 11827) GN=PIIN_01611 PE=3 SV=1
K5WY18;L8X715;A0A066WCJ3;A0A0H2RJR8;S7RUE4;A0A074S7Y0;A0A0C3S2I1;A0A0K6G971;A0A0H2QXA5;R9AEE2;W6MMH1;I4Y9Z8	>tr K5WY18 K5WY18_PHACS Uncharacterized protein OS=Phanerochaete carnosae (strain HHB-10118-sp) GN=PHACADRAFT_255953 PE=3 SV=1;>tr L8X715 L8X715_THACA Heat shock 70 kDa protein OS=Thanatephorus cucumeris (strain AG1-IA) GN=AG1IA_01161 PE=3 SV=1;>tr A0A066WC
A0A0C7BNQ4;A0A0C7C1Z8;A0A0A1NWD1;A0A0C9MNC5;S2JJA3;A0A0C9M5E0;F4NSN3;A0A060SFD3;R1EH27;K2QU21	>tr A0A0C7BNQ4 A0A0C7BNQ4_9FUNG Putative Heat shock protein 70 OS=Rhizopus microsporus GN=RMATCC62417_07835 PE=3 SV=1;>tr A0A0C7C1Z8 A0A0C7C1Z8_9FUNG Putative FAFR114Wp OS=Rhizopus microsporus GN=RMATCC62417_12173 PE=3 SV=1;>tr A0A0A1NWD1 A0A0A1NWD1_9FUNG
Q8J1Y0;Q9UVM0;A0A098VQ59;A0A093YWL1;A0A094ECP4;A0A063C9F2;A0A093ZFG9;A0A094ASX7;A0A094B334;A0A094D6F5;A0A094FCQ2;A0A094H3X8;A0A094H6N8;A0A094HTP7;A0A0C3CG25;A0A0G2EWK6;K2SBA2;L8GD43;A0A086T808;A0A094FUQ2;A0A093Z0Q8;A0A094DWM5;A0A093XL50	>tr Q8J1Y0 Q8J1Y0_RHIST 70 kDa heat shock protein 2 OS=Rhizopus stolonifer PE=3 SV=1;>tr Q9UVM0 Q9UVM0_RHIST Hsp70 protein 2 (Fragment) OS=Rhizopus stolonifer PE=2 SV=2
A0A068RI60;A0A077W9W7	>tr A0A068RI60 A0A068RI60_9FUNG Heat shock protein 70 OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_01079.1 PE=3 SV=1;>tr A0A077W9W7 A0A077W9W7_9FUNG Putative Molecular chaperones HSP70/HSC70,HSP70 superfamily OS=Lichtheimia ramosa GN=LRAMOS06771 PE=
A0A0D2A626	>tr A0A0D2A626 A0A0D2A626_9PEZI Hsp72-like protein OS=Verruconis gallopava GN=PV09_06491 PE=3 SV=1
A0A0C3PGF1;S2JJG9;A0A0C9LSP0;S2JJN1;A0A0C9MWC3;K1VQV2;J5TFA6;I1CJ10;A0A0C7BA89;I1C2A3;A0A0A1NMK2;A0A0A1NS3;A0A0C7B940;A0A068RT59;A0A068S7N5;A0A0B7N686;A0A077X3J0;A0A077X4V1	>tr A0A0C3PGF1 A0A0C3PGF1_PHLGI Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Phlebiopsis gigantea 11061_1 CR5-6 GN=PHLGIDRAFT_109109 PE=3 SV=1;>tr S2JJG9 S2JJG9_MUCC1 Succinate dehydrogenase [ubiquinone] flavoprotein subunit,

S8E591;A0A067LTX7;A0A0B7F7I9;A0A0K6G1V0;I4YI24;R9APP0;A0A0H2S3C1;M5BJT8;M2PEX5;S7QFH4;A0A0C2XMF7;A0A074SXX6;X8JU80;J4IBP9;K5V0E9;W4KHV4;A0A066WCS2;A0A0C3H5N0;A0A0C3M193;A0A0J0XUR3;F4P8I9;A0A0D7BLQ7;A0A060S3K5;A0A077WAH1;A0A068RDP6;G4TEW1;A0A068RE64;G4T8Z7	>tr S8E591 S8E591_FOMPI Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial OS=Fomitopsis pinicola (strain FP-58527) GN=FOMPIDRAFT_1024584 PE=3 SV=1;>tr A0A067LTX7 A0A067LTX7_9HOMO Succinate dehydrogenase [ubiquinone] flavoprotein subu
J4H4B9;A0A074S3I5;A0A0B7F4H9;A0A0K6G1T3;M2RII6;S8DIF5;W4KJD2;L8X5F9;X8JQQ6	>tr J4H4B9 J4H4B9_9APHY Uncharacterized protein OS=Fibroporia radiculosa GN=FIBRA_06912 PE=3 SV=1;>tr A0A074S3I5 A0A074S3I5_9HOMO Small COPII coat GTPase SAR1 OS=Rhizoctonia solani 123E GN=V565_050310 PE=3 SV=1;>tr A0A0B7F4H9 A0A0B7F4H9_THACB Small COPII c
M5BTK8	>tr M5BTK8 M5BTK8_THACB Uncharacterized protein OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=BN14_04584 PE=4 SV=1
A0A0C9LUJ9;I1BVT6;A0A077WGS7;S2JIW1;A0A0B7NP27;A0A0A1N4X0;A0A0C7B2R6;I1BI20	>tr A0A0C9LUJ9 A0A0C9LUJ9_9FUNG Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial-like OS=Mucor ambiguus GN=MAM1_0083d04624 PE=4 SV=1;>tr I1BVT6 I1BVT6_RHIO9 Uncharacterized protein OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-462
A0A0C3BAH3;G4TFU0	>tr A0A0C3BAH3 A0A0C3BAH3_9HOMO Uncharacterized protein OS=Serendipita vermifera MAFF 305830 GN=M408DRAFT_85799 PE=4 SV=1;>tr G4TFU0 G4TFU0_PIRID Probable VAC8-vacuolar membrane protein, required for the cytoplasm-to-vacuole targeting OS=Piriformospora ind
O19908	>tr O19908 O19908 · GLMS_CYACA Uncharacterized protein OS=Cyanidium caldarium (Red alga) GN=glmS PE=4 SV=1
CON__P02769	>P02769 SWISS-PROT:P02769 (Bos taurus) Bovine serum albumin precursor
A0A060SEU9;S7S592;A0A0D7BAH1;A0A0B7FQ52;A0A074SYS0;X8JQQ7;A0A0K6G4Y4;M5BLY9;A0A066VWE6;R9ADF6;A0A063C8N6;W4KPE0;K5VCP8;M2QWN7;J4G569;R7SRR8;A0A0C3NF21;S8E8B2;A0A0H2SSW8;A0A0C3QXC3;A0A0J0XWG4;A0A0D2AAC4;A0A0C7B8T6;A0A0C9LRX0;S2JCL4;A0A0B7NJU5;I1CHF5;I4Y6W9;A0A086T2R8;I1C414;A0A0A1N492;L8X2R6;A0A068RE87;A0A093ZDF3;A0A094C0T8;A0A067MPW9;A0A094ICM5;A0A094HNNK8;A0A0G2G560;A0A0B7NLQ5;S2JF14;A0A068RR42;A0A077WE79;A0A077W893;K2RQ39;A0A0G2DSF5;A0A0C3DQE9;A0A094DDQ1;A0A094EUV2;A0A094I5U7;L8G105;A0A093XSG9;A0A093YM56;A0A093ZSX8;A0A094D6B2;A0A094F5L5;A0A094G4U3;A0A0E9KR89;R1GGS0;J6EZI7;K1VJ85;A0A068RTA4	>tr A0A060SEU9 A0A060SEU9_PYCCI Uncharacterized protein OS=Pycnoporus cinnabarinus GN=BN946_scf184829.g26 PE=4 SV=1;>tr S7S592 S7S592_GLOTA Vacuolar protein 8 OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=GLOTRDRAFT_53895 PE=4 SV=
A0A068S8X7;A0A077WU53	>tr A0A068S8X7 A0A068S8X7_9FUNG Cyclophilin b OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_09667.1 PE=4 SV=1;>tr A0A077WU53 A0A077WU53_9FUNG Peptidyl-prolyl cis-trans isomerase OS=Lichtheimia ramosa GN=LRAMOSA11346 PE=3 SV=1
F4P8S5;A0A068RSV3;A0A0E9NIJ0;A0A0E9NHQ4;S2JF96;A0A0C9MU37;I1BLW4;A0A098VY11;A0A0B7NAH2;I1BRY0;A0A077WET7;A0A0A1N3A5;A0A086J510;H8ZDB7;I3EH54;I3ESE3;A0A0A1NFL8	>tr F4P8S5 F4P8S5_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_90846 PE=3 SV=1;>tr A0A068RSV3 A0A068RSV3_9FUNG V-type atpase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_04643.1 PE=3

A0A0C7B0J7;A0A068S9F6;A0A077WUN0;A0A0A1NEY6;I1BMN7;A0A0A1NRT5	>tr A0A0C7B0J7 A0A0C7B0J7_9FUNG Putative Fumarate reductase OS=Rhizopus microsporus GN=RMATCC62417_01445 PE=4 SV=1;>tr A0A068S9F6 A0A068S9F6_9FUNG Fumarate reductase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_09840.1 PE=4 SV=1;>tr A0A077WUN0 A0A077WU
G5EFT4	>tr G5EFT4 G5EFT4 · AMP1_CAEEL Uncharacterized protein OS=Caenorhabditis elegans GN=Itah-1.1 PE=4 SV=1
I4YG40;A0A0C3S297;R9AH20	>tr I4YG40 I4YG40_WALMC Putative heat shock protein sks2 OS=Walleimia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WALSEDRAFT_31612 PE=3 SV=1;>tr A0A0C3S297 A0A0C3S297_PHLGI Uncharacterized protein OS=Phlebiopsis gigantea 11061_1 CR5-6 GN=PHLGIDRAFT_131
L8WMQ4;A0A0B7FPD0;M5C8C3	>tr L8WMQ4 L8WMQ4_THACA Glutamate carboxypeptidase OS=Thanatephorus cucumeris (strain AG1-IA) GN=AG1IA_07899 PE=4 SV=1;>tr A0A0B7FPD0 A0A0B7FPD0_THACB Cytosolic nonspecific dipeptidase OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=RSOLAG11
A0A0A1N4F1;A0A0C7AYE6;A0A0A1NWB8;A0A0B7N5L8;I1CCN8;I1CD28;S2K2C3;Q86ZV6;A0A0A1P8Q5;A0A068RWU8;A0A077WM97;A0A077X2J3;A0A0B7N6U9;S2K026;I1BLT0;I1BW85;A0A0C9MCF3;A0A0C7CMV2;A0A0C9N9R4;I4YD25;M5BQX3;A0A074SD21;A0A0K6G1V7;X8JTU3;K5UHW9;A0A0C9N6X4;A0A0C7AZV4;Q86ZP0;Q86Z78;A0A0C7CKD0	>tr A0A0A1N4F1 A0A0A1N4F1_9FUNG Putative Heat shock protein Hsp70 OS=Rhizopus microsporus GN=RMCBS344292_01957 PE=3 SV=1;>tr A0A0C7AYE6 A0A0C7AYE6_9FUNG Putative Heat shock protein SSB1 OS=Rhizopus microsporus GN=RMATCC62417_01145 PE=3 SV=1;>tr A0A0A1NWB8
A0A0C9LUF2;A0A0B7N9R5;S2J528;A0A0C9LU68;A0A0B7NLC6;J4I9S1;L8X2U5;A0A067MB41;A0A0C3SF43;A0A0A1NF09;A0A0C7C1V9;A0A0A1NHK0;A0A0B7NF22;A0A0C9LVX6;F4P844;I1CVC9;S2J358;S2JJB7;A0A060S739;A0A066WEC2;A0A074SD44;A0A0C3RVA7;A0A0D7BBM7;A0A0K6G218;B8PCZ7;G4TBY1;K5WNU2;M5BI B2;S7S0S0;S8E2U8;W4KQ62;X8JT68	>tr A0A0C9LUF2 A0A0C9LUF2_9FUNG 40S ribosomal protein S27 OS=Mucor ambiguus GN=MAM1_0077d04387 PE=3 SV=1;>tr A0A0B7N9R5 A0A0B7N9R5_9FUNG 40S ribosomal protein S27 OS=Parasitella parasitica GN=PARPA_05601.1 scaffold 18730 PE=3 SV=1;>tr S2J528 S2J528_MUCC1 4
A0A0C2WRM4;L8X7J5;A0A067MUU1;J5RHW0;K1WGY0;S7RUM4;W4KI26;G4U2H4;A0A0C3LG17;A0A0J0XWJ8	>tr A0A0C2WRM4 A0A0C2WRM4_9HOMO Uncharacterized protein OS=Serendipita vermifera MAFF 305830 GN=M408DRAFT_329262 PE=3 SV=1;>tr L8X7J5 L8X7J5_THACA Heat shock 70 kDa protein OS=Thanatephorus cucumeris (strain AG1-IA) GN=AG1IA_01361 PE=3 SV=1;>tr A0A067MUU1
J4HWH2;W4KDD2;J6ESF9;K1VZ22;M2PZI1;B8P5U8;G4TE11;A0A067MJ95;A0A0C3ND99;S8FCW8;S7S2V8;A0A0D7B8F2;A0A0C2X1V8	>tr J4HWH2 J4HWH2_9APHY Uncharacterized protein OS=Fibroporia radiculosa GN=FIBRA_04340 PE=4 SV=1;>tr W4KDD2 W4KDD2_9HOMO Uncharacterized protein OS=Heterobasidion irregulare TC 32-1 GN=HETIRDRAFT_102449 PE=4 SV=1;>tr J6ESF9 J6ESF9_TRIAS RVB1 protein OS=Tr
A0A0D7B9U2;J4HWU1;M2PPY6;R7S039;A0A086TBG7;S8ENZ4;A0A060SEA2;A0A067N2L7;A0A098VMZ8	>tr A0A0D7B9U2 A0A0D7B9U2_9HOMO Heat shock protein 70 OS=Cylindrobasidium torrendii FP15055 ss-10 GN=CYLTODRAFT_423557 PE=3 SV=1;>tr J4HWU1 J4HWU1_9APHY Uncharacterized protein OS=Fibroporia radiculosa GN=FIBRA_04964 PE=3 SV=1;>tr M2PPY6 M2PPY6_CERS8 Uncha
W6MRS9	>tr W6MRS9 W6MRS9_9ASCO Uncharacterized protein OS=Kuraishia capsulata CBS 1993 GN=KUCA_T00005055001 PE=3 SV=1

A0A093XRI9;A0A093Y152;A0A0G2H051;K2S985;A0A0D2B891;A0A0C3HBC9;A0A086TL55;A0A094E7M3;A0A094BPY7;A0A094CPM6;A0A094AP44;G4TW40;R1GMW7;A0A0J0XBT9;A0A0C3BMP3	>tr A0A093XRI9 A0A093XRI9_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3557 GN=V490_03954 PE=4 SV=1;>tr A0A093Y152 A0A093Y152_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3808 GN=O988_07165 PE=4 SV=1;>tr A0A0G2H051 A
CON__P04204;CON__ENSEMBL:ENSBTAP00000038255;CON__Q3TTY5;CON__Q5XQN5;CON__Q922U2;CON__Q7Z794;CON__Q6IFZ6;CON__P50446;CON__Q8BGZ7;CON__Q6NXH9;CON__Q9R0H5	>P04264 SWISS-PROT:P04264 Tax_Id=9606 Gene_Symbol=KRT1 Keratin, type II cytoskeletal 1
A0A086TL19	>tr A0A086TL19 A0A086TL19_9FUNG Uncharacterized protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_12038 PE=4 SV=1
CON__P35908	>P35908 SWISS-PROT:P35908 Tax_Id=9606 Gene_Symbol=KRT2 Keratin, type II cytoskeletal 2 epidermal
A0A077WLH4	>tr A0A077WLH4 A0A077WLH4_9FUNG Lysine--tRNA ligase OS=Lichtheimia ramosa GN=LRAMOSA01326 PE=3 SV=1
F4NYZ0;F4P4N1;W6MUG6;A0A077WGW1;A0A0B7NU35;A0A0C7BMH7;A0A0C9MDV1;I1CTP2;S2K3D5;A0A0C7C1S7;A0A0A1NED8;A0A0A1P346	>tr F4NYZ0 F4NYZ0_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_34585 PE=3 SV=1;>tr F4P4N1 F4P4N1_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 /
A0A0A1MYW3;A0A0C7AXH1;I1CLF9;A0A0C7AX60	>tr A0A0A1MYW3 A0A0A1MYW3_9FUNG Lysine--tRNA ligase OS=Rhizopus microsporus GN=RCMBS344292_00065 PE=3 SV=1;>tr A0A0C7AXH1 A0A0C7AXH1_9FUNG Lysine--tRNA ligase OS=Rhizopus microsporus GN=RMATCC62417_00400 PE=3 SV=1;>tr I1CLF9 I1CLF9_RHIO9 Lysine--tRNA ligas
A0A0H2ST47	>tr A0A0H2ST47 A0A0H2ST47_9HOMO ATP-sulfurylase OS=Schizopora paradoxa GN=SCHPADRAFT_923513 PE=3 SV=1
A0A060SHX7;W4KGT4	>tr A0A060SHX7 A0A060SHX7_PYCCI Uncharacterized protein OS=Pycnoporus cinnabarinus GN=BN946_scf185043.g172 PE=4 SV=1;>tr W4KGT4 W4KGT4_9HOMO Uncharacterized protein OS=Heterobasidion irregulare TC 32-1 GN=HETIRDRAFT_416211 PE=4 SV=1
A0A0D1XIB0;R1EHF1;A0A0G2EMF0	>tr A0A0D1XIB0 A0A0D1XIB0_9PEZI Dihydroxy-acid dehydratase OS=Verruconis gallopava GN=PV09_06521 PE=3 SV=1;>tr R1EHF1 R1EHF1_BOTPV Putative dihydroxy-acid dehydratase protein OS=Botryosphaeria parva (strain UCR-NP2) GN=UCRNP2_6335 PE=3 SV=1;>tr A0A0G2EMF0
A0A060SPC0;J4GR18;G4TKC4;A0A0J0XXR4;A0A0H2SF38;A0A074RRZ0;A0A0B7FS66;A0A0K6FKR4;A0A0C3S650;S8EHB9;A0A067NCJ6;M2Q5P5;W4K4F3;J6ETY0;K1WD45;A0A0D7B8U0;A0A0C2WUI6;K5WVU5;L8X0P8;A0A066WGH9;M5BKG4	>tr A0A060SPC0 A0A060SPC0_PYCCI Uncharacterized protein OS=Pycnoporus cinnabarinus GN=BN946_scf184665.g8 PE=3 SV=1;>tr J4GR18 J4GR18_9APHY Uncharacterized protein OS=Fibroporia radiculosa GN=FIBRA_05458 PE=3 SV=1;>tr G4TKC4 G4TKC4_PIRID Probable CCT6-compo
M5BXZ8;I4Y622;F4NWD2;A0A060SID8;A0A067MLE0;A0A074RHP8;A0A0B7FX03;A0A0C3PRH7;A0A0D7BMK9;G4TVC2;L8WLY4;M2QZ74;X8J4V5	>tr M5BXZ8 M5BXZ8_THACB 60S ribosomal protein L2 OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=BN14_06157 PE=4 SV=1;>tr I4Y622 I4Y622_WALMC Uncharacterized protein OS=Wallemia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WALSEDRAFT_663
A0A086TKJ4	>tr A0A086TKJ4 A0A086TKJ4_9FUNG Calnexin OS=Mortierella verticillata NRRL 6337 GN=MVEG_11680 PE=3 SV=1

A0A086TLU9;M2RIZ9	>tr A0A086TLU9 A0A086TLU9_9FUNG Asparagine synthetase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11450 PE=4 SV=1
A0A0E9NMH7;A0A0D2B675	>tr A0A0E9NMH7 A0A0E9NMH7_9ASCO Adenosylhomocysteinase OS=Saitoella complicata NRRL Y-17804 GN=G7K_5199-t1 PE=3 SV=1;>tr A0A0D2B675 A0A0D2B675_9PEZI Adenosylhomocysteinase OS=Verruconis gallopava GN=PV09_02437 PE=3 SV=1
A0A086TLG7	>tr A0A086TLG7 A0A086TLG7_9FUNG Methylcrotonoyl-CoA carboxylase beta chain, mitochondrial OS=Mortierella verticillata NRRL 6337 GN=MVEG_11320 PE=4 SV=1
A0A0C3MKF4;R9AH81;A0A0E9KXY6;X8J4R2;L8WT12;A0A0B7FU M8;M5C9C5;A0A086TF81;A0A060A7B8;A0A060S9X3;R7S7K5;S7 QA78;S8EFE5;A0A0C3BK44;A0A0C3NCK8;K5VUX3;A0A0D7B0U3 ;A0A067MVA0;G4TFE2;A0A0J0XNG6;A0A074RJX9;A0A0K6FU43;I 4Y6G6;A0A063BPF7;F4NZ07	>tr A0A0C3MKF4 A0A0C3MKF4_9HOMO Uncharacterized protein OS=Tulasnella calospora MUT 4182 GN=M407DRAFT_64771 PE=3 SV=1;>tr R9AH81 R9AH81_WAL19 Putative phosphoglucomutase OS=Wallemia ichthyophaga (strain EXF-994 / CBS 113033) GN=J056_001956 PE=4 SV=1;>tr A0
A0A0H2RMX5	>tr A0A0H2RMX5 A0A0H2RMX5_9HOMO Phosphoglucomutase OS=Schizopora paradoxa GN=SCHPADRAFT_921129 PE=3 SV=1
A0A0B7N6W9;A0A0C7B3P6;A0A0C9M5V6;S2K045;I1BN74;A0A0A 1NUW4	>tr A0A0B7N6W9 A0A0B7N6W9_9FUNG Eukaryotic translation initiation factor 3 subunit L OS=Parasitella parasitica GN=PARPA_04539.1 scaffold 14269 PE=3 SV=1;>tr A0A0C7B3P6 A0A0C7B3P6_9FUNG Eukaryotic translation initiation factor 3 subunit L OS=Rhizopus micros
CON__P35527	>P35527 SWISS-PROT:P35527 Tax_Id=9606 Gene_Symbol=KRT9 Keratin, type I cytoskeletal 9
F4PCF8;A0A068RJP4;A0A077WF71;A0A077WGT8;A0A068S784	>tr F4PCF8 F4PCF8_BATDJ Glucose-6-phosphate isomerase OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEEDRAFT_36092 PE=3 SV=1;>tr A0A068RJP4 A0A068RJP4_9FUNG Glucose-6-phosphate isomerase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR
A0A0J1ATL2;L8WGT3;A0A0C3QLT8;A0A0H2R9G0;W4KMK2;A0A 067MXA2;M2R0X7;J4GRY0;M5C9X9;G4TI66;G4TL51;M5CBP8;A0 A0D7BG56;A0A0D2BBR9;A0A0C3HKY0;W6MG61	>tr A0A0J1ATL2 A0A0J1ATL2_9TREE T-complex protein 1 subunit gamma OS=Trichosporon oleaginosus GN=CC85DRAFT_331420 PE=3 SV=1;>tr L8WGT3 L8WGT3_THACA T-complex protein 1 subunit gamma OS=Thanatephorus cucumeris (strain AG1-1A) GN=AG1IA_08818 PE=3 SV=1;>tr A0
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A0A086TKB6;A0A0H2RR76	>tr A0A086TKB6 A0A086TKB6_9FUNG 5-(Carboxyamino)imidazole ribonucleotide synthase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11602 PE=3 SV=1;>tr A0A0H2RR76 A0A0H2RR76_9HOMO Phosphoribosylaminoimidazole carboxylase OS=Schizopora paradoxa GN=SCHPADRAFT_88

A0A0K6G2D6;L8WQE1;A0A0B7G207;A0A074RP00;X8J9E4;R9AEW9;I4YCY8;A0A060S6A2;A0A0H2RU87;S7RJU6;W4K6G4;J4G162;K5UQH4;S8G535;M2PU12;A0A0D7BHM1;A0A0C3PKL1;G4TS99;L8FS48;A0A094DZN9;A0A094AYP3;A0A093YTW3;A0A094E842;A0A094H0B4;A0A093XPR4;A0A093YCI0;A0A094AAK4;A0A094BCD2;A0A094CS34;A0A094GNG8;A0A094J414;A0A094CMW6;A0A0C3CP65;A0A0E9N9F6;A0A0G2DWN4;A0A067MK97;A0A0C3B2Q0;A0A0J0XHZ3;J4U8Q2;K1VI91;R9APB2;I4Y844;F4NV94;W6MF71;A0A068RHU8;A0A077WIL1;A0A0C3Q8L6	>tr A0A0K6G2D6 A0A0K6G2D6_9HOMO Nucleolar protein 56 OS=Rhizoctonia solani GN=RSOLAG22IIIB_04925 PE=4 SV=1;>tr L8WQE1 L8WQE1_THACA Small nuclear ribonucleoprotein OS=Thanatephorus cucumeris (strain AG1-IA) GN=AG1IA_06971 PE=4 SV=1;>tr A0A0B7G207 A0A0B7G207
I4YJI5;A0A094ICZ8;A0A094F613;A0A094BIL6;A0A094D624;K2RQ86;A0A094DU08;A0A094HEJ1;A0A093XYC3;A0A0G2DWW2;A0A0E9N9G1;A0A0J0XSG0;I1CCR5;A0A0D1YQ92;A0A0G2EXK4;A0A093YYC0;A0A094A6R5;A0A094BQ69;A0A094EB85;A0A094GQU6;A0A0C3CPZ7;J4UFE0;K1WGI1;L8GB28;R1EW30;A0A063C035;F4P433;A0A0A1P192;A0A0A1N8W7;R9AH87;A0A086T8P7;A0A0D7BST4;W6MQL9;A0A093ZB36	>tr I4YJI5 I4YJI5_WALMC Uncharacterized protein OS=Wallemia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WALSEDRAFT_59108 PE=3 SV=1;>tr A0A094ICZ8 A0A094ICZ8_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-4520 (FW-2644) GN=V502_01895
A0A068RJX6;A0A077WHF8;A0A0C3AW30	>tr A0A068RJX6 A0A068RJX6_9FUNG Glucose-6-phosphate isomerase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_01663.1 PE=3 SV=1;>tr A0A077WHF8 A0A077WHF8_9FUNG Glucose-6-phosphate isomerase OS=Lichtheimia ramosa GN=LRAMOSA08570 PE=3 SV=1;>tr A0A0C3AW30 A0
A0A0G2EC75;A0A0D1YN30;A0A0G2EL87;A0A0C3DYX5;A0A086THR9;A0A0E9L3B1	>tr A0A0G2EC75 A0A0G2EC75_9EURO Putative t-complex protein theta OS=Phaeomoniella chlamydospora GN=UCRPC4_g04238 PE=3 SV=1;>tr A0A0D1YN30 A0A0D1YN30_9PEZI T-complex protein 1, theta subunit OS=Verruconis gallopava GN=PV09_06646 PE=3 SV=1;>tr A0A0G2EL87 A0A
A0A0E9NL23;I1BIV3;S2K910;A0A0C9MEB4	>tr A0A0E9NL23 A0A0E9NL23_9ASCO Protein disulfide-isomerase OS=Saitoella complicata NRRL Y-17804 GN=G7K_4498-t1 PE=3 SV=1;>tr I1BIV3 I1BIV3_RHIO9 Protein disulfide-isomerase OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN
A0A068RU20;A0A077X4Z3	>tr A0A068RU20 A0A068RU20_9FUNG Alanine transaminase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_04494.1 PE=4 SV=1;>tr A0A077X4Z3 A0A077X4Z3_9FUNG Uncharacterized protein OS=Lichtheimia ramosa GN=LRAMOSA06372 PE=4 SV=1
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A0A086TJ33;A0A0C3QPP5;F4NSZ0	>tr A0A086TJ33 A0A086TJ33_9FUNG Prolyl-tRNA synthetase OS=Mortierella verticillata NRRL 6337 GN=MVEG_12114 PE=3 SV=1;>tr A0A0C3QPP5 A0A0C3QPP5_9HOMO Uncharacterized protein OS=Tulasnella calospora MUT 4182 GN=M407DRAFT_6275 PE=3 SV=1;>tr F4NSZ0 F4NSZ0_BATD

A0A0C7BV33;A0A0C9MPW0;E2D2C5;A0A0B7NLP9;S2J744;I1CU U5;A0A068RWQ9;A0A077X1R3;A0A0C7CEK5	>tr A0A0C7BV33 A0A0C7BV33_9FUNG Putative 2-isopropylmalate synthase OS=Rhizopus microsporus GN=RMATCC62417_09767 PE=3 SV=1;>tr A0A0C9MPW0 A0A0C9MPW0_9FUNG 2-isopropylmalate synthase OS=Mucor ambiguus GN=MAM1_0086c04752 PE=3 SV=1;>tr E2D2C5 E2D2C5_PHYBL 2-i
A0A0J0XKQ3;J6FAA9;K1WAZ1	>tr A0A0J0XKQ3 A0A0J0XKQ3_9TREE Putative cyclohydrolase OS=Trichosporon oleaginosus GN=CC85DRAFT_296902 PE=4 SV=1;>tr J6FAA9 J6FAA9_TRIAS Cyclohydrolase OS=Trichosporon asahii var. asahii (strain ATCC 90039 / CBS 2479 / JCM 2466 / KCTC 7840 / NCYC 2677 / U
A0A0A1N1V9;A0A068RUQ5;A0A063C5N0;A0A086T213;A0A068S7 11;A0A077WC91;A0A077WQK1;A0A0A1NLB7;A0A0C7B5F6;A0A0 77X2P3;A0A0A1NG79	>tr A0A0A1N1V9 A0A0A1N1V9_9FUNG Putative 40S ribosomal protein S5 OS=Rhizopus microsporus GN=RMCBS344292_05135 PE=3 SV=1;>tr A0A068RUQ5 A0A068RUQ5_9FUNG 40s ribosomal protein s5 OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_05077.1 PE=3 SV=1;>tr A0A063C
F4P350	>tr F4P350 F4P350_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_19595 PE=3 SV=1
S2JTS1;A0A0H2RRT6;A0A0A1N0B5;A0A0A1NHM4;A0A0C7B1H8;I 1BKR8;A0A077WKC9;A0A0B7NLF9;A0A0C9LVV5;A0A060S5F8;A0 A0C3LB20	>tr S2JTS1 S2JTS1_MUCC1 Delta-1-pyrroline-5-carboxylate dehydrogenase OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_01345 PE=3 SV=1;>tr A0A0H2RRT6 A0A0H2RRT6_9HOMO Delta-1-pyrroline-5-carboxylate dehydrogenase 1 OS=Schizopora par
A0A068SF45;A0A077X012;I1BV29;A0A0C7AYI6;A0A0C9MWC5;A0 A0B7NLT4;S2KCP1;A0A0C7C4L9;A0A0A1NTK4	>tr A0A068SF45 A0A068SF45_9FUNG T-complex protein eta subunit (Tcp-1-eta) OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_10692.1 PE=3 SV=1;>tr A0A077X012 A0A077X012_9FUNG Putative T-complex protein 1 subunit eta OS=Lichtheimia ramosa GN=LRAMOSA04631 PE=3
A0A0C3GU79	>tr A0A0C3GU79 A0A0C3GU79_9PEZI Uncharacterized protein OS=Oidiodendron maius Zn GN=OIDMADRAFT_34310 PE=4 SV=1
Q9QZ86	>tr F4P9U1 Q9QZ86 · NOP58_RAT Putative uncharacterized protein OS=Rattus norvegicus (Rat) GN=Nop58 PE=4 SV=1
CON__P02538;CON__P04259;CON__P48668	>P02538 SWISS-PROT:P02538 Tax_Id=9606 Gene_Symbol=KRT6A Keratin, type II cytoskeletal 6A;>P04259 SWISS-PROT:P04259 Tax_Id=9606 Gene_Symbol=KRT6B Keratin, type II cytoskeletal 6B;>P48668 SWISS-PROT:P48668 Tax_Id=9606 Gene_Symbol=KRT6C Keratin, type II cytos
A0A098VVI1;A0A086T8P0;A0A063BZN8;A0A0D2A827;A0A0E9L3X 8	>tr A0A098VVI1 A0A098VVI1_9MICR Uncharacterized protein OS=Mitosporidium daphniae GN=DI09_126p40 PE=3 SV=1;>tr A0A086T8P0 A0A086T8P0_ACRCH T-complex protein 1 subunit-like protein OS=Acremonium chrysogenum ATCC 11550 GN=ACRE_034800 PE=3 SV=1;>tr A0A063BZN8
A0A0B7MZJ4;A0A0C9MAY6;S2KH72;A0A094GJU5;A0A094C1R3; A0A094BWW8;A0A094BVR6;I4YFZ8;A0A0C2X6Q2;A0A066V2F8; R9AGW5;A0A068RJ45;A0A060SRY6;K5VL84;S8E3P8;A0A0C7B8 M2;I1BQP4;A0A0C3S6G4;R1GHJ6;A0A0G2GN43;K2RP84;A0A094 GY37;L8G256;A0A093XED8;A0A094CSX4;A0A094DBU6;A0A094E V82;A0A094HRS8;A0A0G2E3Q3;A0A093YKG3;A0A094ALA2;A0A0 A1P819;A0A0A1UII8	>tr A0A0B7MZJ4 A0A0B7MZJ4_9FUNG T-complex protein 1 subunit gamma OS=Parasitella parasitica GN=PARPA_05267.1 scaffold 16736 PE=3 SV=1;>tr A0A0C9MAY6 A0A0C9MAY6_9FUNG T-complex protein 1 subunit gamma OS=Mucor ambiguus GN=MAM1_0173c07224 PE=3 SV=1;>tr S2KH7
A0A093Y066;A0A093YQZ7;A0A093ZBQ2;A0A094A7Y8;A0A094AB C3;A0A094BPC0;A0A094BR44;A0A094DD97;A0A094EZE3;A0A09 4FLP1;A0A094GBU8;A0A094GUG9;A0A094H063;A0A094HRA1;L8 FM71	>tr A0A093Y066 A0A093Y066_9PEZI ATP synthase subunit alpha OS=Pseudogymnoascus pannorum VKM F-3808 GN=O988_05424 PE=3 SV=1;>tr A0A093YQZ7 A0A093YQZ7_9PEZI ATP synthase subunit alpha OS=Pseudogymnoascus pannorum VKM F-3557 GN=V490_00951 PE=3 SV=1;>tr A0A093

J6ETH4;K1VXT4;A0A098VPV4;A0A0B7NAY6;A0A0C7BB21;A0A0J0XRA8;I1CAE2;I1CIS2;S2J058;A0A068RL55;A0A077X1S1;A0A0C9MDS4;A0A0A1NTX2	>tr J6ETH4 J6ETH4_TRIAS T-complex protein 1, theta subunit (Tcp-1-theta) OS=Trichosporon asahii var. asahii (strain ATCC 90039 / CBS 2479 / JCM 2466 / KCTC 7840 / NCYC 2677 / UAMH 7654) GN=A1Q1_05429 PE=3 SV=1;>tr K1VXT4 K1VXT4_TRIAC T-complex protein 1, t
A0A086TL99;F4PB09	>tr A0A086TL99 A0A086TL99_9FUNG Propionyl-CoA carboxylase beta chain, mitochondrial OS=Mortierella verticillata NRRL 6337 GN=MVEG_11253 PE=4 SV=1
CON_P13645;CON_P02535-1;CON_Q2M2I5;CON_P13646-1;CON_P08730-1;CON_ENSEMBL:ENSP00000377550	>P13645 SWISS-PROT:P13645 Tax_Id=9606 Gene_Symbol=KRT10 Keratin, type I cytoskeletal 10
A0A0B7MPV9	>tr A0A0B7MPV9 A0A0B7MPV9_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_01235.1 scaffold 1359 PE=4 SV=1
A0A086TL29	>tr A0A086TL29 A0A086TL29_9FUNG T-complex protein 1 subunit epsilon OS=Mortierella verticillata NRRL 6337 GN=MVEG_12048 PE=3 SV=1
A0A077WBA4	>tr A0A077WBA4 A0A077WBA4_9FUNG T-complex protein 1 subunit gamma OS=Lichtheimia ramosa GN=LRAMOSA07245 PE=3 SV=1
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A0A0J0XVB3	>tr A0A0J0XVB3 A0A0J0XVB3_9TREE Isocitrate lyase OS=Trichosporon oleaginosus GN=CC85DRAFT_282916 PE=3 SV=1
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I4YHK2	>tr I4YHK2 I4YHK2_WALMC ATP synthase subunit alpha OS=Walleimia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WALSEDRAFT_31514 PE=3 SV=1
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A0A074RW18;A0A0A1UIN5	>tr A0A074RW18 A0A074RW18_9HOMO GDP/GTP exchange factor Sec2p OS=Rhizoctonia solani 123E GN=V565_114540 PE=4 SV=1;>tr A0A0A1UIN5 A0A0A1UIN5_9HOMO GDP/GTP exchange factor Sec2p OS=Rhizoctonia solani AG-3 Rhs1AP GN=RSOL_271500 PE=4 SV=1
R7RZW8	>tr R7RZW8 R7RZW8_STEHR Uncharacterized protein OS=Stereum hirsutum (strain FP-91666) GN=STEHDRAFT_87380 PE=4 SV=1
A0A086TKX3	>tr A0A086TKX3 A0A086TKX3_9FUNG V-type proton ATPase subunit B OS=Mortierella verticillata NRRL 6337 GN=MVEG_11992 PE=3 SV=1
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A0A086TJZ2	>tr A0A086TJZ2 A0A086TJZ2_9FUNG Translation initiation factor eIF-2 alpha subunit OS=Mortierella verticillata NRRL 6337 GN=MVEG_11480 PE=4 SV=1

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A0A086TIP2	>tr A0A086TIP2 A0A086TIP2_9FUNG Uncharacterized protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_12328 PE=4 SV=1
A0A068SHY5;A0A077WR68;A0A0B7N3D6;A0A0C9MLP6;S2KCX7;A0A0A1MX20;I1BV94	>tr A0A068SHY5 A0A068SHY5_9FUNG Glutamate dehydrogenase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_11698.1 PE=3 SV=1;>tr A0A077WR68 A0A077WR68_9FUNG Glutamate dehydrogenase OS=Lichtheimia ramosa GN=LRAMOSA10542 PE=3 SV=1;>tr A0A0B7N3D6 A0A0B7N3D6_9FU
A0A063C8H9;A0A086SVZ6;A0A0C3CKL8;A0A063C5R3;A0A068RZY5;A0A077WI09;A0A093YAK3;A0A093ZHE7;A0A094AJ49;A0A094ARI8;A0A094C2F2;A0A094CZ83;A0A094DDE2;A0A094DKS5;A0A094DZQ3;A0A094FS89;A0A094GE02;A0A094HGJ7;A0A094HKU1;L8G7K8;A0A093Y877	>tr A0A063C8H9 A0A063C8H9_9HYPO Cell division control protein 12 OS=Ustilaginoidea virens GN=UV8b_2410 PE=3 SV=1;>tr A0A086SVZ6 A0A086SVZ6_ACRCH Septin-like protein OS=Acremonium chrysogenum ATCC 11550 GN=ACRE_079970 PE=3 SV=1;>tr A0A0C3CKL8 A0A0C3CKL8_9PE
S7QBK3	>tr S7QBK3 S7QBK3_GLOTA UTP--glucose-1-phosphate uridylyltransferase OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=GLOTRDRAFT_127697 PE=4 SV=1
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I1BQA8;I1C5W7	>tr I1BQA8 I1BQA8_RHIO9 T-complex protein 1 subunit beta OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_03092 PE=3 SV=1;>tr I1C5W7 I1C5W7_RHIO9 T-complex protein 1 subunit beta OS=Rhizopus delemar (strain RA 99-880

A0A0E9NMY0;A0A0C9M1I7;S2JP10	>tr A0A0E9NMY0 A0A0E9NMY0_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_5148-t1 PE=4 SV=1;>tr A0A0C9M1I7 A0A0C9M1I7_9FUNG NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial OS=Mucor ambiguus GN=MAM1_0019d01707 PE=4 SV=
A0A094DEB2;A0A094GDY6;A0A094IA05;A0A094EZT1;A0A094A091;A0A094C1I1;A0A094FM45;A0A086T1V0;A0A0C3CFR8;A0A063C1X7;A0A0D1Z8K3;L8FZN2;A0A0G2GR53;K2S8J0;R1GJH5;A0A0C9MI94;A0A094EP03;A0A094HSB6;A0A093XDC6;A0A094A3B8;A0A094ACP6;A0A094B177;A0A094B9F1;A0A068S9H5;A0A077WV15;A0A0B7NAV9;A0A0C7B9I7;A0A0C7BU78;I1C0A0;S2K9L1;A0A0C3AP34;G4TQ23;A0A0B2UHZ4;A0A0A1NMV7;A0A0C7BA21;A0A0C7BVD9;I1C2U4;A0A077WUW1;A0A0A1NV33	>tr A0A094DEB2 A0A094DEB2_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-4515 (FW-2607) GN=V496_03156 PE=4 SV=1;>tr A0A094GDY6 A0A094GDY6_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-4517 (FW-2822) GN=V498_03951 PE=4 S
A0A086STY4	>tr A0A086STY4 A0A086STY4_ACRCH Cytochrome p450 protein OS=Acremonium chrysogenum ATCC 11550 GN=ACRE_087420 PE=3 SV=1
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A0A0B7N6K6;S2JQ19	>tr A0A0B7N6K6 A0A0B7N6K6_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_08100.1 scaffold 31862 PE=3 SV=1;>tr S2JQ19 S2JQ19_MUCC1 2,3-bisphosphoglycerate-independent phosphoglycerate mutase OS=Mucor circinelloides f. circinelloides (strain
K5VVM7	>tr K5VVM7 K5VVM7_PHACS Coronin OS=Phanerochaete carnosae (strain HHB-10118-sp) GN=PHACADRAFT_264349 PE=3 SV=1
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A0A067MTN2;S8ET35;A0A0C3QID3;M2R1D0;A0A0B7F6I6;M5BKT9;A0A067N1I6	>tr A0A067MTN2 A0A067MTN2_9HOMO Uncharacterized protein OS=Botryobasidium botryosum FD-172 SS1 GN=BOTBODRAFT_29386 PE=3 SV=1;>tr S8ET35 S8ET35_FOMPI Uncharacterized protein OS=Fomitopsis pinicola (strain FP-58527) GN=FOMPIDRAFT_1021155 PE=3 SV=1;>tr A0A0C3
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A0A086TIW8;R1GS12;S7QFA7;A0A0C3RWP1;K5W7U5;A0A060S709;J4H458;M2RI42;R7S816;S8FSB8;A0A0H2S0B6;G4TBV5;A0A0D7AW29;A0A0G2FTH8;A0A0G2HK23;K2R9P7;S2IXF5;A0A0B7NTB1;A0A0B7NV10;S2IV94;S2JMW0;A0A0C3DAR4;A0A063BTZ5;A0A0B7NKX5;A0A0E9KPU1;S2JSX3;A0A094FKW9;A0A093Y130;A0A094CCY4;A0A086T4D9;A0A093YJ93;A0A093YYZ0;A0A094AHL3;A0A094AZX0;A0A094CLF5;A0A094ER67;A0A094F9W0;A0A094H1P8;A0A094HTK0;L8G6D5;A0A0B7N476;S4W3H3	>tr A0A086TIW8 A0A086TIW8_9FUNG ATP synthase subunit beta OS=Mortierella verticillata NRRL 6337 GN=MVEG_12229 PE=3 SV=1
A0A094ALX3;A0A093Y9Q2;A0A094C0Z7;A0A094CJZ6;A0A0G2HJA4;A0A063CB91;A0A093YY62;A0A093ZSK8;A0A093ZXS1;A0A094C1X7;A0A094D5S8;A0A094ETB1;A0A094FSM1;A0A094G8D6;A0A094GR52;A0A094KMR8;A0A0C3HEH3;L8FZ63;A0A0D1YL95;A0A0G2EJ32;K2R9C1;R1GXC5;I4YHV2	>tr A0A094ALX3 A0A094ALX3_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-4281 (FW-2241) GN=V493_01968 PE=3 SV=1;>tr A0A093Y9Q2 A0A093Y9Q2_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3808 GN=O988_05697 PE=3 SV=1;>tr A0
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A0A0C9M4R3;S2JPK6;A0A068RTU4;A0A077WDJ3;A0A0B7N3T9;A0A0C7B2B2;A0A0A1NAY0;A0A0A1NGI8;I1C290;A0A098VV31;I1CE69	>tr A0A0C9M4R3 A0A0C9M4R3_9FUNG Obg-like ATPase 1 OS=Mucor ambiguus GN=MAM1_0060c03776 PE=3 SV=1;>tr S2JPK6 S2JPK6_MUCC1 Obg-like ATPase 1 OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_00840 PE=3 SV=1;>tr A0A068RTU4 A0A068RTU4_9F

R1EJP5;A0A086T6S5;A0A063BRE5;A0A0G2EFB8;A0A0E9KNU5;K2RGN0	>tr R1EJP5 R1EJP5_BOTPV Isocitrate dehydrogenase [NADP] OS=Botryosphaeria parva (strain UCR-NP2) GN=UCRNP2_5478 PE=3 SV=1;>tr A0A086T6S5 A0A086T6S5_ACRCH Isocitrate dehydrogenase [NADP] OS=Acremonium chrysogenum ATCC 11550 GN=ACRE_041610 PE=3 SV=1;>tr A0A0
F4P8M2;A0A094D1B5;A0A0D1XDC3;A0A093Y422;A0A093Y6A7;A0A094BTE8;A0A094D871;A0A094D968;A0A094F897;A0A094FSP8;A0A094H0P6;A0A094HDN0;A0A094HWB7;L8FUD0;A0A0C3D379;A0A086T7A0;A0A063C3K6	>tr F4P8M2 F4P8M2_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_90451 PE=3 SV=1;>tr A0A094D1B5 A0A094D1B5_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-4515 (FW-2607) G
W4K0N8	>tr W4K0N8 W4K0N8_9HOMO Dihydrolipoyl dehydrogenase OS=Heterobasidion irregulare TC 32-1 GN=HETIRDRAFT_440676 PE=4 SV=1
A0A0C3G956;F4NT48	>tr A0A0C3G956 A0A0C3G956_9PEZI UDP-glucose 6-dehydrogenase OS=Oidiodendron maius Zn GN=OIDMADRAFT_139098 PE=3 SV=1;>tr F4NT48 F4NT48_BATDJ UDP-glucose 6-dehydrogenase OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_18273 PE=3 S
A0A086TMD8;A0A0J0XY42	>tr A0A086TMD8 A0A086TMD8_9FUNG Fumarate hydratase, mitochondrial OS=Mortierella verticillata NRRL 6337 GN=MVEG_11152 PE=3 SV=1
A0A0J1B8C7;A0A060SCF7;S8E3B3;J4GLG5;A0A0C3S748;A0A0H2S4G2;K5W058;R7SSK0;R9AD07;A0A067MYZ0;J4UF97;K1WGW5;I4Y6M8;K5VMS8	>tr A0A0J1B8C7 A0A0J1B8C7_9TREE Adenylosuccinate lyase OS=Trichosporon oleaginosus GN=CC85DRAFT_271894 PE=3 SV=1;>tr A0A060SCF7 A0A060SCF7_PYCCI Uncharacterized protein OS=Pycnoporus cinnabarinus GN=BN946_scf184836.g38 PE=4 SV=1;>tr S8E3B3 S8E3B3_FOMPI Ade
A0A0B7FVJ6;M5C8J7;F4P386;A0A0C2XZX4	>tr A0A0B7FVJ6 A0A0B7FVJ6_THACB Leucyl aminopeptidase OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=RSOLAG1B_09492 PE=3 SV=1;>tr M5C8J7 M5C8J7_THACB Leucine aminopeptidase 3 OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=L
J4HWT1;K5WAF4;A0A063BZ29;A0A0E9KT34;A0A0C3DRA1;J6EP S9;K1VK91;S8G1G7;S2KIR3;A0A0B7NH14;A0A0C9MEY4	>tr J4HWT1 J4HWT1_9APHY 6-phosphogluconate dehydrogenase, decarboxylating OS=Fibroporia radiculosa GN=FIBRA_04913 PE=3 SV=1;>tr K5WAF4 K5WAF4_PHACS 6-phosphogluconate dehydrogenase, decarboxylating OS=Phanerochaete carnosae (strain HHB-10118-sp) GN=PHACADRA
A0A086TKG6;A0A0G2H8I6;A0A094B6R6;A0A093Z3B6;A0A0E9NIM06;A0A068RF59;A0A094F147;A0A094KB46;F4NYU5;A0A0D1Z3V5;A0A093XKS3;A0A094BUJ7;A0A094DAH8;L8FVV4;A0A094CE94;A0A094GCP9;A0A0C3HP80;K2T0E2;R1GU34;A0A086TFA8;A0A0G2ENE3;A0A0B7NLJ1;A0A0C2XS49;S2KC68;I1C383;A0A077WKV6;A0A093YBH1;A0A094H968;A0A094HAH4;A0A093YW11;A0A094B274;I1C070	>tr A0A086TKG6 A0A086TKG6_9FUNG NADH dehydrogenase (Quinone), D subunit OS=Mortierella verticillata NRRL 6337 GN=MVEG_11652 PE=3 SV=1
P55250;D6R7B6;D1LGU2;I1BQ89;M2QX92;A0A0D7BRI6;S2JHF5;A0A0C9MID6;W4KPM1;S7S025;A0A0C3QA10;A0A0B7NBR4;A0A068S032;A0A077WKH3;A0A074RLZ1;X8JKQ5;A0A067MW10;J4GN74;A0A0C3BC52;A0A068RRH2;A0A077WD27;A0A0A1NLR4;A0A0E9NEH2;B8PJ09;A0A066VCN7;A0A0B7FIP8;A0A0K6FYM5;W6MHA8;S8EGJ3;A0A0H2S7J8;K5WP02;M5CCN9	>sp P55250 FUMH_RHIOR Fumarate hydratase, mitochondrial OS=Rhizopus oryzae GN=FUMR PE=3 SV=1;>tr D6R7B6 D6R7B6_RHIOR Fumarase OS=Rhizopus oryzae GN=FUM1 PE=2 SV=1;>tr D1LGU2 D1LGU2_RHIOR Fumarase OS=Rhizopus oryzae GN=fumR PE=2 SV=1;>tr I1BQ89 I1BQ89_RHIO9
A0A0C9MWE1	>tr A0A0C9MWE1 A0A0C9MWE1_9FUNG NADH dehydrogenase I, D subunit OS=Mucor ambiguus GN=MAM1_0177c07331 PE=3 SV=1

A0A060SGL6;A0A074RZK8;L8X7J6;A0A0B7F0P1;A0A0C3L302;A0A0A1UK27;A0A0K6FPG5;A0A0D7AYS8;B8P9H7;J4IBI4;M2QML4;S8DKN2;A0A0C3PWC1;K5W853;S7QGG5;M5BK38;A0A0C3Q3Y1	>tr A0A060SGL6 A0A060SGL6_PYCCI Uncharacterized protein OS=Pycnopus cinnabarinus GN=BN946_scf185014.g15 PE=4 SV=1;>tr A0A074RZK8 A0A074RZK8_9HOMO E3 ubiquitin ligase complex SCF subunit SconC protein OS=Rhizoctonia solani 123E GN=V565_045280 PE=4 SV=1;>t
J9DLC8	>tr J9DLC8 J9DLC8_EDHAE V-type proton ATPase subunit B OS=Edhazardia aedis (strain USNM 41457) GN=EDEG_03395 PE=3 SV=1
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R9AG48;I4YJ95	>tr R9AG48 R9AG48_WALI9 ATP-dependent RNA helicase DBP5 OS=Wallemia ichthyophaga (strain EXF-994 / CBS 113033) GN=J056_004510 PE=3 SV=1;>tr I4YJ95 I4YJ95_WALMC ATP-dependent RNA helicase DBP5 OS=Wallemia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WAL
A0A0E9NBG9;I4YF62;R9AAG1;A0A0C3KFM7;A0A074S361;A0A0B7G075;X8IVP2;A0A067MMD7;L8WNS7;A0A0K6GCD9;A0A0K6GIA7	>tr A0A0E9NBG9 A0A0E9NBG9_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_1394-t1 PE=4 SV=1;>tr I4YF62 I4YF62_WALMC Uncharacterized protein OS=Wallemia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WALSEDRAFT_53906 PE=4 SV=1;>t
W6MI81	>tr W6MI81 W6MI81_9ASCO Uncharacterized protein OS=Kuraishia capsulata CBS 1993 GN=KUCA_T00001563001 PE=4 SV=1
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A0A0B7NRI8;A0A0C9MTS2;A0A068RR57;A0A0C7BR51;A0A086TII7;I1CIE5;S2JME5;A0A077WS80;A0A0C9M506;S2IU73;A0A077WRT5	>tr A0A0B7NRI8 A0A0B7NRI8_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_12427.1 scaffold 45109 PE=3 SV=1;>tr A0A0C9MTS2 A0A0C9MTS2_9FUNG O-acetylhomoserine aminocarboxypropyltransferase OS=Mucor ambiguus GN=MAM1_0136c06292 PE=3 SV=1;>tr
G4TGU5	>tr G4TGU5 G4TGU5_PIRID Related to CYS3-cystathionine gamma-lyase OS=Piriformospora indica (strain DSM 11827) GN=PIIN_04475 PE=3 SV=1
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A0A0A1NY55;A0A0C7BK82;I1BKM1;I1CT49;A0A068RTJ1;A0A077WMJ8;A0A0B7NH87;A0A0C9MHG7;S2JSP4;R9AKA9;I4Y628;A0A0G2GRF6;A0A0G2GIY0;K2SHR7;R1GFC5;F4PD47	>tr A0A0A1NY55 A0A0A1NY55_9FUNG Elongation factor Tu OS=Rhizopus microsporus GN=RMCBS344292_10831 PE=3 SV=1;>tr A0A0C7BK82 A0A0C7BK82_9FUNG Elongation factor Tu OS=Rhizopus microsporus GN=RMATCC62417_07181 PE=3 SV=1;>tr I1BKM1 I1BKM1_RHIO9 Elongation facto
I1BQ04;A0A077WAT2;A0A0C7CDD6;A0A0B7NG15;A0A0A1NSZ0;A0A0A1P4I0;A0A0C7BDX4;A0A0C7CFP2;W6MWN3;I1CK88;A0A0A1P9K0	>tr I1BQ04 I1BQ04_RHIO9 Uncharacterized protein OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_02988 PE=3 SV=1;>tr A0A077WAT2 A0A077WAT2_9FUNG Uncharacterized protein OS=Lichtheimia ramosa GN=LRAMOSA00645 PE=3 SV=1;
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CON__P02533;CON__Q9QWL7;CON__Q04695;CON__Q6IFX2	>P02533 SWISS-PROT:P02533 Tax_Id=9606 Gene_Symbol=KRT14 Keratin, type I cytoskeletal 14;>Q9QWL7 SWISS-PROT:Q9QWL7 Tax_Id=10090 Gene_Symbol=Krt17 Keratin, type I cytoskeletal 17;>Q04695 SWISS-PROT:Q04695 Tax_Id=9606 Gene_Symbol=KRT17 Keratin, type I cytoske
Q91YI0	>tr Q91YI0 Q91YI0_AKLY_MOUSE Uncharacterized protein OS=mus musculus (mouse) GN=AS1 PE=3 SV=1
O74212	>sp O74212 D5FAD_MORAP Acyl-lipid (8-3)-desaturase OS=Mortierella alpina GN=DES1 PE=1 SV=1
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S7S0M2;W4KEX3	>tr S7S0M2 S7S0M2_GLOTA Proteasome-domain-containing protein OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=GLOTRDRAFT_33104 PE=4 SV=1;>tr W4KEX3 W4KEX3_9HOMO 1-cysteine peroxiredoxin OS=Heterobasidion irregulare TC 32-1 GN=HETIRDR
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L7PAC3	>tr L7PAC3 L7PAC3_MORAP Phenylalanine hydroxylase OS=Mortierella alpina PE=2 SV=1
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A0A074S8N2;A0A0K6G0Z8;M5BJ27;X8JQN3;G4T6E6;A0A0C3BA44;A0A066WDY9	>tr A0A074S8N2 A0A074S8N2_9HOMO Peptide chain release factor eRF subunit 1 OS=Rhizoctonia solani 123E GN=V565_033580 PE=4 SV=1;>tr A0A0K6G0Z8 A0A0K6G0Z8_9HOMO Eukaryotic peptide chain release factor subunit 1 OS=Rhizoctonia solani GN=RSOLAG22IIB_00863 PE=
S2JB07;S8DHB9	>tr S2JB07 S2JB07_MUCC1 Uncharacterized protein OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_05876 PE=4 SV=1;>tr S8DHB9 S8DHB9_FOMPI Uncharacterized protein OS=Fomitopsis pinicola (strain FP-58527) GN=FOMPIDRAFT_1056437 PE=4 SV=
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P40327	>tr P40327 P40327 · PRS4_YEAST Uncharacterized protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast) GN=RPT2 PE=3 SV=1
A0A0E9N834;A0A0H2SEK7;A0A0J1AT25;A0A094E9M6;J4U7P1;G1ESZ5;W4KND2;A0A0C2WQA0;S7S2K2;I4YIH2;K1VX15;M1T7M3;A0A0C3Q921;A0A067MQW6;A0A0C2XSJ6;A0A0E9KQZ5;A0A0G2HIU6;A0A093YJC3;A0A094ALI5;A0A094EWD7;A0A094F002;A0A094FXE9;A0A094GNA8;A0A0C3I026;L8FVD1;A0A063C4L5;A0A086TCN0;A0A0G2EA67;K2QW76;R1G1X1;A0A094AD36;A0A094HC55;G4TRK3;A0A093X9V7;A0A094CZU7;A0A093Z7N2;J4GMA7;K5WPX0;S8FCM8;A0A0C3S3E0;A0A0B7NIS1;A0A068LCN6;B8PFM6;A0A060S287;A0A0D7BT08;F4PAQ1;A0A0D2APK8;B8P5U3;M2P6G5;G4I1H5	>tr A0A0E9N834 A0A0E9N834_9ASCO Mitogen-activated protein kinase OS=Saitoella complicata NRRL Y-17804 GN=G7K_0234-t1 PE=3 SV=1;>tr A0A0H2SEK7 A0A0H2SEK7_9HOMO Mitogen-activated protein kinase OS=Schizopora paradoxa GN=SCHPADRAFT_898207 PE=3 SV=1;>tr A0A0J1
A0A086TM40	>tr A0A086TM40 A0A086TM40_9FUNG Saccharopine dehydrogenase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11055 PE=4 SV=1
A0A0C3DIP5;A0A094EIT4;A0A093X5Z2;A0A093XNJ8;A0A093YYN5;A0A093ZBT0;A0A094BBS4;A0A094BDF2;A0A094CY14;A0A094D821;A0A094DME3;A0A094F5S7;A0A094GJX9;A0A094HLK3;A0A094IJH6;L8FLD1;A0A086SZ70	>tr A0A0C3DIP5 A0A0C3DIP5_9PEZI Adenosylhomocysteinase OS=Oidiodendron maius Zn GN=OIDMADRAFT_161511 PE=3 SV=1;>tr A0A094EIT4 A0A094EIT4_9PEZI Adenosylhomocysteinase OS=Pseudogymnoascus pannorum VKM F-103 GN=V499_08245 PE=3 SV=1;>tr A0A093X5Z2 A0A093X5Z2_9

A0A086TII5;A0A068S4P5;A0A077W6G3;I1CJM1;A0A068RJY3;A0A077X1C5;A0A0A1NJ25;A0A0A1PFM8;A0A0A1PHW1;A0A0C3QWT8;A0A067MY23;A0A0K6G1R3;L8X632;A0A074S9W1;A0A0B7F3W1;X8JU77;A0A068S6X8;A0A0C9MCK8;A0A077WNI3;A0A0B7NTN1;S2JKZ4;A0A0B7MNX3;S2KKC5;I1CFJ4;A0A0C9MD38	>tr A0A086TII5 A0A086TII5_9FUNG Uncharacterized protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_12403 PE=3 SV=1
A0A0D2AN29;A0A0D2BA27;K2RZI3;A0A0G2GC88;A0A077WLM7;I1BN10;I1CME2	>tr A0A0D2AN29 A0A0D2AN29_9PEZI Succinyl-CoA ligase subunit beta OS=Verruconis gallopava GN=PV09_01058 PE=3 SV=1;>tr A0A0D2BA27 A0A0D2BA27_9PEZI Succinyl-CoA ligase subunit beta OS=Verruconis gallopava GN=PV09_01058 PE=3 SV=1;>tr K2RZI3 K2RZI3_MACPH Succin
A0A0C9MUE4;S2KBE4	>tr A0A0C9MUE4 A0A0C9MUE4_9FUNG GroES-like protein OS=Mucor ambiguus GN=MAM1_0146d06552 PE=3 SV=1;>tr S2KBE4 S2KBE4_MUCC1 Uncharacterized protein OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_03562 PE=3 SV=1
A0A0C3BM97	>tr A0A0C3BM97 A0A0C3BM97_9HOMO Uncharacterized protein OS=Serendipita vermifera MAFF 305830 GN=M408DRAFT_150498 PE=4 SV=1
P32390	>tr P32390 P32390 · ARP3_SCHPO Uncharacterized protein OS=Schizosaccharomyces pombe (strain 972 / ATCC 24843) (Fission yeast) GN=act2 PE=4 SV=1
A0A0L0DDE8	>tr A0A0L0DDE8 A0A0L0DDE8_THETB Uncharacterized protein OS=Thecamonas trahens ATCC 50062 GN=AMSG_06400 PE=3 SV=1
A0A086TKN4;A0A093YJV1;A0A094CDV0;A0A094AX91;A0A094F3P5;A0A094I1I6;A0A094GBH7;A0A0B7NWB4;F4P813;A0A093ZQ08;A0A094AWK7;A0A094C043;A0A094GPD8;A0A094JR52;A0A0C3H348;L8FV44;A0A094D2Y8;A0A068RPQ1;A0A077X1V6;A0A0A1NA60;A0A0C7BQ94;A0A0C9M2G9;I1C4D0;S2IZY3;A0A094A8I8;A0A0C7CCW0	>tr A0A086TKN4 A0A086TKN4_9FUNG Aspartate aminotransferase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11904 PE=4 SV=1
A0A0B7MWP6;A0A0A1MJ15;A0A0A1NX77;I1BX31	>tr A0A0B7MWP6 A0A0B7MWP6_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_04143.1 scaffold 11792 PE=3 SV=1;>tr A0A0A1MJ15 A0A0A1MJ15_9FUNG Putative Enolase OS=Rhizopus microsporus GN=RMATCC62417_02079 PE=3 SV=1;>tr A0A0A1NX77 A0A0A1NX77_9F
A0A0A1NKD0;A0A0A1NSG5	>tr A0A0A1NKD0 A0A0A1NKD0_9FUNG Putative Enolase OS=Rhizopus microsporus GN=RMATCC62417_09688 PE=3 SV=1;>tr A0A0A1NSG5 A0A0A1NSG5_9FUNG Putative Enolase OS=Rhizopus microsporus GN=RMCBS344292_09758 PE=3 SV=1
A0A0B7NWE6;A0A0C9MIX1;S2J8L6	>tr A0A0B7NWE6 A0A0B7NWE6_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_13974.1 scaffold 47516 PE=3 SV=1;>tr A0A0C9MIX1 A0A0C9MIX1_9FUNG Enolase OS=Mucor ambiguus GN=MAM1_0157d06840 PE=3 SV=1;>tr S2J8L6 S2J8L6_MUCC1 Enolase OS=Mucor
I3EE17;I3ERN6	>tr I3EE17 I3EE17_NEMP3 Nucleolar protein OS=Nematocida parisii (strain ERTm3) GN=NEQG_02345 PE=4 SV=1;>tr I3ERN6 I3ERN6_NEMP1 Nucleolar protein OS=Nematocida parisii (strain ERTm1 / ATCC PRA-289) GN=NEPG_00066 PE=4 SV=1

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Q9HGA1;Q9HG99;Q9HGA2;Q9HGA0;C4MMK4;Q9HGB4;A0A0A0P4S1;A0A0A0P4S9;A0A0A0P5H0;A0A0A0P9I9;D8WM67;D8WM37;D8WM68;L7SVC0;L7SVE6;L7SXW6;L7T0Z7;A0A0A0P4S7;D8WM46;A0A0A0P3I6;A0A0A0P9B6;I1YZQ1;S5PUX4;A0A0A0P4M8;Q207E0;G8GLH9;G8GLJ6;G8GLI5;G8GLI6;G8GLI9;R4QJK0;Q308K6;R4QJJ1;G8GLJ2;R4QUW1;G8GLI8;L7SWZ6;R4QRN5;Q5EG83;G8GLJ0;Q1W601;L7SXX7;R4QU30;G8GLJ1;D4NZB5;M4H1X4;M4H291;M4H2L6;M4H2P3;G8GLK0;G1FK77;D3YFQ1;A0A0A6ZEX5;D3YFQ2;A0A0A6ZFF1;A0A0A6ZHA0;A0A0A6ZHG6;D5JGN0;G9IZM3;A0A0A0P6M2;J7GXF3;J7GXF3;J7GXF8;J7H0F1;J7H2W8;G8GLK5;X4Y2I9	>tr Q9HGA1 Q9HGA1_9FUNG Elongation factor 1-alpha (Fragment) OS=Gamsiella multidivariata GN=EF-1alpha PE=3 SV=1;>tr Q9HG99 Q9HG99_9FUNG Elongation factor 1-alpha (Fragment) OS=Mortierella verticillata GN=EF-1alpha PE=3 SV=1;>tr Q9HGA2 Q9HGA2_9FUNG Elongat
A0A0B2UH62	>tr A0A0B2UH62 A0A0B2UH62_9MICR Eukaryotic translation initiation factor 2 OS=Ordospora colligata OC4 GN=M896_010580 PE=4 SV=1
F4NWR2;A0A068RPA3;A0A077WZ19;A0A0B7MX4;A0A0C9M3W2;S2JUA1	>tr F4NWR2 F4NWR2_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_9716 PE=3 SV=1;>tr A0A068RPA3 A0A068RPA3_9FUNG Argininosuccinate synthetase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCO
A0A0A1MS69;A0A0B7MZT6;A0A0C7B1X6;A0A0C9MW08;I1BP15;I1CEW2;S2KEY1;A0A068RWH3;A0A077X0Z8;A0A094CH70;A0A094GL70;A0A094GHS7;A0A094AYB2;A0A086TFY7;A0A093Y5X6;A0A093YTE7;A0A093Z2E6;A0A094A9E4;A0A094CKV3;A0A094CV31;A0A094DDU9;A0A094E8A5;A0A094GL60;L8FSF2;F4P6R1;A0A0C3SAY5;K5WYL2;A0A0E9N9L8;A0A0G2H1G6;G4TD50;L8X8L1;A0A0B7F615;A0A067LZX3;J4H2Z8;A0A0G2EB01;K2R8H3;A0A063CCJ2;A0A0D1XKU1;A0A0C3HER2;R1G9B4;W6MG78;A0A060SB76;A0A0C3QHU9;A0A0H2S3S4;W4KKX6;A0A074SX77;A0A0C3AXP7;A0A0K6FQ66;M2QMX6;M5BVC6;S7QFI7;S8EQ68;X8JEG9;I4YJ87;R9AGB0;A0A098VV18;A0A0E9L244;A0A094DZP2	>tr A0A0A1MS69 A0A0A1MS69_9FUNG Putative PRS6_MANSE 26S PROTEASE REGULATORY SUBUNIT 6B (ATPASE MS73) OS=Rhizopus microsporus GN=RMCBS344292_01377 PE=3 SV=1;>tr A0A0B7MZT6 A0A0B7MZT6_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_05407.1 s
A0A068RS22;A0A077W6W8;A0A0C9M4D8;A0A0A1NJJ0;A0A0C7B318;A0A0B7NSQ9;S2JHB7;F4P114;A0A0C7CCT8	>tr A0A068RS22 A0A068RS22_9FUNG Glutaryl-dehydrogenase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_03326.1 PE=3 SV=1;>tr A0A077W6W8 A0A077W6W8_9FUNG Putative Glutaryl-CoA dehydrogenase,mitochondrial OS=Lichtheimia ramosa GN=LRAMOSA00584 PE=3 SV=1;>tr
U5Y3C6;A0A0A7A5D6;D5KSD2;P59668;Q9Y8H5;A8E070	>tr U5Y3C6 U5Y3C6_MORAP Delta 12 desaturase OS=Mortierella alpina PE=2 SV=1

A0A0G2EGU4;A0A0C3HDZ2;A0A0D1YNA7;A0A0G2EQU2;A0A0H2RCV1;A0A093Y2I4;A0A093Y5S9;A0A094AAH9;A0A094D151;A0A094E039;A0A094E3G2;A0A094E5I3;A0A094EWF7;A0A094FMG5;A0A094FUZ0;A0A094H4H2;A0A094HLA3;K2SB76;L8FUC6;R1EYA1;S7RXX1;J0CXY0;M2P8M6;A0A0D7BVQ3;G4TRY5;W4KHW3;A0A086T1C5;A0A063BYY2;A0A094H4V8;A0A0E9N879;L8X6F8;L8WMD6;A0A093X4I4;A0A094BB95;A0A094CND8;A0A060S785;J4H507;M2R8R7;I4Y5C3;R9A9T6;A0A0B7F6V0;A0A0K6G997;A0A067M907;A0A068S518;A0A077WB53;A0A0B7NCG5;A0A0C9MW24;K5W527;R7S165;S2K7K8;A0A0J0XSS4;M5BQU1;D6R7B7;I1BH14;I1C584;W6MWG9;A0A0C2W4H8;J6EZB6;K1V9P1;A0A0H2S7U2;A0A0J0XBM3;A0A0C3PSX0;A0A066W0J7;A0A074RSX6;A0A0B7FNC4;A0A0C3S6T1;A0A0K6FZL9;K5W0T4;W4K4D3;X8IVG1;A0A094E6Z0;A0A0C3CAG6;A0A093ZCS0;A0A094A8A2;A0A094AK95;A0A094B8M8;A0A094FCP9;A0A094FTI6;A0A094H4F9;A0A0G2GV48;K2RTX1;L8FPM0;R1EVC8;A0A0D2ARF0;A0A0D7BHV7;A0A0C3QBB8;A0A0C3QGW7;A0A093ZD04	>tr A0A0G2EGU4 A0A0G2EGU4_9EURO Putative malate dehydrogenase OS=Phaeomoniella chlamydospora GN=UCRPC4_g03714 PE=3 SV=1;>tr A0A0C3HDZ2 A0A0C3HDZ2_9PEZI Malate dehydrogenase OS=Oidiodendron maius Zn GN=OIDMADRAFT_165098 PE=3 SV=1;>tr A0A0D1YNA7 A0A0D1YNA7_9
A0A063BTI3	>tr A0A063BTI3 A0A063BTI3_9HYPO D-3-phosphoglycerate dehydrogenase 1 OS=Ustilagoidea vires GN=UV8b_6623 PE=3 SV=1
F4NVJ5	>tr F4NVJ5 F4NVJ5_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_9167 PE=4 SV=1
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A0A0G2E7K8;R1GUR0	>tr A0A0G2E7K8 A0A0G2E7K8_9PEZI Ribosomal protein OS=Diplodia seriata GN=UCDDS831_g05629 PE=3 SV=1;>tr R1GUR0 R1GUR0_BOTPV Ribosomal protein OS=Botryosphaeria parva (strain UCR-NP2) GN=UCRNP2_1179 PE=3 SV=1
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A0A0B7NB48	>tr A0A0B7NB48 A0A0B7NB48_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_06541.1 scaffold 22734 PE=3 SV=1
A0A068RF15;A0A077WIV1;A0A0C7BC21;A0A0C9MNU0;I1CIR1;S2JR05;A0A0B7NTT9;F4PAI6;A0A0A1NIH1;A0A0A1NZR9	>tr A0A068RF15 A0A068RF15_9FUNG Stomatin family protein OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_00534.1 PE=4 SV=1;>tr A0A077WIV1 A0A077WIV1_9FUNG Putative Cell division cycle 20-like protein 1, cofactor-APC complex OS=Lichtheimia ramosa GN=LRAMOSAO
M4CAS3	>tr M4CAS3 M4CAS3 · M4CAS3_BRACM Putative uncharacterized protein OS=Brassica campestris (Field mustard) PE=4 SV=1
A0A0D2ABF0	>tr A0A0D2ABF0 A0A0D2ABF0_9PEZI ATP-dependent RNA helicase eIF4A OS=Verruconis gallopava GN=PV09_04936 PE=3 SV=1

I4YDT6;R9ACR9;A0A0D7AY16;G4TDL5;A0A0H2S2R2;A0A0C2X710;R7SV02;A0A066VDL7;A0A067MSB0;J4HW07;S7QP90;M2QWB5;B8P2V9;K5XBU2;A0A074SWP2;A0A0B7FMX5;A0A0C3RU50;A0A0K6GGL5;L8WTL1;S8F8U7;X8IXR0;M5BJB1;W4KJI6;A0A060SC13	>tr I4YDT6 I4YDT6_WALMC Chorismate synthase OS=Walleimia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WALSEDRAFT_32267 PE=3 SV=1;>tr R9ACR9 R9ACR9_WALI9 Chorismate synthase OS=Walleimia ichthyophaga (strain EXF-994 / CBS 113033) GN=J056_001196 PE=3 SV=1;
F4PDS1	>tr F4PDS1 F4PDS1_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_36225 PE=3 SV=1
W6MF78;A0A0H2SBC3	>tr W6MF78 W6MF78_9ASCO Uncharacterized protein OS=Kuraishia capsulata CBS 1993 GN=KUCA_T00000320001 PE=3 SV=1;>tr A0A0H2SBC3 A0A0H2SBC3_9HOMO DEAD-domain-containing protein OS=Schizopora paradoxa GN=SCHPADRAFT_903514 PE=4 SV=1
G4TBF6	>tr G4TBF6 G4TBF6_PIRID Probable Actin OS=Piriformospora indica (strain DSM 11827) GN=PIIN_02533 PE=3 SV=1
A0A0E9NL60;Q2TTE1;C4MMH6;Q9C2S4;Q9C2T0;C4MMG5;Q29TR7;D9I7R7	>tr A0A0E9NL60 A0A0E9NL60_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_4662-t1 PE=3 SV=1;>tr Q2TTE1 Q2TTE1_9FUNG Actin (Fragment) OS=Smittium simulii PE=3 SV=1;>tr C4MMH6 C4MMH6_9FUNG Actin (Fragment) OS=Mortierella indohii PE=
A0A0C3D2X0	>tr A0A0C3D2X0 A0A0C3D2X0_9PEZI Uncharacterized protein OS=Oidiodendron maius Zn GN=OIDMADRAFT_141320 PE=3 SV=1
W6MK43	>tr W6MK43 W6MK43_9ASCO Uncharacterized protein OS=Kuraishia capsulata CBS 1993 GN=KUCA_T00002665001 PE=4 SV=1
A0A068S9T5;A0A068S314;A0A077WN88;A0A077WP48	>tr A0A068S9T5 A0A068S9T5_9FUNG Pkinase-domain-containing protein OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_09948.1 PE=4 SV=1;>tr A0A068S314 A0A068S314_9FUNG Calcium calmodulin-dependent protein kinase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCO
I1CR47;A0A0B7NRQ9;S2K8M3;S2IZ04;A0A0D7BJ24;A0A0C9MF84;A0A0B7MZX2;I1CBW3	>tr I1CR47 I1CR47_KRHO9 60S ribosomal protein L37 OS=Rhizopus delemar (strain RA 99-6607 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_15638 PE=3 SV=1;>tr A0A0B7NRQ9 A0A0B7NRQ9_9FUNG Ribosomal protein L37 OS=Parasitella parasitica GN=PARPA_14468.1 scaff
A0A0J1B5H2	>tr A0A0J1B5H2 A0A0J1B5H2_9TREL Actin-like protein OS=Trichosporon breagmosus GN=CC85DRAFT_301886 PE=3 SV=1
A0A0B7NF04;A0A0C9N2K8;S2JD99;M9RTJ9;M9RSC6;A0A0C7B7H8;I1CGE1;I1CJ50;A0A0A1NII6;A0A0C7CH85;A0A0A1N3C0	>tr A0A0B7NF04 A0A0B7NF04_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_10220.1 scaffold 40051 PE=3 SV=1;>tr A0A0C9N2K8 A0A0C9N2K8_9FUNG 26S protease regulatory subunit 8-like isoform X4 OS=Mucor ambiguus GN=MAM1_0226d08335 PE=3 SV=1;>tr
A0A068RYI7;A0A077X422;A0A068RY47;A0A0B7NEI7;A0A0C9M909;S2JDV2;I1CIX6;A0A0C7BEV5;A0A0C7BZ58;I1CA13;A0A0A1P159;A0A0E9NN55;A0A068RN90;A0A093ZA81;A0A094F1D0;L8WVW87;A0A0D1XJQ4;A0A0G2EKP8;K2QM03;R1GIR4;A0A0G2ECV6;J5T7H1;K1V2V5;A0A086SUF7;R9ABQ1;G4TCA8;A0A094EDG1;A0A094GVQ7;A0A063CC75;A0A093Y0F0;A0A093Y0Y6;A0A094AP05;A0A094AUS1;A0A094BEW6;A0A094DC50;A0A094DTJ6;A0A094IFI5;A0A094K646;A0A0C3D7Y2;L8GAE2;A0A094HWI2;A0A0D7BCM3;A0A0H2SP02;A0A0C3BKM7;A0A066W8B3;A0A067MWW9;A0A074SIT0;A0A0B7FDE7;A0A0K6FQF1;S7QDD4;S8E0E0;W4KLV5;A0A077X0E4;A0A0C3M0F6;J4H1L6;S2JNS7;A0A0C3PP80;K5W8G9;M2RH60;W6MTD6;F4P309;A0A068SBT2;A0A077WJ18;I4Y678;A0A0J1B1U1;M5BPG3;A0A093YNP5	>tr A0A068RYI7 A0A068RYI7_9FUNG Pyruvate dehydrogenase E1 component subunit alpha OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_06235.1 PE=4 SV=1;>tr A0A077X422 A0A077X422_9FUNG Pyruvate dehydrogenase E1 component subunit alpha OS=Lichtheimia ramosa GN=

A0A098VVJ9;F4NU41	>tr A0A098VVJ9 A0A098VVJ9_9MICR Uncharacterized protein OS=Mitosporidium daphniae GN=DI09_108p70 PE=3 SV=1;>tr F4NU41 F4NU41_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_29178 PE=3 SV=1
K2SFN6;I4Y7D7;R9AQU9;A0A0G2E448;R1GBC1;A0A0D1XMP3;A0A0B7MSK5;A0A0C9MJF8;S2J362;A0A0B7N322;A0A0C7B474;A0A0C9LRD4;S2JUM3;A0A068RIB8;A0A068SG89;A0A077W929;A0A077WNL0;I1CR91;I1CVL8;A0A0A1N6D8;A0A0A1NIH9;I1BK46;I1CCJ0;K1VT38;J5Q778;A0A074S5A3;X8JR54;W6MVN9;A0A063BP26;A0A086TA28;A0A0C3DTW4;A0A060SDG8;A0A094A0E5;A0A093X4Y3;A0A093XTH2;A0A093Z874;A0A094A5D4;A0A094BBS6;A0A094BDH0;A0A094CMC7;A0A094E0B5;A0A094F3J0;A0A094GPG9;A0A094GX14;A0A094HQP3;A0A094IUK6;L8GDK5;A0A098VLJ1;W4KQ00;A0A066W0B8;F4P0B2;A0A067MW63;A0A0C3LBK2;A0A0J0XT41;M2RRZ5;S7S4Q2;A0A0G2GWU7;A0A0H2RQW7;A0A0D7BGG5;A0A0C3PUU8;B8PCY6;A0A0B7FJS3;A0A0K6G539;M5BKC8;A0A0A1N5J3;A0A0A1NE58;A0A0C7BZ22;A0A0C7BYZ2;A0A0A1NHW2	>tr K2SFN6 K2SFN6_MACPH Prohibitin OS=Macrophomina phaseolina (strain MS6) GN=MPH_07060 PE=4 SV=1;>tr I4Y7D7 I4Y7D7_WALMC Uncharacterized protein OS=Walleimia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WALSEDRAFT_61236 PE=4 SV=1;>tr R9AQU9 R9AQU9_WALI
S8FQM2	>tr S8FQM2 S8FQM2_FOMPI Peptide hydrolase OS=Fomitopsis pinicola (strain FP-58527) GN=FOMPI DRAFT_1115220 PE=3 SV=1
F4NXY0;F4NXY2	>tr F4NXY0 F4NXY0_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_34661 PE=3 SV=1;>tr F4NXY2 F4NXY2_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 /
A0A075QMZ8;A0A075QLA3;CON__ENSEMBL:ENSBTAP00000025008;F4NWC3;A0A086IZS8;A0A0B2UG97;I3EG14;I3EPG4;J9DIF9;H8ZCA1;Q29TJ5;Q9GQU7;B6RUI3;H2DEU1;Q29TJ3;Q29TK4;Q29TK6;Q29TP1;Q29TP8;Q29TP9;Q86ZW8;Q9UVR1;A0A075QHX3;Q9P8Z4;A0A075QHV1;Q7Z860;Q25570	>tr A0A075QMZ8 A0A075QMZ8_9FUNG Beta-tubulin (Fragment) OS=Tieghemiomyces parasiticus PE=3 SV=1;>tr A0A075QLA3 A0A075QLA3_9FUNG Beta-tubulin (Fragment) OS=Dispira cornuta PE=3 SV=1
Q29TG5;I4YDV2	>tr Q29TG5 Q29TG5_9FUNG Beta-tubulin (Fragment) OS=Dissophora decumbens GN=btub1 PE=3 SV=1;>tr I4YDV2 I4YDV2_WALMC Tubulin-domain-containing protein OS=Walleimia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WALSEDRAFT_32276 PE=3 SV=1
A0A0C3BGB0;G4TBG0;A0A060SQK0;M2QZN5;A0A0G2E2N3;A0A0B7N6N4;A0A0C7BH12;R1GGF0;J4H0J4;A0A0C9MSS4;K2RFZ9;S2JAJ4;A0A0C3DPJ8;A0A086T8V3;A0A063BWU2;A0A068RV79;A0A077WMM5;A0A086TLN6;A0A0E9NNL2;F4NWR7;A0A0J0XNP3;W6MJ03;A0A0B7MW57;A0A0C9MQ68;S2J0H4;A0A0A1P8X4;A0A0A1P5Y0;A0A0C7CDV9	>tr A0A0C3BGB0 A0A0C3BGB0_9HOMO Peroxidase OS=Serendipita vermifera MAFF 305830 GN=M408DRAFT_328086 PE=3 SV=1;>tr G4TBG0 G4TBG0_PIRID Probable cytochrome-c peroxidase OS=Piriformospora indica (strain DSM 11827) GN=PIIN_02499 PE=3 SV=1;>tr A0A060SQK0 A0A060
A0A086TLF5	>tr A0A086TLF5 A0A086TLF5_9FUNG Aminocarboxymuconate-semialdehyde decarboxylase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11308 PE=4 SV=1
A0A060SJK7	>tr A0A060SJK7 A0A060SJK7_PYCCI Uncharacterized protein OS=Pycnoporus cinnabarinus GN=BN946_scf184977.g93 PE=3 SV=1

L8X072;A0A0H2S3U7;A0A0K6FLT0;X8JKZ4;A0A0B7FTJ0;M5BTH9	>tr L8X072 L8X072_THACA Vacuolar protein sorting 26 OS=Thanatephorus cucumeris (strain AG1-IA) GN=AG1IA_03502 PE=4 SV=1;>tr A0A0H2S3U7 A0A0H2S3U7_9HOMO Vacuolar protein sorting-associated protein 26 OS=Schizopora paradoxa GN=SCHPADRAFT_93051 PE=4 SV=1;>tr
R1GB62;G4TS22;A0A0C2WYB8;A0A093XKA6;A0A093YGX5;A0A094DFG4;A0A094EM30;F4NZH7;A0A094DSM5;A0A094EZ01;A0A094F052;A0A094HL09;A0A093ZYZ9;A0A094BZR9;A0A094DBU8;A0A094EMH2;A0A094IWW6;L8GB02;A0A0J0XMJ8;A0A0D1YJ17;A0A0E9KWF0;A0A068RGC6;A0A077WM54;K2QKY0	>tr R1GB62 R1GB62_BOTPV Putative phosphatidylserine synthase protein OS=Botryosphaeria parva (strain UCR-NP2) GN=UCRNP2_10206 PE=3 SV=1;>tr G4TS22 G4TS22_PIRID Probable nucleolar rRNA processing protein GAR1 OS=Piriformospora indica (strain DSM 11827) GN=P
A0A094EDS6;A0A094GCB3	>tr A0A094EDS6 A0A094EDS6_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-103 GN=V499_09705 PE=4 SV=1;>tr A0A094GCB3 A0A094GCB3_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-4519 (FW-2642) GN=V501_10575 PE=4 SV=1
A0A086TLM4;F4NV90	>tr A0A086TLM4 A0A086TLM4_9FUNG S-adenosylmethionine synthase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11376 PE=3 SV=1
J0D8Q2	>tr J0D8Q2 J0D8Q2_AURDE Actin 2 OS=Auricularia delicata (strain TFB10046) GN=AURDEDRAFT_154722 PE=3 SV=1
S7RXU6	>tr S7RXU6 S7RXU6_GLOTA Actin 1 OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=GLOTRDRAFT_126057 PE=3 SV=1

<p>A0A0C3NYK6;J4HXD7;K5V887;M2QI81;R7SI12;Q7Z8L2;J5QLA2;K1WQC8;A0A074RNY8;A0A067MF76;A0A0B7FZF8;A0A0C2XDR5;A0A0C3QDP8;A0A0D7BIZ2;A0A0H2RDL0;A0A0K6FSW9;CON__P60712;G4TR71;I4Y631;R7S1T0;R9AE65;X8J2N8;R7S4Z8;S8F895;V5W5W4;L8WKN1;J0LFD0;W4KFQ1;W4KH88;A0A068S4N7;A0A077WS74;A0A077WY33;A0A0A1P664;A0A0B7NR31;A0A0B7NVG6;A0A0C9MA04;A0A0C9MS75;I1CLG1;Q58YD9;S2JRE7;S2K7Q5;S7QKI4;A0A060S811;A0A066V1S8;A0A0A1MZD0;A0A068B367;P26197;A0A068SBD2;A0A074SBD1;A0A0K6G3B5;A0A0H2S796;W6MIT6;F4NW02;P10982;Q9URI4;M5BWT3;L8WKN6;M2PKY1;A0A063BXW9;A0A086ST21;A0A093X056;A0A093XI43;A0A094ALD3;A0A094BAW5;A0A094C981;A0A094CVB5;A0A094DNC6;A0A094EAX5;A0A094EFW1;A0A094ER52;A0A094FBI8;A0A094FE35;A0A094H1F2;A0A094KER6;A0A0C3GFF1;A0A0D1XA17;A0A0G2DYL4;A0A0G2HAT5;K2SFB1;L8FP22;Q9UVW9;R1G944;A0A098VUP0;A0A0B7G167;A0A0A1NTT7;Q7Z9B9;Q7Z9F1;Q3Y5A1;H6VN94;H6VN95;H6VN96;H6VN97;A0A0C2WZP0;A0A066VNX0;M5BZP9;Q2TTD5;Q2TTD8;A0A088NEK1;A0A088NUK7;Q9C1V0;G9M802;Q9C2S6;Q9C2T3;Q9C2T9;Q9C2V0;A0A0H3VBB5;A0A0H3VBS0;A0A0H3VBB2;D9I7R8;Q96WK2;J9A0F1;A0A0B2UN42;I3EGD1;I3EP48;G0LY11;G0LY10;Q2TTD7;Q534I7;A0A088NEH6;A0A088NEI1;A0A088NEI9;A0A088NEJ5;A0A088NEK6;A0A088NEL5;A0A088NF34;A0A088NF38;A0A088NF46;A0A088NF52;A0A088NF58;A0A088NF65;A0A088NF72;A0A088NFG6;A0A088NFH2;A0A088NFH5;A0A088NFI1;A0A088NFI5;A0A088NFJ0;A0A088NFJ6;A0A088NIA1;A0A088NIA7;A0A088NIB4;A0A088NIC0;A0A088NIC4;A0A088NID0;A0A088NUH4;A0A088NUI1;A0A088NUI5;A0A088NUJ0;A0A088NUJ4;A0A088NUJ9;A8BDK2;A8BDM1;A8BDM5;C4MMG2;C4MMG3;C4MMG4;C4MMG6;C4MMG8;C4MMG9;C4MMH1;C4MMH2;C4MMH3;C4MMH4;C4MMH9;C4MMI0;C4MMI1;C4MMI2;C4MMI3;C6F060;C6F061;C6F062;C6F063;C6F064;C6F066;C6F074;C6F075;C6F076;C6F077;C6F078;C6F079;C6F080;Q29TR4;Q29TR5;Q29TR6;Q29TR8;Q29TR9;Q29TS0;Q5I W28;Q5IW29;Q9C153;Q9C1U2;Q9C1U3;Q9C1U9;Q9C1V1;Q9C1V2;Q9C1V3;Q9C1V5;Q9C1V8;Q9C1V9;Q9C1W0;Q9C1X8;Q9C1X9;Q9C1Y0;Q9C1Y1;Q9C1Y2;Q9C1Y4;Q9C1Y5;Q9C1Y6;Q9C1Y7;Q9C1Y8;Q9C1Z0;Q9C200;Q9C201;Q9C202;Q9C203;Q9C204;Q9C205;Q9C207;Q9C2S7;Q9C2S8;Q9C2S9;Q9C2T1;Q9C2T4;Q9C2T5;Q</p>	<p>>tr A0A0C3NYK6 A0A0C3NYK6_PHLGI Uncharacterized protein OS=Phlebiopsis gigantea 11061_1 CR5-6 GN=PHLGIDRAFT_28381 PE=3 SV=1;>tr J4HXD7 J4HXD7_9APHY Uncharacterized protein OS=Fibroporia radiculosa GN=FIBRA_05357 PE=3 SV=1;>tr K5V887 K5V887_PHACS Uncharacte</p>
<p>A0A0J0XVY0</p>	<p>>tr A0A0J0XVY0 A0A0J0XVY0_9TREE Nucleic acid-binding protein OS=Trichosporon oleaginosus GN=CC85DRAFT_299687 PE=4 SV=1</p>

D3JU53;S8EB76;J4GCD1;A0A0C3Q107;A0A067MCK2;A0A074RLS7;A0A0H2RVC8;A0A0K6FR13;L8X2K1;X8JDQ6;A0A0C3B6Z4;I4YC34;M5CES0;A0A0B7MYH7;K5V2F7;A0A0C3S8M2;M2RE32;A0A060STP2;I1CFW2;R7T1M8;S7QF54;W4JUT6;A0A0A1N236;A0A0A1NHV6;A0A0B7N1F2;A0A0C7B3W0;A0A0C9MWM3;I1B XK9;I1CRW7;S2K3F1;A0A068RJM4;A0A077WV66;A0A0D7BC45;A0A068RT68;A0A068RU15;A0A077X4K8;A0A0C9MNS1;G4T7X7;S2K666;R9ANQ1;A0A066W0W4	>tr D3JU53 D3JU53_MORAP GDP-D-mannose 4,6-dehydratase OS=Mortierella alpina GN=gmd PE=3 SV=1
I1CEG8;S2JKB4;A0A0C9MTT0	>tr I1CEG8 I1CEG8_RHIO9 Uncharacterized protein OS=Rhizopus deleamar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_11559 PE=3 SV=1;>tr S2JKB4 S2JKB4_MUCC1 Alanine-glyoxylate transaminase/(R)-3-amino-2-methylpropionate-pyruvate transami
A0A0A1NLJ6;A0A0C7BQI6;I1BUM9;A0A0B7N7B3;A0A0C9M3V8;S2J8C0;I1C1V7;A0A068SEQ9;A0A077WH39;A0A0C7C8U8	>tr A0A0A1NLJ6 A0A0A1NLJ6_9FUNG Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Rhizopus microsporus GN=RMCBS344292_07653 PE=3 SV=1;>tr A0A0C7BQI6 A0A0C7BQI6_9FUNG Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Rhizopus microsporus GN=RM
A0A074SAM9;X8JEQ4;G4TS25;A0A067M1W7;M5CHK5;L8WXY3;A0A0H2R1G0;A0A0D7B6P0;A0A068LCP2;M2P828;A0A060S8F1;B8P757;J4H3I5;S8EEW2;U3PIQ5;W4KC56;A0A0C3S6K1;K5WH41;A0A0K6FTV7;R9A9V0;A0A0C3BM84;A0A0J0XBQ8;S7PZ45;J5SF75;K1VU69;W6MQX9;A0A094GVF3;A0A094BRV3;A0A094DJ06;A0A068S5P0;A0A068S9J5;A0A077WPN0;A0A093X246;A0A093ZIK0;A0A094A443;A0A094A8K0;A0A094CBC5;A0A094CMV4;A0A094EUF9;A0A094HEA6;A0A094HF52;A0A094HJ60;A0A0C3GU35;L8FS91;A0A0G2EG07;K2RWY3;R1GSZ2;I4Y5L9;A0A0D1XG11;A0A086TDZ9;A0A0E9NAD8;A0A063C0T1;A0A094A7H8	>tr A0A074SAM9 A0A074SAM9_9HOMO 60S ribosomal protein L4 OS=Rhizoctonia solani 123E GN=V565_168620 PE=4 SV=1;>tr X8JEQ4 X8JEQ4_9HOMO 60S ribosomal protein L4 OS=Rhizoctonia solani AG-3 Rhs1AP GN=RSOL_395090 PE=4 SV=1;>tr G4TS25 G4TS25_PIRID Probable RPL4A-
A0A086TKK0;F4NXT9	>tr A0A086TKK0 A0A086TKK0_9FUNG Phospho-2-dehydro-3-deoxyheptonate aldolase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11686 PE=3 SV=1
A0A0C3S3Q6;A0A094KM18;A0A094I398;A0A0D2A6L3;A0A0E9L4C5;A0A0G2EKZ7;A0A093XAI6;A0A093XIM7;A0A094BIM8;A0A094CZX3;K2RHZ1;A0A063BR99;K5WL45;M2R8K5;S8EF11;A0A060SN00;W4KDZ3;A0A0K6FTG8;S7S120;A0A067MMB1;G4TRK8;I4YCB6;R9AU94;R7T243;A0A077WVX1;A0A068SCT6;F4P5V7	>tr A0A0C3S3Q6 A0A0C3S3Q6_PHLGI Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Phlebiopsis gigantea 11061_1 CR5-6 GN=PHLGIDRAFT_109404 PE=3 SV=1;>tr A0A094KM18 A0A094KM18_9PEZI Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Pseudogymnoa
K2RTB1	>tr K2RTB1 K2RTB1_MACPH Fumarate reductase/succinate dehydrogenase flavoprotein OS=Macrophomina phaseolina (strain MS6) GN=MPH_04791 PE=4 SV=1

C4MMK2;C4NZR7;Q9HGB7;F1CWF4;F1CWF5;F1CWF6;Q9HGC5;Q9HG98;Q9HG78;Q9HG96;Q9HGA5;C4MMJ5;C4MMJ8;C4MML0;F2X4U3;A0A0A0P5C6;A0A0K2CUS4;A0A0K2CV13;Q0PPX1;A0A075X2G1;F1CWF3;A0A0A0P5G1;A0A0A0P6L5;A0A0A0P6U0;A0A0A0P9B9;A0A0A0P9G9;A0A0A0P9J2;Q4TWI9;Q4PS59;A0A0A0P4K9;A0A0A0P6R9;A0A0A0P9E1;A0A0F6Q4S1;A0A0A0P6M5;A0A0A0P4Q5;A0A0A0P3G2;A0A0A0P4N3;A0A0A0P6Q0;F5BD10;A0A075X3N5;F5BD08;A0A075X2T1;A0A075X3P4;A0A075X8V2;A0A077CZF0;A0A075X212;A0A075X2T6;A0A075X2F5;A0A075X2S6;A0A075X2G7;D3YFP2;F5BD09;A0A0A0P5E8;X4Y5H1;X4YKE6;X4XW45;X4Y2N8;X4Y5G0;X4YIR0;X4YKD7;X4YKE1	>tr C4MMK2 C4MMK2_MORAP Elongation factor 1-alpha (Fragment) OS=Mortierella alpina PE=3 SV=1;>tr C4NZR7 C4NZR7_9LECA Elongation factor 1-alpha (Fragment) OS=Lopezaria versicolor GN=tef-1 PE=4 SV=1
Q70BT2;A0A077W7X2;A0A068RQ97;A0A0A1P474	>tr Q70BT2 Q70BT2_MORAP Acetyl-CoA carboxylase (Fragment) OS=Mortierella alpina GN=acc1 PE=4 SV=1;>tr A0A077W7X2 A0A077W7X2_9FUNG Putative Acetyl-CoA carboxylase OS=Lichtheimia ramosa GN=LRAMOSA00558 PE=4 SV=1;>tr A0A068RQ97 A0A068RQ97_9FUNG Acetyl-carboxy
A0A086TLD8;L8X9W4;A0A0D1YPY0;A0A094ESV2;A0A094GUA9;A0A093XLQ6;A0A093Z757;A0A094BLN9;A0A068SCN5;A0A0B7G5E4;A0A094DXD1;A0A0C3D3R2;A0A0E9NCN1;A0A094FMH0;A0A094HXC1;A0A094ESY6;A0A0C3QFN0;A0A063C1U9;J5QY74;K1VKI2;A0A074S7J5;A0A0C3AMS3;X8JRP4;A0A0B7N7B9;S2JSM8;W4KEX6;A0A0K6FS49;F4PFF6;A0A0C9MQI7;A0A0D7BT95;K5V987;A0A067MXL9;M2PV22;A0A0C3P3Z9;A0A094ALC1;A0A093Y4L8;A0A094BCW6;A0A094FFJ5;M5C3F4;A0A0A1NV53	>tr A0A086TLD8 A0A086TLD8_9FUNG Aspartyl aminopeptidase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11291 PE=3 SV=1
A0A086TKU9	>tr A0A086TKU9 A0A086TKU9_9FUNG Mannose-1-phosphate guanylttransferase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11969 PE=4 SV=1
A0A0A1N6A2;A0A0C7AXH0;A0A0A1NAC2;A0A0A1NM87;I1C4J1;I1C5U1;I1CFJ8;A0A0C7CIR3	>tr A0A0A1N6A2 A0A0A1N6A2_9FUNG Putative Fructose 1,6-bisphosphate aldolase OS=Rhizopus microsporus GN=RMCBS344292_09139 PE=4 SV=1;>tr A0A0C7AXH0 A0A0C7AXH0_9FUNG Putative Fructose-bisphosphate aldolase OS=Rhizopus microsporus GN=RMATCC62417_00617 PE=4 SV=
A0A086TKW0	>tr A0A086TKW0 A0A086TKW0_9FUNG Protein phosphatase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11980 PE=3 SV=1
R9A9I6;J6F6N8;K1VIX6;A0A0C3SC94;A0A0C3M0D7;K3V6K6;S7QJD5;A0A060SA90;M2R8L8;S8EFH1;W4KDS6;A0A0H2SLR1;R7SY S1;A0A0D7BV41;I4YET3;A0A0C9MSF6;S2JK51;A0A0J0XSX9;J4HXA5	>tr R9A9I6 R9A9I6_WALI9 Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Walleimia ichthyophaga (strain EXF-994 / CBS 113033) GN=J056_002743 PE=3 SV=1;>tr J6F6N8 J6F6N8_TRIAS Isocitrate dehydrogenase [NAD] subunit, mitochondrial OS=Trichosporon asah
A0A086TM25;A0A0B7NDD0	>tr A0A086TM25 A0A086TM25_9FUNG Fructose-bisphosphate aldolase 1 OS=Mortierella verticillata NRRL 6337 GN=MVEG_11040 PE=4 SV=1
A0A086TLQ2;A0A0C3QEY9;A0A0A1NAW3;A0A0A1NTV6;A0A0C7AZ26;A0A0B7MV65;A0A0C9M4K5;I1BXT6;S2JFJ0;A0A0B7FVZ6;A0A0K6G7L8;A0A068RGA4;A0A077W9C8;A0A0C2WKU7;G4TAJ3;A0A0C7AYQ0;A0A0C7AYR4;A0A0C7AXW1;M5BSC4	>tr A0A086TLQ2 A0A086TLQ2_9FUNG Cysteine synthase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11403 PE=4 SV=1
A0A074RP07;X8IZX3	>tr A0A074RP07 A0A074RP07_9HOMO Short chain dehydrogenase OS=Rhizoctonia solani 123E GN=V565_115880 PE=3 SV=1;>tr X8IZX3 X8IZX3_9HOMO Short chain dehydrogenase OS=Rhizoctonia solani AG-3 Rhs1AP GN=RSOL_073710 PE=3 SV=1

A0A086TMI9	>tr A0A086TMI9 A0A086TMI9_9FUNG Aspartate-semialdehyde dehydrogenase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11201 PE=3 SV=1
A0A0D7AW94;A0A0C2X4D2;A0A0C3PLH9;A0A0H2RAX8;G4TTA5;J7SBX8;K5W2D0;M2QU39;R7SVH1;S8F0D7;A0A067MP70;S7RHQ0;W4JWC6;A0A0C3KS36;A0A060SQS2;R7SHC6;J8TYH9;A0A0J0XFL9;K1VNG2;L8WU75;A0A094FVM4;A0A094GNI4;A0A094EP08;A0A0E9NEV2;A0A094AP86;A0A063BSM0;A0A074S1Q9;F4NRU3;X8JSA5;A0A0K6GDQ4;M5BJQ1;A0A068RIU3;A0A077WAI8;I4YD62;R9AF41;A0A0C3CZH2;A0A0G2GDM0;A0A0G2DYH7;K2S794;R1FVF1;A0A0C9MMR5;A0A086THK3;A0A093XMI4;A0A094ABY9;A0A094AK14;A0A094ARJ8;A0A094B6C0;A0A094BLF6;A0A094CGN7;A0A094CX38;A0A094GDI2;A0A0D2AU49;A0A094BBP7;A0A094F9C3;A0A0E9KUH6;S2J8W3;A0A0B7NG21;A0A0C7BY81;A0A0C9MC87;A0A0A1MTT4;A0A0A1NK50;L8FYA0;S2JSN6;I1C6Z6;A0A0C7BWF4;I1CMU2;I1CI41;A0A0B2UI02;A0A086J4S4;H8ZDK4;I3EHD9;I3ESM9;A0A066W850;A0A098VS22	>tr A0A0D7AW94 A0A0D7AW94_9HOMO Serine/threonine-protein phosphatase OS=Cylindrobasidium torrendii FP15055 ss-10 GN=CYLTODRAFT_383871 PE=3 SV=1;>tr A0A0C2X4D2 A0A0C2X4D2_9HOMO Serine/threonine-protein phosphatase OS=Serendipita vermifera MAFF 305830 GN=M40
A0A086TLW7	>tr A0A086TLW7 A0A086TLW7_9FUNG Uncharacterized protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_10982 PE=4 SV=1
A0A063C5C0;A0A0E9KWE6	>tr A0A063C5C0 A0A063C5C0_9HYPO Thiosulfate sulfurtransferase OS=Ustilaginoidea virens GN=UV8b_3359 PE=4 SV=1;>tr A0A0E9KWE6 A0A0E9KWE6_9HYPO Uncharacterized protein OS=Ustilaginoidea virens GN=UVI_045660 PE=4 SV=1
A0A094ENV4	>tr A0A094ENV4 A0A094ENV4_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-4514 (FW-929) GN=V495_01025 PE=4 SV=1
A0A0C7B6T1;A0A0C7C1S4;A0A0C9MD92;I1C941;A0A0C7BIJ9;S2IUH5;A0A0B7MR96;A0A068S5T1;A0A0A1NHE6;A0A0A1MN65;A0A077WC12;A0A0C7CNU0;A0A0A1NHM0	>tr A0A0C7B6T1 A0A0C7B6T1_9FUNG Putative GTP binding protein OS=Rhizopus microsporus GN=RMATCC62417_03289 PE=3 SV=1;>tr A0A0C7C1S4 A0A0C7C1S4_9FUNG Putative GTP binding protein OS=Rhizopus microsporus GN=RMATCC62417_12088 PE=3 SV=1;>tr A0A0C9MD92 A0A0C9MD92_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3557 GN=V490_07313 PE=3 SV=1;>tr A0A094AH38 A0A094AH38_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3808 GN=O988_04925 PE=3 SV=1;>tr A0A094DP70 A0A094DP70_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3808 GN=O988_04925 PE=3 SV=1
A0A0L0DS52	>tr A0A0L0DS52 A0A0L0DS52_THETB Uncharacterized protein OS=Thecamonas trahens ATCC 50062 GN=AMSG_10077 PE=4 SV=1
X8JH53;A0A074RXU6;X8JEM8;A0A0K6G8T9;L8X336	>tr X8JH53 X8JH53_9HOMO Small GTPase family Ras-related nuclear family (Ran)/TC4 protein (fragment) OS=Rhizoctonia solani AG-3 Rhs1AP GN=RSOL_415500 PE=4 SV=1;>tr A0A074RXU6 A0A074RXU6_9HOMO GTP-binding nuclear protein GSP1/Ran protein OS=Rhizoctonia solani AG-3 Rhs1AP GN=RSOL_415500 PE=4 SV=1
A0A093XEK5;A0A094AH38;A0A094DP70;A0A094F6H5;A0A094CS S7;A0A094GZL7;L8FUV3;A0A093Z0Q4;A0A063BWC6;A0A0E9KK R4;K2RHF1;A0A0D2A2J8;A0A0G2E143;A0A0G2GS86;R1GV22;A0A093ZE07;A0A094ELX9;A0A094FY99;A0A094H2W4;A0A094KMP1;A0A0C3H9C6;I4Y734;A0A094ASH8;A0A094BZI5;A0A086TF39;R9ADY9;W6MWH3	>tr A0A093XEK5 A0A093XEK5_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3557 GN=V490_07313 PE=3 SV=1;>tr A0A094AH38 A0A094AH38_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3808 GN=O988_04925 PE=3 SV=1;>tr A0A094DP70 A0A094DP70_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3808 GN=O988_04925 PE=3 SV=1
P00636	>tr P00636 P00636 · F16P1_PIG Uncharacterized protein OS=Sus scrofa (Pig) GN=FBP1 PE=3 SV=1
Q9P4D7;A9ZLZ4;A0A0B4ZNK5;A0A0B4ZPU9;A0A0B4ZSH1;A0A0B4ZSY9;A0A0B4ZUK5;A0A0B4ZUL1;D5KSD4;A0A0B4ZSW3;A0A0B4ZSW8;A0A0B4ZUI5	>tr Q9P4D7 Q9P4D7_MORAP Elongation of fatty acids protein OS=Mortierella alpina GN=GLELO PE=2 SV=1;>tr A9ZLZ4 A9ZLZ4_MORAP Elongation of fatty acids protein OS=Mortierella alpina GN=GLELO PE=2 SV=1;>tr A0A0B4ZNK5 A0A0B4ZNK5_MORAP Elongation of fatty acids

B8PMN3;S7RBX6;J4GVG4;A0A060SD24;K5X2T6;S8EFH9;D2KCD4;J5R7P8;K1VBX2;F4PAA6;A0A068RV94;A0A077WCZ0;A0A068SHT7;A0A077WK68;A0A0B7N8P3;A0A0C7BQE4;S2JML5;A0A0A1MZY9;A0A0C9MPH3;I1BQ85;A0A0J0XFK6;W6MIK0;M2RDL0;A0A0C2WF11;A0A0C3PTF4;A0A0C3QJE4;A0A0D7BTH5;G4TD19;R7SLL0;W4JV34;A0A0C3Q7Y2;A0A0C3Q5G3	>tr B8PMN3 B8PMN3_POSPM Predicted protein OS=Postia placenta (strain ATCC 44394 / Madison 698-R) GN=POSPLDRAFT_90853 PE=4 SV=1;>tr S7RBX6 S7RBX6_GLOTA Vacuolar protein sorting-associated protein 26 OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Ma
R1EU67	>tr R1EU67 R1EU67_BOTPV Putative methylenetetrahydrofolate dehydrogenase protein OS=Botryosphaeria parva (strain UCR-NP2) GN=UCRNP2_2081 PE=4 SV=1
A0A0B7NK18;A0A0A1MYB4;A0A0A1NAJ2;A0A0C7BJF7;A0A077WV08	>tr A0A0B7NK18 A0A0B7NK18_9FUNG Serine/threonine-protein phosphatase OS=Parasitella parasitica GN=PARPA_09942.1 scaffold 39144 PE=3 SV=1;>tr A0A0A1MYB4 A0A0A1MYB4_9FUNG Serine/threonine-protein phosphatase OS=Rhizopus microsporus GN=RMCBS344292_06326 PE=3
S7QPT8	>tr S7QPT8 S7QPT8_GLOTA Uncharacterized protein OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=GLOTRDRAFT_31928 PE=4 SV=1
A0A086TKR0	>tr A0A086TKR0 A0A086TKR0_9FUNG Hydroxymethylglutaryl-CoA lyase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11930 PE=4 SV=1
D3JU54;A0A0A1N031;A0A0C9MS07;S2JTA4;A0A068S1Y7;A0A077WGJ2;A0A0C7BA25;A0A0A1NF90	>tr D3JU54 D3JU54_MORAP GDP-keto-6-deoxymannnose 3,5-epimerase/4-reductase OS=Mortierella alpina GN=gmer PE=3 SV=1
B6ZK38;Q9P8G1	>tr B6ZK38 B6ZK38_MORAP Elongation of fatty acids protein OS=Mortierella alpina GN=MAELO PE=3 SV=1;>tr Q9P8G1 Q9P8G1_MORAP Elongation of fatty acids protein OS=Mortierella alpina GN=MAELO PE=2 SV=1
A0A086TJU2	>tr A0A086TJU2 A0A086TJU2_9FUNG 3-hydroxyacyl-CoA dehydrogenase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11857 PE=4 SV=1
A0A0C9M7Y1;Q96UF1;A0A0A1NB49;I1BY51	>tr A0A0C9M7Y1 A0A0C9M7Y1_9FUNG Glyceraldehyde-3-phosphate dehydrogenase OS=Mucor ambiguus GN=MAM1_0119d05807 PE=3 SV=1;>sp Q96UF1 G3P3_MUCCL Glyceraldehyde-3-phosphate dehydrogenase 3 OS=Mucor circinelloides f. lusitanicus GN=GPD3 PE=3 SV=1;>tr A0A0A1NB49
A0A0B7MPY7;A0A0H2RWV6;A0A0C3BPM9;A0A0B7NBR7;A0A0B7MWU6	>tr A0A0B7MPY7 A0A0B7MPY7_9FUNG 40S ribosomal protein S1 OS=Parasitella parasitica GN=PARPA_01285.1 scaffold 1359 PE=3 SV=1;>tr A0A0H2RWV6 A0A0H2RWV6_9HOMO 40S ribosomal protein S1 OS=Schizopora paradoxa GN=RPS1 PE=3 SV=1;>tr A0A0C3BPM9 A0A0C3BPM9_9HOMO 40
I1CPV6;B3FPE3	>tr I1CPV6 I1CPV6_RHIO9 Glyceraldehyde-3-phosphate dehydrogenase OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_15197 PE=3 SV=1;>tr B3FPE3 B3FPE3_9ASCO Glyceraldehyde-3-phosphate dehydrogenase OS=Starmerella bombico
J5SRB9	>tr J5SRB9 J5SRB9_TRIAS Inorganic diphosphatase OS=Trichosporon asahii var. asahii (strain ATCC 90039 / CBS 2479 / JCM 2466 / KCTC 7840 / NCYC 2677 / UAMH 7654) GN=A1Q1_04180 PE=4 SV=1
A0A0B7F9N7	>tr A0A0B7F9N7 A0A0B7F9N7_THACB Inorganic pyrophosphatase OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=RSOLAG1IB_06903 PE=4 SV=1
A0A0D2A969;A0A0G2GI95;K2RXS1;R1G1C7;A0A0G2DXP4	>tr A0A0D2A969 A0A0D2A969_9PEZI Cytochrome c1, heme protein, mitochondrial OS=Verruconis gallopava GN=PV09_05524 PE=4 SV=1;>tr A0A0G2GI95 A0A0G2GI95_9PEZI Putative cytochrome mitochondrial OS=Diplodia seriata GN=UCDDS831_g06764 PE=4 SV=1;>tr K2RXS1 K2RXS1_
A0A068SEV9;A0A077W827;A0A068RY06;A0A077X2G7;A0A068RXA3	>tr A0A068SEV9 A0A068SEV9_9FUNG Vacuolar protein sorting-associated protein 74 OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_11154.1 PE=4 SV=1;>tr A0A077W827 A0A077W827_9FUNG Uncharacterized protein OS=Lichtheimia ramosa GN=LRAMOS00352 PE=4 SV=1;>tr A0

A0A086TLS1	>tr A0A086TLS1 A0A086TLS1_9FUNG Uncharacterized protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_11422 PE=4 SV=1
A0A0B7MW60;A0A0C9MJU2;Q96UF2;S2JFE0;C9E064;A0A0A1N9W8;A0A0A1NTB1;A0A0B7NFP2;C9E066;I1C4E8;S2K7L3;A0A0A1MRG5;A0A0A1NWD9;A0A0C7C3Y3;Q8X1J6	>tr A0A0B7MW60 A0A0B7MW60_9FUNG Glyceraldehyde-3-phosphate dehydrogenase OS=Parasitella parasitica GN=PARPA_00796.1 scaffold 1159 PE=3 SV=1;>tr A0A0C9MJU2 A0A0C9MJU2_9FUNG Glyceraldehyde-3-phosphate dehydrogenase OS=Mucor ambiguus GN=MAM1_0171c07186 PE=3 S
A0A0E9NJ51;F4NY08;A0A074S4K6;X8JJI7;K2RYI7;J4UJ74;A0A063BWB0;K1W193;G4TL88;A0A0J0XGH5;A0A066VV75;A0A067M8U3;A0A0C3QPR9;J4H3N6;A0A086T2K8;A0A0E9KS22;J6F8T0;K1W1L0;S7RPY1;A0A0B7FXE7;S8G4B0;A0A0C3PH48;A0A0H2SG13;M2RL35;A0A093Y4G8;A0A093Y7Q6;A0A093ZEA3;A0A093ZXZ1;A0A094AFT8;A0A094AZL0;A0A094BLZ0;A0A094CNP2;A0A094DX78;A0A094EVM8;A0A094FYF6;A0A094GCE3;A0A094GKE0;A0A094IKU1;A0A0K6FS12;L8FX74;W4K777;A0A0G2EN45;A0A0G2HAE6;R1GJ15;A0A0C3AZM4;A0A068RMP1;A0A077WXX5;A0A0C7BIY1;A0A0C7BVT6;A0A0C3HNV6;A0A0D7BNU9;A0A0A1NAM6;M5BPR8;B8PNN2;A0A0A1NFN1;A0A0A1P5S5;A0A0C7BWM8	>tr A0A0E9NJ51 A0A0E9NJ51_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_4024-t1 PE=4 SV=1;>tr F4NY08 F4NY08_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_19096
A0A0C3S3G7;B8PF53;M2PY69;S8FTS9;W4KPI1;J7S5L3;I4YHM9;R9ANR7	>tr A0A0C3S3G7 A0A0C3S3G7_PHLGI Uncharacterized protein OS=Phlebiopsis gigantea 11061_1 CR5-6 GN=PHLGIDRAFT_18396 PE=4 SV=1;>tr B8PF53 B8PF53_POSPM Predicted protein OS=Postia placenta (strain ATCC 44394 / Madison 698-R) GN=POSPLDRAFT_97600 PE=4 SV=1;>tr M
A0A068RIX3;A0A077WCR1	>tr A0A068RIX3 A0A068RIX3_9FUNG Thioredoxin reductase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_01665.1 PE=3 SV=1;>tr A0A077WCR1 A0A077WCR1_9FUNG Thioredoxin reductase OS=Lichtheimia ramosa GN=LRAMOS07398 PE=3 SV=1
F4NYT7	>tr F4NYT7 F4NYT7_BATDJ Transaldolase OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_18972 PE=3 SV=1
A0A086TKM7	>tr A0A086TKM7 A0A086TKM7_9FUNG Uncharacterized protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_11897 PE=4 SV=1
A0A068RI90;A0A068RJI4;A0A077W8Y5;A0A077WD94;A0A074RZ01;X8IYZ7;S2K009;A0A0C3AHS6;G4TTS2;A0A068RQX0;A0A0A1NTM9;A0A0B7MQ97;A0A0B7NEM0;A0A0C3QN59;A0A0C7BH45;I1BKC1;A0A068RQ34;F4P3L0;A0A066VIS6;I1BRA2;S2JQU1;A0A0A1P1N5;A0A0C7BG95;I1CSK9;A0A0C7BZY7;A0A077WCI0	>tr A0A068RI90 A0A068RI90_9FUNG Guanine nucleotide binding protein beta subunit OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_01103.1 PE=4 SV=1;>tr A0A068RJI4 A0A068RJI4_9FUNG Guanine nucleotide binding protein beta subunit OS=Lichtheimia corymbifera JM
A0A067MUL5;A0A0E9NHR0	>tr A0A067MUL5 A0A067MUL5_9HOMO Uncharacterized protein OS=Botryobasidium botryosum FD-172 SS1 GN=BOTBODRAFT_143406 PE=4 SV=1;>tr A0A0E9NHR0 A0A0E9NHR0_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_3515-t1 PE=4 SV=1
I4YB96;R9APE8;A0A0H2SEG0	>tr I4YB96 I4YB96_WALMC WD40 repeat-like protein OS=Walleimia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WALSEDRAFT_64506 PE=4 SV=1;>tr R9APE8 R9APE8_WALI9 Guanine nucleotide-binding protein subunit beta-like protein OS=Walleimia ichthyophaga (strain E
A0A086TL95;F4P4E3;A0A0A1P983;A0A0C9M6L3;S2J665;A0A0C7B738;A0A0C7B7I7;I1BTA4	>tr A0A086TL95 A0A086TL95_9FUNG Serine/threonine-protein phosphatase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11249 PE=3 SV=1;>tr F4P4E3 F4P4E3_BATDJ Serine/threonine-protein phosphatase OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN

A0A086VL88;Q5EM39	>tr A0A086VL88 A0A086VL88_9FUNG Cytochrome c oxidase subunit 2 OS=Mortierella verticillata NRRL 6337 GN=MVEG_20025 PE=3 SV=1;>tr Q5EM39 Q5EM39_9FUNG Cytochrome c oxidase subunit 2 OS=Mortierella verticillata GN=cox2 PE=3 SV=1
W4K492;A0A0C3NJI8;K5VSP8;M2QLF8;L8X489;A0A067N4G8;A0A0J0XF28;J6EY09;K1VBY6;M5C5Y1;C7EWL6;S7RW04;S8FV45;J4H293;A0A060S8L3;A0A0D7B5K6	>tr W4K492 W4K492_9HOMO Uncharacterized protein OS=Heterobasidion irregulare TC 32-1 GN=HETIRDRAFT_418643 PE=4 SV=1;>tr A0A0C3NJI8 A0A0C3NJI8_PHLGI Uncharacterized protein OS=Phlebiopsis gigantea 11061_1 CR5-6 GN=PHLGIDRAFT_74762 PE=4 SV=1;>tr K5VSP8 K5VSP
A0A086TL69	>tr A0A086TL69 A0A086TL69_9FUNG Malate dehydrogenase OS=Mortierella verticillata NRRL 6337 GN=MVEG_12088 PE=3 SV=1
A0A0C7B157;A0A0C7B0L8;A0A0A1NQL8	>tr A0A0C7B157 A0A0C7B157_9FUNG Uncharacterized protein OS=Rhizopus microsporus GN=RMATCC62417_01466 PE=4 SV=1;>tr A0A0C7B0L8 A0A0C7B0L8_9FUNG Uncharacterized protein OS=Rhizopus microsporus GN=RMATCC62417_01466 PE=4 SV=1;>tr A0A0A1NQL8 A0A0A1NQL8_9FUNG Un
A0A086TMJ7	>tr A0A086TMJ7 A0A086TMJ7_9FUNG Delta-aminolevulinic acid dehydratase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11209 PE=3 SV=1
A0A068RRR8;A0A077WC98	>tr A0A068RRR8 A0A068RRR8_9FUNG Arginase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_03815.1 PE=3 SV=1;>tr A0A077WC98 A0A077WC98_9FUNG Arginase OS=Lichtheimia ramosa GN=LRAMOSA07875 PE=3 SV=1
A0A0C7B430;S2J740;A0A0C7B2V7;A0A0A1NC88;A0A0A1NSM9;A0A0A1NYJ8;A0A0B7N149;I1CRK6;S2JMM3;A0A0C9MK93;A0A0C9MXT0;A0A0C9MVI6;A0A0B7MYH6;A0A0B7NJ77;A0A068SCA5;A0A068SD45;A0A077WDH9;A0A077WPU8;A0A0A1NPE9;A0A0C7AZA0;I1BLS7;I1CJX0;I1CD32;A0A0C7CBE9	>tr A0A0C7B430 A0A0C7B430_9FUNG Putative 40S ribosomal protein S6 OS=Rhizopus microsporus GN=RMATCC62417_02375 PE=4 SV=1;>tr S2J740 S2J740_MUCC1 40S ribosomal protein S6 OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_07732 PE=3 SV
A0A093XPI8;A0A093YJP3;A0A093ZJH8;A0A093ZKI3;A0A094ARU5;A0A094B830;A0A094D1F4;A0A094E3E4;A0A094GGP2;A0A0C3D3C9;L8FPH1;A0A094AI57;A0A094C1V6;A0A094FF25;A0A094HLU8;A0A063CAM0;A0A0D1YZR9;A0A0G2F1Q4;K2R3V9;R1GM64;A0A0G2DY89;A0A0E9KSE0;A0A094EG46	>tr A0A093XPI8 A0A093XPI8_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3808 GN=O988_08946 PE=3 SV=1;>tr A0A093YJP3 A0A093YJP3_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3775 GN=V491_09203 PE=3 SV=1;>tr A0A093ZJH8 A
A0A086TJW9;A0A0A1MZW0;A0A077WDR3;A0A0A1NSE8;A0A0B7NW06;A0A0C7C9T6;I1BR14;S2JAV7;A0A0C7CAA1	>tr A0A086TJW9 A0A086TJW9_9FUNG Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11884 PE=3 SV=1;>tr A0A0A1MZW0 A0A0A1MZW0_9FUNG Putative Phosphoribosylaminoimidazole-succinocarboxamide synthase OS=Rhiz
A0A0H2RZ89;R9ARV1	>tr A0A0H2RZ89 A0A0H2RZ89_9HOMO Mitochondrial carrier OS=Schizopora paradoxa GN=SCHPADRAFT_994686 PE=3 SV=1;>tr R9ARV1 R9ARV1_WALI9 ADP,ATP carrier protein OS=Walleimia ichthyophaga (strain EXF-994 / CBS 113033) GN=J056_000323 PE=3 SV=1
A0A068SBP3;A0A077WJ05	>tr A0A068SBP3 A0A068SBP3_9FUNG Erythrocyte band 7 integral membrane protein OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_10515.1 PE=4 SV=1;>tr A0A077WJ05 A0A077WJ05_9FUNG Uncharacterized protein OS=Lichtheimia ramosa GN=LRAMOSA09652 PE=4 SV=1
A0A086TLG5	>tr A0A086TLG5 A0A086TLG5_9FUNG 3-hydroxybutyryl-CoA dehydrogenase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11318 PE=4 SV=1

A0A077WNV7;J4H572;A0A0B7FHL1;A0A060S965;A0A0H2SBC8;A0A074SS25;X8J422;A0A0C3S1P6;A0A067MWP7;S7QEZ1;S8FXV7;A0A0C2XUD5;L8WSN7;W4KIP2;A0A0K6FRD7;I4Y690;R9ABW6;A0A0B7NUF3;A0A0C9MES2;F4NXN4;S2JB92;A0A0A1P5M0;A0A0C7B0Z2;A0A068S3S3;I1CDH3;K5UZC5;M2QN91;M5BXU9;A0A0D7BTG3;A0A066WCX9;A0A0C7C7B1	>tr A0A077WNV7 A0A077WNV7_9FUNG Putative Pyridoxine biosynthesis protein PDX1 OS=Lichtheimia ramosa GN=LRAMOSA10174 PE=3 SV=1;>tr J4H572 J4H572_9APHY Uncharacterized protein OS=Fibroporia radiculosa GN=FIBRA_08480 PE=3 SV=1;>tr A0A0B7FHL1 A0A0B7FHL1_THACB
W6MJG9;A0A066VRT1;A0A0B7NNC2;A0A0C9LW22;J6EXB0;K1VAS3;A0A098VTJ4;A0A0H2RVA8;R7S469;C0LEE6;G4TCS7;A0A074S4W4;M5BJ97;S7PTN1;X8IVT8;A0A0K6GFZ3;I4Y5K9;J4G0R5;W4KPC1;A0A060SGU1;A0A0C3NMR7;A0A0C3PUL4;A0A0C3QX68;A0A0J0XVD5;K5XDJ9;M2RUI2;S7QMD2;S8EI11;K5V5K6;A0A0B7NP86;A0A0C9M3G9;S2J0K3;S2JL87;A0A068S0S7;I1BRC7;A0A068RUH0;A0A068SAW7;A0A068SE89;A0A077WP97;A0A077WSE7;L8WTQ0;A0A0A1MRY0;A0A0A1NZQ9;A0A067MBE3;A0A077WRA9;A0A0C3ALB9;A0A0D7B0S1	>tr W6MJG9 W6MJG9_9ASCO Uncharacterized protein OS=Kuraishia capsulata CBS 1993 GN=KUCA_T00002089001 PE=3 SV=1;>tr A0A066VRT1 A0A066VRT1_9HOMO Uncharacterized protein (Fragment) OS=Rhizoctonia solani AG-8 WAC10335 GN=RSAG8_06499 PE=3 SV=1;>tr A0A0B7NNC2 A0
I1BSK3;A0A0C7BEG2;A0A0C7C4G9;A0A0C7BDN9;A0A0C7BD09	>tr I1BSK3 I1BSK3_RHIO9 Uncharacterized protein OS=Rhizopus deleamar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RO3G_03888 PE=4 SV=1;>tr A0A0C7BEG2 A0A0C7BEG2_9FUNG Putative Nitrilase OS=Rhizopus microsporus GN=RMATCC62417_05249 PE=4 SV=
A0A086TLX5	>tr A0A086TLX5 A0A086TLX5_9FUNG Uncharacterized protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_10990 PE=3 SV=1
I4YC99;R9AU65	>tr I4YC99 I4YC99_WALMC Glucosamine-6-phosphate isomerase OS=Walleimia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WALSEDRAFT_68866 PE=3 SV=1;>tr R9AU65 R9AU65_WALI9 Glucosamine-6-phosphate isomerase OS=Walleimia ichthyophaga (strain EXF-994 / CBS 11303
Q9ZVF6	>tr Q9ZVF6 Q9ZVF6 · PAHX_ARATH Uncharacterized protein OS=Arabidopsis thaliana (Mouse-ear cress) GN=F2I9.11 PE=4 SV=1
A0A0B7NJS7;A0A077WNQ8;A0A0J0XCF5;A0A0C3H330;A0A0C9LW23;S2JYB9;A0A0C7BR52;A0A0C7CEY8;I1BR68;R9AB96;A0A0D2A3R4;A0A0G2GB38	>tr A0A0B7NJS7 A0A0B7NJS7_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_09845.1 scaffold 39137 PE=3 SV=1;>tr A0A077WNQ8 A0A077WNQ8_9FUNG Putative Urease accessory protein UreG OS=Lichtheimia ramosa GN=LRAMOSA02330 PE=3 SV=1;>tr A0A0J0XCF
P35182	>tr P35182 P35182 · PP2C1_YEAST Uncharacterized protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast) GN=PTC1 PE=4 SV=1
S7PT43	>tr S7PT43 S7PT43_GLOTA Multifunctional beta-oxidation protein (Fragment) OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=GLOTRDRAFT_50401 PE=4 SV=1
A0A067M2D7;W4K8E6	>tr A0A067M2D7 A0A067M2D7_9HOMO Uncharacterized protein OS=Botryobasidium botryosum FD-172 SS1 GN=BOTBODRAFT_36736 PE=4 SV=1;>tr W4K8E6 W4K8E6_9HOMO Mitochondrial porin OS=Heterobasidion irregulare TC 32-1 GN=HETIRDRAFT_143221 PE=4 SV=1
I1BV01;A0A068SCV4;A0A0A1P281;A0A068RW29;A0A077WVS3;A0A0A1MZL1;A0A0C7B003;I1C0Z0;F4P953;A0A077X161;A0A098VVG1;I1C5S8;I1C7X4;A0A0A1P5C6;A0A0A1PDU7	>tr I1BV01 I1BV01_RHIO9 40S ribosomal protein S0 OS=Rhizopus deleamar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=RPS0 PE=3 SV=1;>tr A0A068SCV4 A0A068SCV4_9FUNG 40s ribosomal protein s0 OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_108
G3FNL8	>tr G3FNL8 G3FNL8_MORAP Sepiapterin reductase OS=Mortierella alpina PE=2 SV=1
C4T9C3;A0A098VPJ9	>tr C4T9C3 C4T9C3_MORAP Succinate dehydrogenase [ubiquinone] iron-sulfur subunit, mitochondrial OS=Mortierella alpina GN=sdhB PE=3 SV=1

A0A068SGQ6;A0A077W5R7	>tr A0A068SGQ6 A0A068SGQ6_9FUNG Serine 3-dehydrogenase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_11241.1 PE=3 SV=1;>tr A0A077W5R7 A0A077W5R7_9FUNG Uncharacterized protein OS=Lichtheimia ramosa GN=LRAMOSA00146 PE=3 SV=1
A0A068RX72;A0A077X1I2	>tr A0A068RX72 A0A068RX72_9FUNG Pyrroline-5-carboxylate reductase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_05811.1 PE=3 SV=1;>tr A0A077X1I2 A0A077X1I2_9FUNG Pyrroline-5- carboxylate reductase OS=Lichtheimia ramosa GN=LRAMOSA05885 PE=3 SV=1
Q9UVH0	>tr Q9UVH0 Q9UVH0_MORAP Putative thioredoxin-like protein OS=Mortierella alpina PE=4 SV=1
Q9C2V2;Q9C2T7;Q9C2T2;C4MMH7;C4MMH8;Q9C2V6;Q9C2S5;D 9I7S1	>tr Q9C2V2 Q9C2V2_9FUNG Actin (Fragment) OS=Lobosporangium transversale GN=act-1 PE=3 SV=1;>tr Q9C2T7 Q9C2T7_9FUNG Actin (Fragment) OS=Mortierella chlamydospora GN=act-1 PE=3 SV=1;>tr Q9C2T2 Q9C2T2_9FUNG Actin (Fragment) OS=Gamsiella multivaricata GN=act
G3FNL6;G3FNL5;A0A086TLQ7	>tr G3FNL6 G3FNL6_MORAP GTP cyclohydrolase I OS=Mortierella alpina PE=2 SV=1;>tr G3FNL5 G3FNL5_MORAP GTP cyclohydrolase I OS=Mortierella alpina PE=2 SV=1;>tr A0A086TLQ7 A0A086TLQ7_9FUNG GTP cyclohydrolase I OS=Mortierella verticillata NRRL 6337 GN=MVEG_114
A0A0B7NHH0;A0A0A1N6F1;A0A0A1NEA3;A0A0A1NTB4;I1C4C3;A 0A0C9MF47;I1BTL8;I1CNU9;A0A0A1NXL4;A0A0B7NKK4;A0A0C7 BIE9;S2JL32	>tr A0A0B7NHH0 A0A0B7NHH0_9FUNG 40S ribosomal protein S4 OS=Parasitella parasitica GN=PARPA_09139.1 scaffold 35524 PE=3 SV=1;>tr A0A0A1N6F1 A0A0A1N6F1_9FUNG 40S ribosomal protein S4 OS=Rhizopus microsporus GN=RMCBS344292_01779 PE=3 SV=1;>tr A0A0A1NEA3 A0A0 >tr J4H5D0 J4H5D0_9APHY Uncharacterized protein OS=Fibroporia radiculosa GN=FIBRA_08797 PE=4 SV=1
J4H5D0	
A0A0B7N732;A0A0B7NAL5;A0A0B7NPE0;A0A0C9M4X9;S2KDR9; A0A0A1NZC7;F4NXW5;S2JG79;S2JL13;A0A0C7BEK8;A0A0C7BK 41;A0A0C7BM58;A0A0C7CEI0	>tr A0A0B7N732 A0A0B7N732_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_05070.1 scaffold 16330 PE=4 SV=1;>tr A0A0B7NAL5 A0A0B7NAL5_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_09770.1 scaffold 38623 PE=4 SV=1;>tr A0A0
A0A098VRU3	>tr A0A098VRU3 A0A098VRU3_9MICR Ribosomal protein L4 OS=Mitosporidium daphniae GN=DI09_27p120 PE=4 SV=1
J4I9C5;W4KPD7;A0A067LWW0;A0A0C3LJX9;A0A0C3SFS4;S7S4 K1;S8FSP1;A0A060SDT8;A0A066VMF0;A0A074S4Z2;A0A0K6GG4 4;M5BJ64;X8IXG9;A0A0H2S8G8;A0A0C2WKR6;I1CJK8	>tr J4I9C5 J4I9C5_9APHY Uncharacterized protein OS=Fibroporia radiculosa GN=FIBRA_02967 PE=3 SV=1;>tr W4KPD7 W4KPD7_9HOMO Uncharacterized protein OS=Heterobasidium irregulare TC 32-1 GN=HETIRDRAFT_377553 PE=3 SV=1;>tr A0A067LWW0 A0A067LWW0_9HOMO Uncharacte
A0A0G2H0Z0;K2RQG0;R1ECI6;A0A0D2A3F2;A0A0G2GIA1	>tr A0A0G2H0Z0 A0A0G2H0Z0_9EURO Putative proteasome component OS=Phaeomoniella chlamydospora GN=UCRPC4_g00187 PE=4 SV=1;>tr K2RQG0 K2RQG0_MACPH Proteasome subunit alpha/beta OS=Macrophomina phaseolina (strain MS6) GN=MPH_07892 PE=4 SV=1;>tr R1ECI6 R1ECI6 B

A0A067MI01;K1VRY4;G4T5J6;M2R7N0;A0A0B7G143;R7T2Z0;A0A060SS70;A0A066V8A5;A0A074SFV6;M5C1H7;J0LGN5;J8TS75;A0A0C3SBX5;K5W735;A0A0C3AMT4;A0A0J0XID4;J7SBZ9;S8E5Z7;A0A0D7BUE3;A0A0K6FS08;K2RZL5;A0A0C3Q6K8;F4P7H4;Q562H7;L8X4T0;A0A068RY22;A0A068RYV1;A0A077WIA8;A0A0B7N8Q4;A0A0C7AWU8;A0A0C9MEV4;I1CGT0;I1CHI5;S2K7V3;W4KEN3;A0A077WTY7;X8JQY8;A0A0E9NRJ2;A0A094ET07;A0A063BVZ2;R1EAT2;A0A086TEY4;A0A094ERD6;A0A094F0H5;A0A0G2E9Z0;A0A094AUT5;A0A094BM49;A0A094C3Z9;A0A094GC95;A0A094HCP2;A0A0G2ER93;A0A093XZ02;A0A093ZT19;A0A094AQ85;A0A094CBQ3;A0A094FHS3;A0A0C3HPI9;A0A0D1Z6N1;I4Y9U6;L8FZ56;A0A094JJV0;R9AKQ1;A0A068RVR2;A0A068RTW3;A0A077WLE0;S7QIN8;A0A068SBC6;A0A0H2RAQ4;A0A0C7BVA3;I1C141;I1CEW8;A0A068RI63;S2KAQ4;W6MTD9;A0A0B7NFS1;A0A0C9MK21;I1BPN7;S2JT16;A0A0C9MAU7;A0A077W9G0;A0A0A1MVI1;A0A0C7C818;A0A063BWL9;R1EP10;A0A094CHC3;A0A093ZVE0;A0A093ZU00;A0A094EF99;A0A094GFX9;A0A093XAL9;A0A093Z1S4;A0A094B003;A0A094B3P4;A0A094BPU3;A0A094FV56;A0A0D1XLB1;L8G2P2;A0A094F2Q1;A0A094H0M2;A0A0G2E6E3;A0A0C3HNU0;A0A086T8T0;K2SCW4;A0A094FG61;A0A098VLT4;J8ZPW9;A0A0B2ULY7;A0A077WC19;A0A068RPL1;A0A0C7B7R5;A0A077WGH1;A0A0A1N3I8;A0A0A1NWB4;A0A0C7AY10;A0A086J205;H8ZBA5;I3EIC0;I3ENM0;A0A0G2EAH1;A0A0A1NAD3;I1BWN7;A0A0C7B833;A0A0B7NJS4;A0A068SEK5;A0A0A1NNX0	>tr A0A067MI01 A0A067MI01_9HOMO Uncharacterized protein OS=Botryobasidium botryosum FD-172 SS1 GN=BOTBODRAFT_31704 PE=3 SV=1;>tr K1VRY4 K1VRY4_TRIAC Uncharacterized protein OS=Trichosporon asahii var. asahii (strain CBS 8904) GN=A1Q2_03404 PE=3 SV=1;>tr G4
A0A086TK63	>tr A0A086TK63 A0A086TK63_9FUNG 6-phosphogluconolactonase OS=Mortierella verticillata NRRL 6337 GN=MVEG_11550 PE=4 SV=1
Q9H4Y5	>tr Q9H4Y5 Q9H4Y5 · GSTO2_HUMAN Uncharacterized protein OS=Homo sapiens (Human) GN=GSTO2 PE=4 SV=1
A0A0J0XW62;A0A0G2DRY7;K2RB33;R1FV32;G4TM45;A0A0C3BBG3	>tr A0A0J0XW62 A0A0J0XW62_9TREE Adenylate kinase OS=Trichosporon oleaginosus GN=ADK1 PE=3 SV=1;>tr A0A0G2DRY7 A0A0G2DRY7_9PEZI Adenylate kinase OS=Diplodia seriata GN=ADK1 PE=3 SV=1;>tr K2RB33 K2RB33_MACPH Adenylate kinase OS=Macrophomina phaseolina (strai
A0A0C9N3I4;I1CJM6;S2K726	>tr A0A0C9N3I4 A0A0C9N3I4_9FUNG Adenylate kinase OS=Mucor ambiguus GN=ADK1 PE=3 SV=1;>tr I1CJM6 I1CJM6_RHIO9 Adenylate kinase OS=Rhizopus delemar (strain RA 99-880 / ATCC MYA-4621 / FGSC 9543 / NRRL 43880) GN=ADK1 PE=3 SV=1;>tr S2K726 S2K726_MUCC1 Adenylat
A0A0J1BAT6;J6F0N6;K1W6Y0	>tr A0A0J1BAT6 A0A0J1BAT6_9TREE Ribosomal protein L13 OS=Trichosporon oleaginosus
A0A068RPE9;C1J9S0	>tr A0A068RPE9 A0A068RPE9_9FUNG Elongation factor 1-alpha OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_03433.1 PE=4 SV=1
F4P1U4	>tr F4P1U4 F4P1U4_BATDJ Putative uncharacterized protein (Fragment) OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_11284 PE=4 SV=1
A0A068RH60;A0A068SHA5;A0A077WKL5;A0A077WPR0	>tr A0A068RH60 A0A068RH60_9FUNG 40s ribosomal protein s2 OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_00745.1 PE=3 SV=1;>tr A0A068SHA5 A0A068SHA5_9FUNG 40s ribosomal protein s2 OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_12181.1 PE=3 SV=1;>tr A0A0

A0A0B7N3X6	>tr A0A0B7N3X6 A0A0B7N3X6_9FUNG Proteasome subunit alpha type OS=Parasitella parasitica GN=PARPA_06986.1 scaffold 25188 PE=3 SV=1
A0A086TKX7	>tr A0A086TKX7 A0A086TKX7_9FUNG Proteasome subunit alpha type OS=Mortierella verticillata NRRL 6337 GN=MVEG_11996 PE=3 SV=1
W4KGX4;A0A0C3AZV1;A0A0C3QFK6;A0A067M9L5;A0A0C3S7V3;A0A0D7BTB5;J4IBL1;K5V9B0;R7SKC2;S8FND5	>tr W4KGX4 W4KGX4_9HOMO Proteasome subunit alpha type OS=Heterobasidion irregulare TC 32-1 GN=HETIRDRAFT_35088 PE=3 SV=1;>tr A0A0C3AZV1 A0A0C3AZV1_9HOMO Proteasome subunit alpha type OS=Serendipita vermifera MAFF 305830 GN=M408DRAFT_331074 PE=3 SV=1;>tr A0
A0A0B7NK98	>tr A0A0B7NK98 A0A0B7NK98_9FUNG Eukaryotic translation initiation factor 6 OS=Parasitella parasitica GN=PARPA_09572.1 scaffold 36923 PE=3 SV=1
P35860	>tr P35860 P35860 · PSBA_CHLEL OS=Chlorella ellipsoidea GN=psbA PE=2 SV=1
A0A068SFR4;A0A077W9F0;A0A0B7N828;A0A077WKC2;F4NTL9;A0A0A1NUA3;A0A0C7B151;A0A0C9N1Q9;I1BW04;I1CCV6;S2K2K7	>tr A0A068SFR4 A0A068SFR4_9FUNG NADH-quinone 25 kDa OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_11448.1 PE=3 SV=1;>tr A0A077W9F0 A0A077W9F0_9FUNG Putative NADH dehydrogenase OS=Lichtheimia ramosa GN=LRAMOSA00122 PE=3 SV=1;>tr A0A0B7N828 A0A0B7N828_9FUNG
S7RIP5	>tr S7RIP5 S7RIP5_GLOTA Eukaryotic translation initiation factor 6 OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=TIF6 PE=3 SV=1
A0A060SBW9;A0A0C9T717;A0A0C9T7X5;B6P770;J4GUX4;S6EAT1;W4KC40;A0A0D7BM24;L8WTC4;M5BSI2;A0A0K6FM71;A0A0J1B6E7;J6FCV8;K1WHG8;A0A066V8F6;A0A067MSX6;A0A074SKI7;A0A0B7FC46;A0A0C3B5J9;A0A0C3MLQ2;A0A0H2RD08;G4T5R8;M2PDV0	>tr A0A060SBW9 A0A060SBW9_PYCCI Eukaryotic translation initiation factor 6 OS=Pycnoporus cinnabarinus GN=TIF6 PE=3 SV=1;>tr A0A0C9T717 A0A0C9T717_PLICR Eukaryotic translation initiation factor 6 OS=Plicaturopsis crispa FD-325 SS-3 GN=TIF6 PE=3 SV=1;>tr A0A
A0A077WBR9;A0A068RND2;A0A0E9NL65;A0A0G2HLL5;K2S066;A0A0G2GUW4;R1GKD9;F4P1J1;A0A068RU67;A0A077X4D7;W6MTZ1	>tr A0A077WBR9 A0A077WBR9_9FUNG Putative Uracil phosphoribosyltransferase 1 OS=Lichtheimia ramosa GN=LRAMOSA07440 PE=4 SV=1;>tr A0A068RND2 A0A068RND2_9FUNG Uracil phosphoribosyltransferase OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_03260.1 PE=4 SV=1;
A0A0C5B2T6	>tr A0A0C5B2T6 A0A0C5B2T6_9HYPO EF1 protein (Fragment) OS=Acremonium sp. A JSM-2015 GN=EF1 PE=4 SV=1
A9RA84	>tr A9RA84 A9RA84 · HMGB1_PAPAN Uncharacterized protein OS=Papio anubis (Olive baboon) GN=HMGB1 PE=4 SV=1
CON__P00761	>P00761 SWISS-PROT:P00761 TRYP_PIG Trypsin - Sus scrofa (Pig).

A0A0B7MZ27;A0A0B7N9I9;S2J3B9;A0A0A1MML3;A0A0A1MRP2;A0A068REE5;A0A077WBY4;A0A0C9LX66;A0A0C9LVF5;A0A0C7AW82;I1C5L7;I1BGZ5;A0A094DR66;A0A094FEE0;A0A093ZJT3;A0A063BVU3;A0A094CVJ0;S2JSD1;A0A094AVI4;A0A077WAP3;A0A0G2DUN4;K2RRU0;A0A068RKT9;A0A0E9NHF7;A0A094F3U8;A0A094E7I9;A0A094JPE7;A0A067MUR2;A0A0G2EBQ3;A0A094A8C1;A0A094BWL5;A0A094DDW1;A0A0B7NBD8;R1H3B6;F4PDN6;A0A068RHF3;A0A077X3I6;K1VE35;A0A0C3HUS7;A0A0J0XIH4;I1C5X0;A0A0A1N260;A0A0C7BTB2;A0A0C7CNM2;R9AMY4;A0A086T1H5;A0A093Z9C3;A0A094B995;A0A094C2Q9;A0A094GEK6;A0A094H0Y2;L8G1W9;A0A0D2AI17;I1CF95;A0A063CBP1;A0A0E9KW04;I4Y7M5;W6MJK8;A0A0A1N032;A0A0A1NIW6;A0A0D1XWT1;A0A086T3B6;A0A093WZL4;A0A093XYD3;A0A093ZZN8;A0A094AS22;A0A094CDM4;A0A094D4C8;A0A094G0I0;A0A094GX43;A0A094IRV7;A0A094IZQ5;A0A0C3GN63;K2RA92;L8FX32;R1G8Z0;A0A0G2G701;A0A0G2EVE9;A0A0C3AF15;A0A0H2S8C9;W4KP48;W6MH93;A0A066W5P7;K5XEH6;M2RTP1;S8FQB8;A0A060SFY4;A0A0C3S6A6;A0A074SXR7;A0A0B7FJ09;A0A0C9LTB5;A0A0K6FN03;S7RYU3;A0A0D7BSQ1;G4TS49;I4YDF6;J4H578;R9AC12;S2J148;A0A0C9MWZ6;A0A0B7N2F1;A0A0B2UDK7;A0A0J0XSU3;K1V9R6;S2KIV2;A0A0C3QBV0	>tr A0A0B7MZ27 A0A0B7MZ27_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_05116.1 scaffold 16505 PE=4 SV=1;>tr A0A0B7N9I9 A0A0B7N9I9_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_05968.1 scaffold 20345 PE=4 SV=1;>tr S2J3
A0A086TL67	>tr A0A086TL67 A0A086TL67_9FUNG GTP-binding nuclear protein GSP1/Ran OS=Mortierella verticillata NRRL 6337 GN=MVEG_12086 PE=4 SV=1
Q6F5H8	>tr Q6F5H8 Q6F5H8_MORAP Orotate phosphoribosyl transferase OS=Mortierella alpina GN=ura5 PE=3 SV=1
A0A086TLG2;A0A0B7NF44;A0A068S7S7;A0A068S9C1;S2JDT7;A0A068RR21;A0A077WDE2;A0A077WTA1;A0A0A1MSX7;A0A0B7NRN0;A0A0C7AXH3;A0A0C9MWB0;I1BSM6;I1C5T4;I1C972;I1CF62;S2JPH2;A0A0E9NAL1;A0A0A1N698	>tr A0A086TLG2 A0A086TLG2_9FUNG 60S ribosomal protein L13 OS=Mortierella verticillata NRRL 6337 GN=MVEG_11315 PE=3 SV=1

A0A068RFB0;A0A077W8L8;A0A077WRR0;A0A0A1NTU0;A0A0A1PJB8;S2JVG0;A0A0B7N8J4;A0A0B7NB39;A0A0A1N4W7;A0A0A1PE99;S2J3Z6;A0A0C7BXC6;A0A0E9N8V2;L8WGB2;A0A094ATX0;K1WPC8;J4UIX4;L8FT53;F4P8Z5;A0A094FGI9;G4TWQ4;R1GYC5;A0A094B721;J4GTB3;A0A067MW80;A0A0C9N1J6;A0A0G2GGV9;R7SR35;S7S5E8;A0A0C3S8H1;J4G5L5;M2PX63;S8F8R3;W4JXU8;A0A0G2EFN8;A0A0H2S947;F4PAL0;G4TRG3;K2SU76;A0A074SDI4;A0A086TLZ9;A0A0C3APK9;A0A0D7BVI6;A0A0K6GFV7;I1BM56;X8IXA8;A0A060SI62;A0A0D2ANX9;A0A0G2H5Y3;A0A0J0XW38;R7SJF3;S2JT43;A0A0B7MRP2;A0A0C3NQM7;I4YBR0;R9ACX4;S8ELH2;A0A060S8V7;A0A066WIX9;A0A067MXR9;A0A0B7FGD6;A0A0C3B6Q7;A0A0C3QJ48;A0A0C3S1P9;A0A0D7B1A4;A0A0K6GBX1;K5V0T5;K5W8K8;M2QBD4;M5BJC4;S4TIT4;W6MJD0;A0A063C4Y4;A0A077WP46;A0A086T2Z3;A0A0J0XKD2;S7RYB8;A0A074RRU1;A0A0E9KXL2;R9APE9;X8JPL2;A0A094BJH1;A0A094C6H1;A0A094DNK9;A0A094EVG8;A0A094FR45;A0A094HU28;A0A094HUY4;A0A094K172;S8FJ46;A0A060SRF1;I1CS57;A0A093ZUX9;A0A066VLY9;A0A094BCJ8;A0A0B7FMV4;I1BZB3;A0A0C7CNB2	<div> <div>>tr A0A068RFB0 A0A068RFB0_9FUNG Gtp-binding protein sas1 OS=Lichtheimia corymbifera</div> <div>JMRC:FSU:9682 GN=LCOR_00104.1 PE=4 SV=1;>tr A0A077W8L8 A0A077W8L8_9FUNG Putative Ras-like protein Rab-8A OS=Lichtheimia ramosa GN=LRAMOS01108 PE=4 SV=1;>tr A0A077WRR0 A0A0</div> </div>
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<p>A0A068RLX2;A0A077WVG6;A0A0E9NA88;A0A0C3QP62;A0A0C9MSC4;A0A0G2GHA2;R9AGT3;A0A0H2S1P2;R7T273;A0A0C3SEF2;M2PV61;J4GU31;S8EDY0;A0A0D7BTR2;K5W628;S7QK62;W4KH C8;A0A060S339;A0A093XEX5;A0A094CRT4;A0A094BFC0;J9DV05;A0A093YCY6;A0A0J0XJX3;G4U2C5;A0A0B7FYQ5;A0A094DVS4;A0A0C3BGJ5;A0A074S949;W4KMY1;X8IXI7;A0A0D7B2J9;A0A0H2RZ66;S7S466;A0A094GST2;L8WVH1;S8FT24;A0A067MA27;M2PYU1;A0A0C3S674;K5WAV5;A0A0E9NL93;A0A0J0XZT0;J4G1B2;A0A093XMR0;A0A094F8F6;A0A0C7B7J9;G4TAU7;A0A077X506;K5VUR6;A0A067MQR1;A0A0C3B2D3;A0A0H2SBZ9;A0A094KF39;A0A060SGI4;A0A0C3SA10;A0A0D7BRG7;S7QEZ9;W4KL68;A0A094F2H7;A0A094H3M6;A0A0C3PXS5;S8DUI9;A0A093Z2W7;A0A074SAL2;A0A0A1UK26;A0A0B7F1V7;A0A0K6FX73;A0A0C9M4Q8;A0A0E9NIB9;S2JH38;A0A068SCJ2;A0A077X0P5;A0A093XTA8;A0A093ZJR3;A0A094AI06;A0A094BQ30;A0A094DFE9;A0A094DIB7;A0A094ISK7;A0A0B7NHE2;L8G7X5;A0A094D2G0;A0A0C7AXH5;A0A0C7CN22;A0A0E9L4M0;I4YJY1;A0A068S8A3;A0A086SY90;A0A0A1N5R2;A0A0C7AXP0;A0A0C7CM33;A0A0D1ZYW2;A0A077WP78;A0A0A1NZI8;A0A068SDU6;A0A077WV33;A0A0B7NDY9;A0A0B7NSM7;A0A0C9LV12;A0A0C9MUC0;A0A0G2EU45;R1E769;S2J875;S2JI47;S2JIZ1;A0A068SEG1;A0A077WM57;A0A0A1NW36;A0A0C7AXT3;F4PA58;I1C5S9;A0A086J559;H8ZD63;I3EH04;I3ES91;W6MMB0;A0A0A1NRV0;A0A0B2UKG6;L8WED4;A0A0A1NT97;L8FRM0;A0A0A1MTL9;A0A098VT49;A0A0C3LL12;A0A0C3HAJ4;A0A0K6FQ14;A0A0B7NCJ0;I1C174;A0A063BWV9;I1BTA3;K2S958;I1CN31;I1BVA2;M5CEE3;M5C5W3;A0A066V2S9;A0A066V269</p>	<p>>tr A0A068RLX2 A0A068RLX2_9FUNG Ras-related protein rab-6a OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_02327.1 PE=4 SV=1;>tr A0A077WVG6 A0A077WVG6_9FUNG Putative Ras-like protein Rab-6B OS=Lichtheimia ramosa GN=LRAMOSA03884 PE=4 SV=1;>tr A0A0E9NA88 A0</p>
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A0A086TL30	>tr A0A086TL30 A0A086TL30_9FUNG Proteasome subunit beta type OS=Mortierella verticillata NRRL 6337 GN=MVEG_12049 PE=3 SV=1
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A0A0G2E484;K2SFN1;R1G2A9;A0A066W5C9;A0A0E9N7J2;A0A0D2AAS1;A0A0C9MBV8;A0A0C7C2D0;M5BLR2	>tr A0A0G2E484 A0A0G2E484_9PEZI Putative rab small monomeric gtpase OS=Diplodia seriata GN=UCDDS831_g06251 PE=4 SV=1;>tr K2SFN1 K2SFN1_MACPH Ras GTPase OS=Macrophomina phaseolina (strain MS6) GN=MPH_07055 PE=3 SV=1;>tr R1G2A9 R1G2A9_BOTPV Putative rab smal
A0A0B7N1Q7;A0A0C9M4W5;I1BS69;I1BWA8;I1C1E6;S2J135;S2JC42;S2JG50;A0A0C9L7W9;A0A0C9LX78;A0A0B7N4R8;A0A0B7NHI9;R7RXR1	>tr A0A0B7N1Q7 A0A0B7N1Q7_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_05192.1 scaffold 16505 PE=3 SV=1;>tr A0A0C9M4W5 A0A0C9M4W5_9FUNG 40S ribosomal protein S5 OS=Mucor ambiguus GN=MAM1_0007c00822 PE=3 SV=1;>tr I1BS69 I1BS69_RHIO9 40S
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A0A086TKM3;A0A0E9NFM5;J4GVI6;A0A0C3QEM7;A0A0B7N0W7;G4TUX8;A0A068S3X2;A0A077W832;A0A0C3KQ51;A0A068S475;R7S3W1;R7T2D2;A0A0C3N9K9;A0A0D7BNG4;S7RCZ1;A0A0C3A7A1;A0A0G2DV66;A0A0C9SX70;S8EWE0;W4K4Y3;K5WPD4;A0A0H2SHM5;M2QGE7;A0A067M962;A0A074S984;A0A0K6FZX9;X8IVE9;A0A0H2R1A8;M5BSI5;A0A066VSA9;A0A0A1NBR8;A0A0J0XBA1;A0A0C3HUI0;A0A0C3SBF2;A0A0D1XRU5;F4NSS9;R9AAW1;W6MFF2;A0A0B7NME2;A0A0C2W3Y4;A0A0C9MTS0;I1CJL6;I4Y6L5;S2JAC7;A0A063BUT7;A0A074RQL6;A0A086SUI3;A0A0B7FGS7;A0A0C3MCR0;G4TRX9;K5VSY5;Q8TG28;W4JS04;X8JGR3;A0A060SN63;A0A067MK11;A0A077WZZ1;A0A093XJ05;A0A093ZRY5;A0A094A522;A0A094B9A9;A0A094CDT1;A0A094CFK1;A0A094FB26;A0A094GP77;A0A094H6A0;A0A094IEQ1;A0A094K5B1;A0A0D7BCB1;L8FMA8;M2QQV6;R7T2T7;S4THT8;S4TK20;S7Q632;S8FFL0;A0A077WDY1;A0A094CQD2;A0A0A1P0W1;A0A0C7AWC0;A0A0C9M5E6;A0A0G2F1D4;F4NZR6;G4T988;I1BMD2;I1BPV4;I1BUI7;I1CEG5;S2J5Z6;K2SGG5;R1GGY5;R7S8J0;A0A0C2X8N7;M5C3K1;A0A0C7CF74;L8WFH2;A0A093ZHT3	>tr A0A086TKM3 A0A086TKM3_9FUNG GTP-binding protein rhoA OS=Mortierella verticillata NRRL 6337 GN=MVEG_11893 PE=4 SV=1;>tr A0A0E9NFM5 A0A0E9NFM5_9ASCO Uncharacterized protein OS=Saitoella complicata NRRL Y-17804 GN=G7K_2659-t1 PE=4 SV=1;>tr J4GVI6 J4GVI6_9
L7PB94	>tr L7PB94 L7PB94_MORAP Dihydropteridine reductase (Fragment) OS=Mortierella alpina PE=2 SV=1
S7PW03	>tr S7PW03 S7PW03_GLOTA Uncharacterized protein OS=Gloeophyllum trabeum (strain ATCC 11539 / FP-39264 / Madison 617) GN=GLOTRDRAFT_132852 PE=4 SV=1
P27882	>tr P27882 P27882 · ERV1_YEAST Uncharacterized protein OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) (Baker's yeast) GN=ERV1 PE=4 SV=1

A0A086TJ62;A0A0C9MLA2;A0A0E9NKE4;A0A077WY64;A0A068R SJ2;A0A068RTH5;A0A068S7E8;A0A077WS51;A0A077WUB4;A0A 0A1NM61;A0A0C9M700;F4PE27;I1CMC5;S2J7J6;S2JWK8;S2K8W 1;A0A0A1MWH9;F4PE86;A0A0C7C6Y5;A0A0C9MJC2;L8WJ27;A0 A0K6GAW4;A0A074RQK8;A0A0B7FGH5;X8JKV7;B8P5C1;A0A0D7 BRK6;I4YAJ4;R9AL23;S8EI58;W4KMP2;A0A067MWH2;A0A0C3P3 C0;K5VDU0;M2QYE2;S7QMP1;A0A060SLW0;F4NUT9;J4I0L0;A0A 0B7NEI2	>tr A0A086TJ62 A0A086TJ62_9FUNG Ras-like C3 botulinum toxin substrate 1 OS=Mortierella verticillata NRRL 6337 GN=MVEG_12143 PE=4 SV=1;>tr A0A0C9MLA2 A0A0C9MLA2_9FUNG RAS-related C3 botulinum toxin substrate 1 isoform X3 OS=Mucor ambiguus GN=MAM1_0025c02073
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A0A086T4Y2	>tr A0A086T4Y2 A0A086T4Y2_ACRCH Nuclear movement protein-like protein OS=Acremonium chrysogenum ATCC 11550 GN=ACRE_047720 PE=4 SV=1

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A0A086TIW5	>tr A0A086TIW5 A0A086TIW5_9FUNG 60S ribosomal protein L18-B OS=Mortierella verticillata NRRL 6337 GN=MVEG_12226 PE=4 SV=1
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A0A0A1P0B7	>tr A0A0A1P0B7 A0A0A1P0B7_9FUNG Uncharacterized protein OS=Rhizopus microsporus GN=RMCBS344292_11581 PE=4 SV=1
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A0A086TKQ1	>tr A0A086TKQ1 A0A086TKQ1_9FUNG Ferritin OS=Mortierella verticillata NRRL 6337 GN=MVEG_11921 PE=3 SV=1
A0A0C3BCW3	>tr A0A0C3BCW3 A0A0C3BCW3_9HOMO Uncharacterized protein OS=Serendipita vermifera MAFF 305830 GN=M408DRAFT_328417 PE=3 SV=1
A0A086TLY2	>tr A0A086TLY2 A0A086TLY2_9FUNG F-type H+-transporting ATPase subunit D OS=Mortierella verticillata NRRL 6337 GN=MVEG_10997 PE=4 SV=1
A0A094AU57	>tr A0A094AU57 A0A094AU57_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-3808 GN=O988_02672 PE=4 SV=1
S2JQ68;A0A0A1P518;A0A0C7BLV2;A0A0C7CB17;A0A0C7CC91;A0A0A1NDH6;I1BS24;A0A0C9MF99	>tr S2JQ68 S2JQ68_MUCC1 Uncharacterized protein OS=Mucor circinelloides f. circinelloides (strain 1006PhL) GN=HMPREF1544_08490 PE=4 SV=1;>tr A0A0A1P518 A0A0A1P518_9FUNG Uncharacterized protein OS=Rhizopus microsporus GN=RMATCC62417_07369 PE=4 SV=1;>tr A0A0
A0A074RNF6;X8JK72;A0A0C2XDB5;A0A066VRA3;A0A0K6FRC2	>tr A0A074RNF6 A0A074RNF6_9HOMO Peptidyl-prolyl cis-trans isomerase OS=Rhizoctonia solani 123E GN=V565_211840 PE=3 SV=1;>tr X8JK72 X8JK72_9HOMO Peptidyl-prolyl cis-trans isomerase OS=Rhizoctonia solani AG-3 Rhs1AP GN=RSOL_490230 PE=3 SV=1;>tr A0A0C2XDB5 A0

A0A0D1XQE2;K2RIC4	>tr A0A0D1XQE2 A0A0D1XQE2_9PEZI 40S ribosomal protein S18 OS=Verruconis gallopava GN=PV09_04018 PE=3 SV=1;>tr K2RIC4 K2RIC4_MACPH Ribosomal protein S13 OS=Macrophomina phaseolina (strain MS6) GN=MPH_10322 PE=3 SV=1
A0A086T1T3	>tr A0A086T1T3 A0A086T1T3_ACRCH Eukaryotic translation initiation factor 1A, X-chromosomal-like protein OS=Acremonium chrysogenum ATCC 11550 GN=ACRE_059280 PE=3 SV=1
A0A066VRU0	>tr A0A066VRU0 A0A066VRU0_9HOMO 40S ribosomal protein S19-A (Fragment) OS=Rhizoctonia solani AG-8 WAC10335 GN=RSAG8_05474 PE=4 SV=1
K5WVC0	>tr K5WVC0 K5WVC0_PHACS Uncharacterized protein OS=Phanerochaete carnosae (strain HHB-10118-sp) GN=PHACADRAFT_29586 PE=4 SV=1
A0A0A1NLJ3	>tr A0A0A1NLJ3 A0A0A1NLJ3_9FUNG Putative 60S ribosomal protein L12 OS=Rhizopus microsporus GN=RMATCC62417_01709 PE=3 SV=1
J4ICF6;S8EJF2;A0A066VXC6;A0A067MI69;A0A0B7FJC7;A0A0C3NGS5;K5WAT4;X8JNG3;A0A074S326;A0A0J1BA94;L8X1X8	>tr J4ICF6 J4ICF6_9APHY Uncharacterized protein OS=Fibroporia radiculosa GN=FIBRA_08579 PE=3 SV=1;>tr S8EJF2 S8EJF2_FOMPI Uncharacterized protein OS=Fomitopsis pinicola (strain FP-58527) GN=FOMPIDRAFT_1021997 PE=3 SV=1;>tr A0A066VXC6 A0A066VXC6_9HOMO Uncharacterized protein OS=Homo sapiens GN=HOMO_000000000 PE=3 SV=1
A0A068L7F7	>tr A0A068L7F7 A0A068L7F7_9APHY Peptidyl-prolyl cis-trans isomerase OS=Wolfiporia cocos GN=CYP PE=2 SV=1
Q9XVP0;P62843;Q01855	>tr Q9XVP0 Q9XVP0 · RS15_CAEEL Uncharacterized protein OS=Caenorhabditis elegans GN=rps-15 PE=3 SV=1;>tr P62843 P62843 · RS15_MOUSE=Mus musculus (Mouse) GN=Rps15 PE=3 SV=1
A0A086TK70	>tr A0A086TK70 A0A086TK70_9FUNG Ubiquinol-cytochrome c reductase cytochrome c1 subunit OS=Mortierella verticillata NRRL 6337 GN=MVEG_11557 PE=4 SV=1
A0A0B7NES0;A0A0C9MZI9;S2JM62;A0A0K6FTI7;A0A066WBG0;A0A060SJR3;A0A0C3S662;M2PQ18;A0A0A1PG52;A0A0C7B3H2;I1CBB4;F4NWR6	>tr A0A0B7NES0 A0A0B7NES0_9FUNG Nucleoside diphosphate kinase OS=Parasitella parasitica GN=PARPA_11282.1 scaffold 43311 PE=3 SV=1;>tr A0A0C9MZI9 A0A0C9MZI9_9FUNG Nucleoside diphosphate kinase OS=Mucor ambiguus GN=MAM1_0240d08579 PE=3 SV=1;>tr S2JM62 S2JM62 Uncharacterized protein OS=Homo sapiens GN=HOMO_000000000 PE=3 SV=1
L8WU57;M5BSF7	>tr L8WU57 L8WU57_THACA Inorganic diphosphatase OS=Thanatephorus cucumeris (strain AG1-IA) GN=AG1IA_05668 PE=4 SV=1;>tr M5BSF7 M5BSF7_THACB Inorganic pyrophosphatase OS=Thanatephorus cucumeris (strain AG1-IB / isolate 7/3/14) GN=BN14_04148 PE=4 SV=1
R7SG08;A0A0C3LQH9	>tr R7SG08 R7SG08_FOMME Ubiquitin-conjugating enzyme E2 4 OS=Fomitiporia mediterranea (strain MF3/22) GN=FOMMEDRAFT_24276 PE=3 SV=1;>tr A0A0C3LQH9 A0A0C3LQH9_9HOMO Uncharacterized protein OS=Tulasnella calospora MUT 4182 GN=M407DRAFT_244708 PE=3 SV=1
G4TIQ4	>tr G4TIQ4 G4TIQ4_PIRID Probable Calmodulin OS=Piriformospora indica (strain DSM 11827) GN=PIIN_05133 PE=4 SV=1
A0A086TKH8;F4NSB7;S2IUZ3	>tr A0A086TKH8 A0A086TKH8_9FUNG 40S ribosomal protein OS=Mortierella verticillata NRRL 6337 GN=MVEG_11664 PE=3 SV=1
A0A067MGM3;J4UB84;K1VK41;L8WEQ3;F4P2K6;A0A0J0XL23;A0A0D7B4F4;W4JNN2;A0A0B7G0Q0;A0A0C3PEY3;A0A0H2R148;B8PDU5;E7E161;I4Y835;I7H4Q8;J4GPE1;K5WS92;M2QW12;R7S4C2;R9APA2;S7PV21;A0A066VRY3;A0A060SMY7;A0A0K6FUX8	>tr A0A067MGM3 A0A067MGM3_9HOMO Uncharacterized protein OS=Botryobasidium botryosum FD-172 SS1 GN=BOTBODRAFT_36044 PE=4 SV=1;>tr J4UB84 J4UB84_TRIAS ATP-dependent DNA helicase OS=Trichosporon asahii var. asahii (strain ATCC 90039 / CBS 2479 / JCM 2466 / KC) GN=TRIAS_000000000 PE=3 SV=1
R9AVT5	>tr R9AVT5 R9AVT5_WALI9 40S ribosomal protein S10-B OS=Walleimia ichthyophaga (strain EXF-994 / CBS 113033) GN=J056_002299 PE=4 SV=1

A0A094FKG9;A0A094HB71	>tr A0A094FKG9 A0A094FKG9_9PEZI Uncharacterized protein (Fragment) OS=Pseudogymnoascus pannorum VKM F-4518 (FW-2643) GN=V500_09402 PE=4 SV=1;>tr A0A094HB71 A0A094HB71_9PEZI Uncharacterized protein (Fragment) OS=Pseudogymnoascus pannorum VKM F-4520 (FW-2644)
Q9UVH1;A0A0B7NNQ5;L8WXJ8;S2JW84;S2JDX6;S2JW25;A0A077WEC8;S2KA89;A0A0G2EG41;K2RBK9;R1E8W0;R9A950;F4NV06;A0A060S8G0;A0A066VMJ3;A0A066VVX0;A0A067MCV9;A0A074RRC0;A0A0C2X4G1;A0A0C3S3Z8;A0A0H2RAX3;A0A0K6GG11;J4H3H6;K5V4J6;M2QTW6;R7SNR2;S8DIL0;W4JYP9;X8IX22;A0A068RLF1;A0A077WVE9;A0A0A1NCG2;A0A0B7N2R9;A0A0B7NJ12;A0A0C7CBE3;A0A0C9LUS2;I1CB86;A0A0J0XUK1;A0A0G2GY39;A0A0C3HEX9;A0A063BX41;A0A086T8C6;A0A093XFU8;A0A093Y0T1;A0A093YZV9;A0A094BDW7;A0A094C1C2;A0A094C1T9;A0A094CFG9;A0A094D8S6;A0A094DBT4;A0A094E1S2;A0A094HXX0;A0A094I0D9;A0A094I3P0;A0A094IZ52;A0A0D2A8R9;L8FVQ6;A0A0D7AZU8;B8P3N0;G4TQB2;M5BJ99;S7PXR4;I4YIK3;A0A098VSF3;A0A0C9MP21;A0A0E9NEN7	>tr Q9UVH1 Q9UVH1_MORAP Putative 60S ribosomal protein L27A OS=Mortierella alpina GN=rpl27A PE=3 SV=1;>tr A0A0B7NNQ5 A0A0B7NNQ5_9FUNG Uncharacterized protein OS=Parasitella parasitica GN=PARPA_13339.1 scaffold 46779 PE=3 SV=1;>tr L8WXJ8 L8WXJ8_THACA 60S ri
F4P3E3;A0A077WXN2;A0A068RUG6;A0A077WY95;A0A068S7S4;A0A077WSD3;A0A068S2T9;K1V056;A0A0E9NBH7;A0A0C7B3W5;R9AGN4;A0A0C7BX76;I1CRA2;A0A0C9MNR5;S2JD01;A0A0B7MYM5;A0A0C9LSQ3;S2JFW7;A0A0B7NQF5;A0A0C3K4T9;M2REF0;S7S1J8;A0A0C3NWH2;J4GDJ8;R7S3Z0;S8FB91;A0A0A1P953;I1BZ65;J6EYJ1;K1VE25;A0A0D7BHA8;I4YJZ0;A0A060SKY2;A0A0C7BQ17	>tr F4P3E3 F4P3E3_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_88596 PE=3 SV=1;>tr A0A077WXN2 A0A077WXN2_9FUNG Putative 40S ribosomal protein S17-B OS=Lichtheimia ramosa GN=LRAMOSA04600
A0A086TLA7;A0A094GYU1;A0A093ZZU9;A0A094BFX3;A0A094GLP7;A0A094GXX9;A0A0E9KW48;S7RZU3;A0A063C2F2;A0A094AWA0;A0A094CFC5;A0A094F3R1;A0A094ILR3;A0A0C3C7J1;L8FZG4;A0A0E9NBV7;A0A0C7BU37;A0A0G2DUI4;A0A068RSP0;F4P0I4;A0A0G2E2J0;K2SCG4;R1EM59;A0A0D2BA92;I1CUB3;A0A068RVW6;A0A077WR67;A0A0A1NZD0;A0A0B7NEI8;A0A0C9MNE3;I1BPP0;I1CHI4;S2JDI4;A0A0C9M6M2;S2KAZ2	>tr A0A086TLA7 A0A086TLA7_9FUNG 40S ribosomal protein S16 OS=Mortierella verticillata NRRL 6337 GN=MVEG_11261 PE=3 SV=1;>tr A0A094GYU1 A0A094GYU1_9PEZI Uncharacterized protein OS=Pseudogymnoascus pannorum VKM F-4520 (FW-2644) GN=V502_09659 PE=3 SV=1;>tr A0
A0A086TL32	>tr A0A086TL32 A0A086TL32_9FUNG 40S ribosomal protein S23 OS=Mortierella verticillata NRRL 6337 GN=MVEG_12051 PE=3 SV=1
A0A067YM27;A0A067YMC9;A0A067YMG5	>tr A0A067YM27 A0A067YM27_9PEZI Actin (Fragment) OS=Penidiella columbiana PE=3 SV=1;>tr A0A067YMC9 A0A067YMC9_9PEZI Actin (Fragment) OS=Pseudoramichloridium henryi PE=3 SV=1;>tr A0A067YMG5 A0A067YMG5_9PEZI Actin (Fragment) OS=Pseudoramichloridium henryi PE
A0A098VV46	>tr A0A098VV46 A0A098VV46_9MICK Histone H3 OS=Mitosporidium ophryosporum GN=D109_11p180 PE=3 SV=1
R1GRD4;K2REH6;A0A093XXC4;A0A093YQ28;A0A094BDF5;A0A094BV69;A0A094CMR8;A0A094DDT6;A0A094DMJ2;A0A094ENK0;A0A094EZ81;A0A094HWD1;A0A094ICG9;A0A094IDU2;A0A0C3H5S1;A0A0E9KL39;A0A0G2EB03;L8FXE8;A0A063BRC6	>tr R1GRD4 R1GRD4_BOTPV Putative 60s ribosomal protein I23 protein OS=Botryosphaeria parva (strain UCR-NP2) GN=UCRNP2_4811 PE=3 SV=1;>tr K2REH6 K2REH6_MACPH Ribosomal protein L14b/L23e OS=Macrophomina phaseolina (strain MS6) GN=MPH_09906 PE=3 SV=1;>tr A0A0

A0A077WGE9;A0A068SC08;S2K9B5;A0A0C9LTV8;A0A0B7N7K9;F4P7A4;A0A068RRS3;A0A077W950;A0A0A1N9W0;A0A0B7N8H4;A0A0C7BNQ1;A0A0C9MC65;I1C4Y4;Q9HDF5;S2JDC3;A0A0G2GK25;A0A093Z3G4;A0A086TBU9;A0A093XC64;A0A093XW01;A0A093YXF9;A0A093Z3I4;A0A093ZVE8;A0A094AZ83;A0A094BPA9;A0A094DX52;A0A094E4J2;A0A094EKZ8;A0A094FZ68;A0A094G611;A0A094GVQ2;A0A094HGS2;A0A0C3CR11;A0A0D2A1K7;A0A0E9KLX4;A0A0E9L167;A0A0G2DQB5;A0A0G2G1E8;A0A0G2G7E9;K2RSI5;K2SDU3;L8G1I0;R1GNU3;R1GWB1;W6MN64;A0A0J0XL38;J6EWW4;K1VI65;A0A063C8Z1;A0A0C3D7I4;A0A063BSC3;A0A0J1BCP9;A0A0E9NAT8;L8WQP5;A0A060S2Y1;R7S2Y0;R9AI30;A0A060SFT0;M2RTR9;J0WY00;A0A060S806;A0A066W187;A0A067MJK0;A0A074RSF7;A0A098VVU5;A0A0C2WZZ9;A0A0C3PNP6;A0A0C3S831;A0A0D7B877;A0A0H2S249;A0A0H2S794;A0A0K6GFH1;B8PD36;G4TE33;I4YIF8;J4I9W3;K5XEB5;M2RK03;M5CFN0;P62792;R7STV3;R9A992;S7QKJ2;S8DYW6;W4KMU5;X8JJK1;W4KMM8;I4Y618;G4TW39;A0A0D7BDQ6;S7QBJ0;W4K0F2;R7SYI2;A0A0C3Q0D4;A0A068RQK8;L8X1Z2;S8FSR6;A0A0A1N552;A0A066VYN8	>tr A0A077WGE9 A0A077WGE9_9FUNG Histone H4 OS=Lichtheimia ramosa GN=LRAMOS08656 PE=3 SV=1;>tr A0A068SC08 A0A068SC08_9FUNG Histone H4 OS=Lichtheimia corymbifera JMRC:FSU:9682 GN=LCOR_09635.1 PE=3 SV=1;>tr S2K9B5 S2K9B5_MUCC1 Histone H4 OS=Mucor circinelloi
A0A086TK04	>tr A0A086TK04 A0A086TK04_9FUNG Large subunit ribosomal protein L14e OS=Mortierella verticillata NRRL 6337 GN=MVEG_11492 PE=4 SV=1
A0A0B7MYL6;A0A0C9LWJ7;S2KC07	>tr A0A0B7MYL6 A0A0B7MYL6_9FUNG Uncharacterized protein OS=Parasitena parasitica GN=PARPA_01517.1 scaffold 1359 PE=3 SV=1;>tr A0A0C9LWJ7 A0A0C9LWJ7_9FUNG Ribosomal protein S22 OS=Mucor ambiguus GN=MAM1_0216d08160 PE=3 SV=1;>tr S2KC07 S2KC07_MUCC1 40S ribo
I4YHN6;R9ANY7;A0A086TJW6	>tr I4YHN6 I4YHN6_WALM1C NADH dehydrogenase, alpha subcomplex, subunit 6 OS=Wallemia mellicola (strain ATCC MYA-4683 / CBS 633.66) GN=WALSEDRAFT_59217 PE=4 SV=1;>tr R9ANY7 R9ANY7_WALI9 NADH dehydrogenase 1 alpha subcomplex subunit 6 OS=Wallemia ichthyophaga
A0A0C3SFF5;K5XDA6	>tr A0A0C3SFF5 A0A0C3SFF5_PHLGI Uncharacterized protein OS=Phlebiopsis gigantea 11061_1 CR5-6 GN=PHLGIDRAFT_17794 PE=4 SV=1;>tr K5XDA6 K5XDA6_PHACS Uncharacterized protein OS=Phanerochaete carnosa (strain HHB-10118-sp) GN=PHACADRAFT_247298 PE=4 SV=1

W6MGP7;A0A094C140;A0A094BJL8;A0A094CX20;A0A093YW15;A0A094EFP9;A0A093XDE0;A0A094J8Y6;A0A0B7FUX6;I4Y5E2;A0A0G2ENB9;L8WVIO;A0A094G3L5;A0A094CFM7;A0A094BZT0;A0A0K6FM12;A0A094BL17;A0A094B0J8;K2RHN1;A0A0B7F544;A0A0D2A5S2;A0A074REZ6;X8JC86;A0A0K6GHK5;M2RS96;S7QMQ7;S8EGN3;A0A093Z6G9;M5BSU7;A0A074S5X3;A0A093XRD9;A0A093YBW5;A0A094AZF9;A0A094CAE5;A0A094D0Y3;A0A094DEY0;A0A094EZL2;A0A094GR62;A0A094H4P9;A0A094HXC0;A0A0A1UMB1;A0A0C3SC27;A0A0D7B7K4;A0A0D7BBL8;J4HVR0;L8G786;Q01867;S7RSG0;V5W5W7;W4K5Q8;A0A0E9NL44;V5W4M0;J4GLR5;A0A067MAF3;A0A067N0B7;A0A074S901;A0A094A6D7;A0A0C3H1B0;A0A0C3QRE6;A0A0C3SFG3;A0A0G2E8U8;A0A0G2F3Q7;F4P187;K1VJU6;K2S8T2;K5UVQ3;K5WNF4;R7SWR5;S8FT96;X8JHG0;L8FU04;A0A0E9NG97;I1CHT2;I1CB85;A0A0C2W6G4;A0A0C3BEU3;A0A0J0XBY6;C0L941;J5SNQ9;W6MRE5;A0A0A1PDZ1;A0A0C7B428;A0A067MLF1;M5BR31;G4TG81;L8X4R2;C7DJP9;G4TDP0;F4NVC1;L8WIL1;A0A060SSV8;J5TB49;K1VV15;A0A0J0XYI9;A0A0C2XZ38;A0A060SBK4;A0A067M4V2;A0A074SQ86;A0A0C3S841;A0A0D7B053;A0A0K6G2W8;B8P0U2;J4G7Q1;K5VVN7;M2QQD8;M5BYZ6;R7STE5;S7RT35;S8EEM3;U3PLF0;W4JYT1;X8JA52;A0A0C3QF37;G4THG3;K5WK55;L8FSG6;A0A0C3GY18;A0A0D2AES0;A0A0G2EWR7;A0A0G2GEQ7;R1GSJ4;A0A086T9I0;W6MM66;A0A0D2BBL5;A0A060SGW1;A0A098VQF5;G4T8R6;A0A066VCU3;A0A0A1NBJ9;A0A0K6GDE1;I1BXB6;M5C250;W4KNW8;X8IV60;A0A0G2EK29;K2RZ76;J4G0P3;B8P7F5;S8FQ56;A0A066WAU3;J6F255;K1VMG6;A0A0C3RQ26;A0A0D7B7N6;J0WVP8;S7QK97;A0A0C3I1U7;A0A0C2X840;A0A0C3L513;F4P6V2;A0A063BYS4;A0A0H2R6Y5;R9A9C1;L8WZL1;A0A063BRZ2;A0A0A1NQH0;X8IV06;A0A066VL52;I4Y7K4;A0A0H2S8J0;A0A063BLP3;A0A0B7MN52;J9DRV3;A0A098VV94;S2JLB1;A0A0B7N6Y7;R9AGK1;I4YDZ1;J9D6B5;Q01868;A0A0K6FXY4;B8NZA2;A0A0C9M1Z1;M2QJ42;R9AQR6;A0A086J351;H8Z9W5;A0A0B2UML3;A0A0D7AV74;A0A086J197;H8ZF93;A0A0C3LC17;A0A0B7MTC2;A0A0B7NUV8;A0A0B7MQ95;I3EDX0;I3ERI9;A0A0B2UMA6;A0A0C3GDQ5;A0A0C3QM92	>tr W6MGP7 W6MGP7_9ASCO Uncharacterized protein OS=Kuraishia capsulata CBS 1993 GN=KUCA_T00000963001 PE=4 SV=1;>tr A0A094C140 A0A094C140_9PEZI Uncharacterized protein (Fragment) OS=Pseudogymnoascus pannorum VKM F-4515 (FW-2607) GN=V496_10504 PE=4 SV=1;>tr
F4P4R3	>tr F4P4R3 F4P4R3_BATDJ Putative uncharacterized protein OS=Batrachochytrium dendrobatidis (strain JAM81 / FGSC 10211) GN=BATDEDRAFT_25278 PE=4 SV=1
Q9UVA4	>tr Q9UVA4 Q9UVA4_9APHY Beta-tubulin (Fragment) OS=Lentinus tigrinus PE=3 SV=1
Q9Y706;A0A0C3AKT2;G4TQ19	>sp Q9Y706 CYB5_MORAP Cytochrome b5 OS=Mortierella alpina PE=1 SV=1;>tr A0A0C3AKT2 A0A0C3AKT2_9HOMO Uncharacterized protein OS=Serendipita vermifera MAFF 305830 GN=M408DRAFT_74759 PE=3 SV=1;>tr G4TQ19 G4TQ19_PIRID Probable cytochrome b5 OS=Piriformospora i

A0A066W9Q0;A0A0B7G1I8;A0A0D7BRA2;W4KFZ9;G4T6P7;J9D7E0;A0A0C3S356;F4NUX4;M2QVF9;A0A0A1N0M4;A0A0A1P7X0;I1C6Z8;I1CIC3;I1CMU0;S7QJ23	>tr A0A066W9Q0 A0A066W9Q0_9HOMO Uncharacterized protein (Fragment) OS=Rhizoctonia solani AG-8 WAC10335 GN=RSAG8_03640 PE=4 SV=1;>tr A0A0B7G1I8 A0A0B7G1I8_THACB 60S ribosomal protein L29 OS=Schizosaccharomyces pombe (Strain 972 / ATCC 24843) GN=rpl29 PE=3 S
A0A086TMI4;A0A093Z2B7;A0A0C9MG99;A0A0B7MZ05;A0A0B7F6T7;M5C3Q6;A0A0G2F2P4;A0A063C0J1;A0A086SZQ3;A0A0K6G2P9;A0A0C3DQG1;A0A0D2ASW8;A0A0G2EAV2;K2QT22;R1GRJ7;A0A0C2W1L2;G4TF25;A0A093Y9V4;A0A093YJL0;A0A093Z3N9;A0A094AH57;A0A094BM92;A0A094C3X6;A0A094F2Y2;A0A094FF40;A0A094G5M1;A0A094GXE3;A0A094H7L2;A0A094JUJ4;A0A094KSC4;L8FWE9;A0A0A1N2V7;A0A0A1NJG0;A0A0B7MWW2;A0A0C9LP64;S2K167;I1BUQ1;I1BX71;W6MG82	>tr A0A086TMI4 A0A086TMI4_9FUNG 50S ribosomal protein L34e OS=Mortierella verticillata NRRL 6337 GN=MVEG_11198 PE=4 SV=1
A0A0H2RUL8;A0A067LUU1;A0A0J0XUK7;A0A060SBH6;A0A066WD85;A0A074S3D9;A0A0B7FGP4;A0A0C9N2R4;A0A0C9SLC5;A0A0K6GBT4;B8P796;J4I3S1;K5X6R0;R9AK74;X8JNV0;S2J264;A0A0A1NGP5;A0A0C7C221	>tr A0A0H2RUL8 A0A0H2RUL8_9HOMO Cytochrome c OS=Schizopora paradoxa GN=SCHPADRAFT_849824 PE=3 SV=1;>tr A0A067LUU1 A0A067LUU1_9HOMO Uncharacterized protein OS=Botryobasidium botryosum FD-172 SS1 GN=BOTBODRAFT_167354 PE=3 SV=1;>tr A0A0J0XUK7 A0A0J0XUK7_9TREE
A0A063BZZ2	>tr A0A063BZZ2 A0A063BZZ2_9HYPO 40S ribosomal protein S20 OS=Ustilagoidea virens GN=UV8b_5416 PE=3 SV=1
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A0A086SUB5	>tr A0A086SUB5 A0A086SUB5_ACRCH Cytochrome c-like protein OS=Acremonium chrysogenum ATCC 11550 GN=ACRE_086030 PE=3 SV=1
A0A086TLA8	>tr A0A086TLA8 A0A086TLA8_9FUNG NADH dehydrogenase (Ubiquinone) Fe-S protein 5 OS=Mortierella verticillata NRRL 6337 GN=MVEG_11262 PE=4 SV=1
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L7PA84	>tr L7PA84 L7PA84_MORAP 4a-hydroxytetrahydrobiopterin dehydratase OS=Mortierella alpina PE=2 SV=1
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P56301	>tr P56301 P56301 · PSAC_CHLVU Putative uncharacterized protein OS=Chlorella vulgaris (Green alga) GN=psaC PE=4 SV=1
A0A063CBC0	>tr A0A063CBC0 A0A063CBC0_9HYPO Uncharacterized protein OS=Ustilagoidea virens GN=UV8b_163 PE=4 SV=1

A0A086TM47	>tr A0A086TM47 A0A086TM47_9FUNG 40S ribosomal protein S28 OS=Mortierella verticillata NRRL 6337 GN=MVEG_11062 PE=4 SV=1
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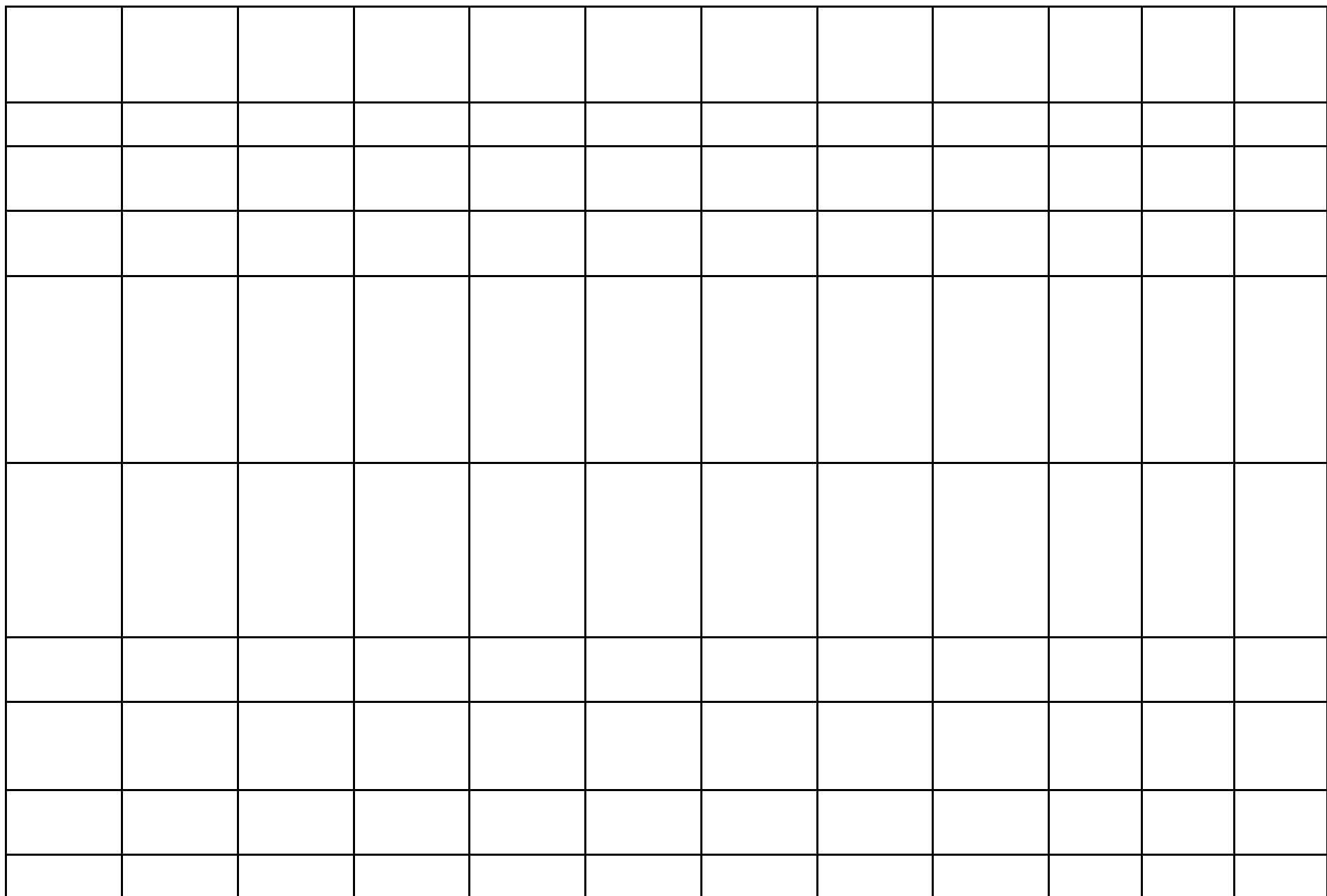
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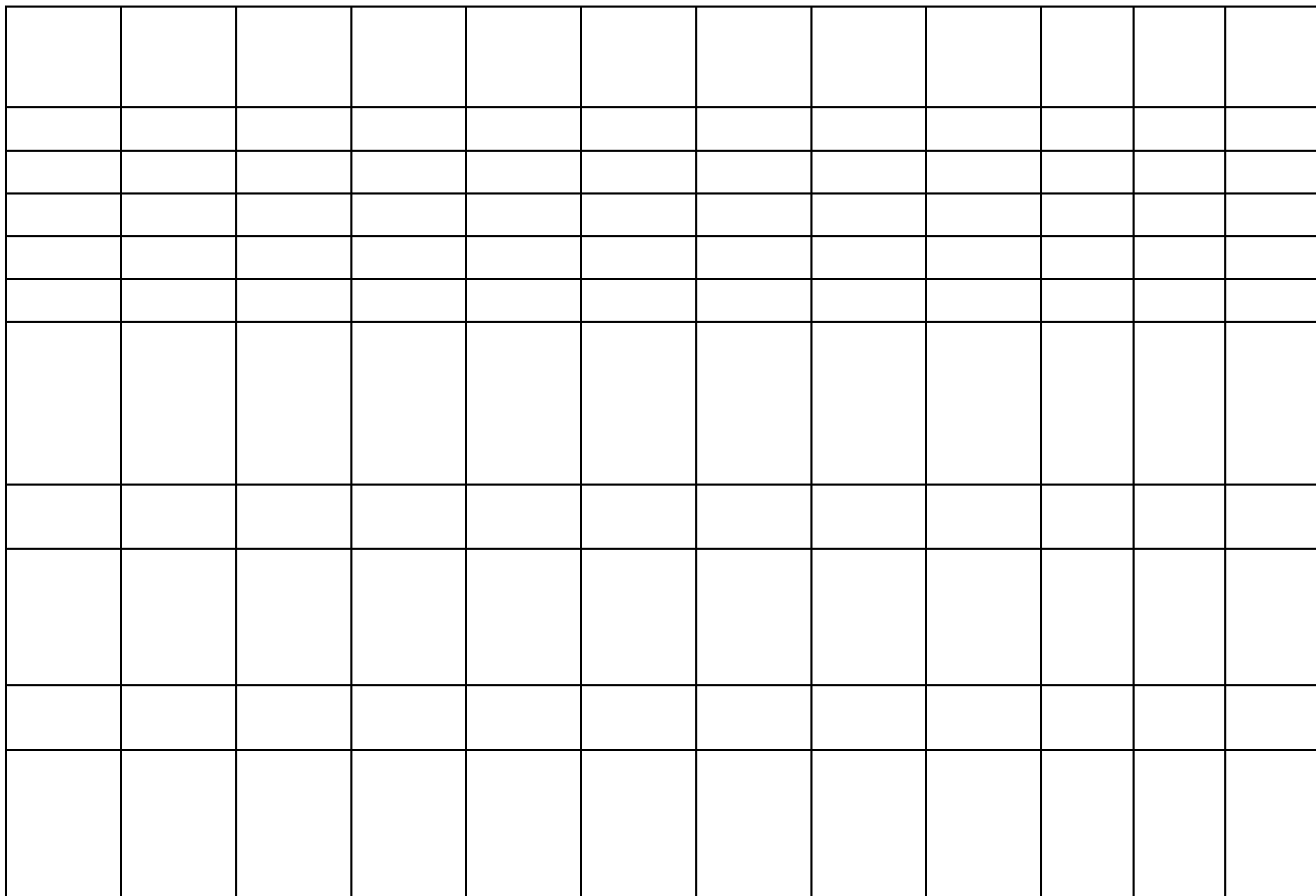


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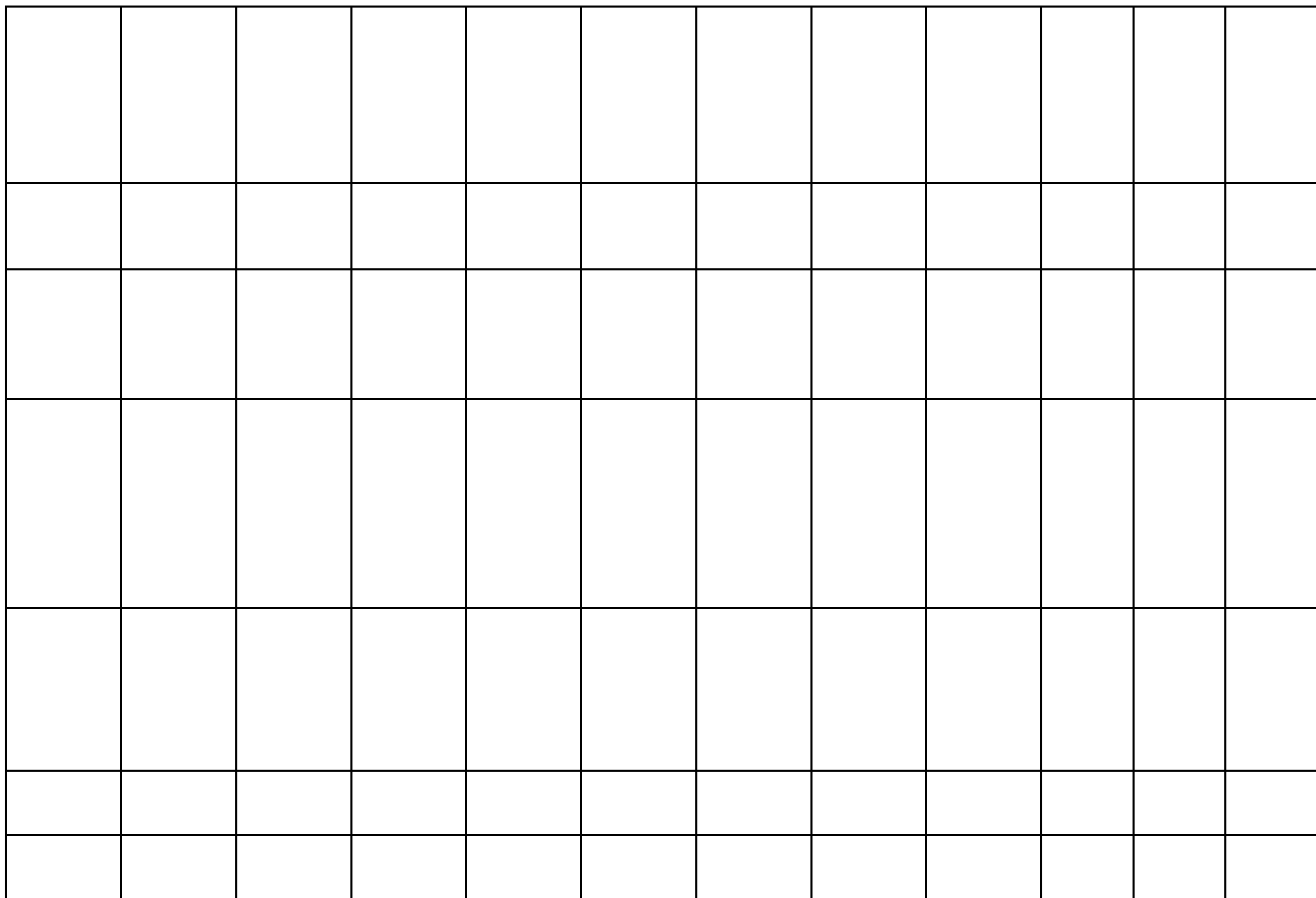


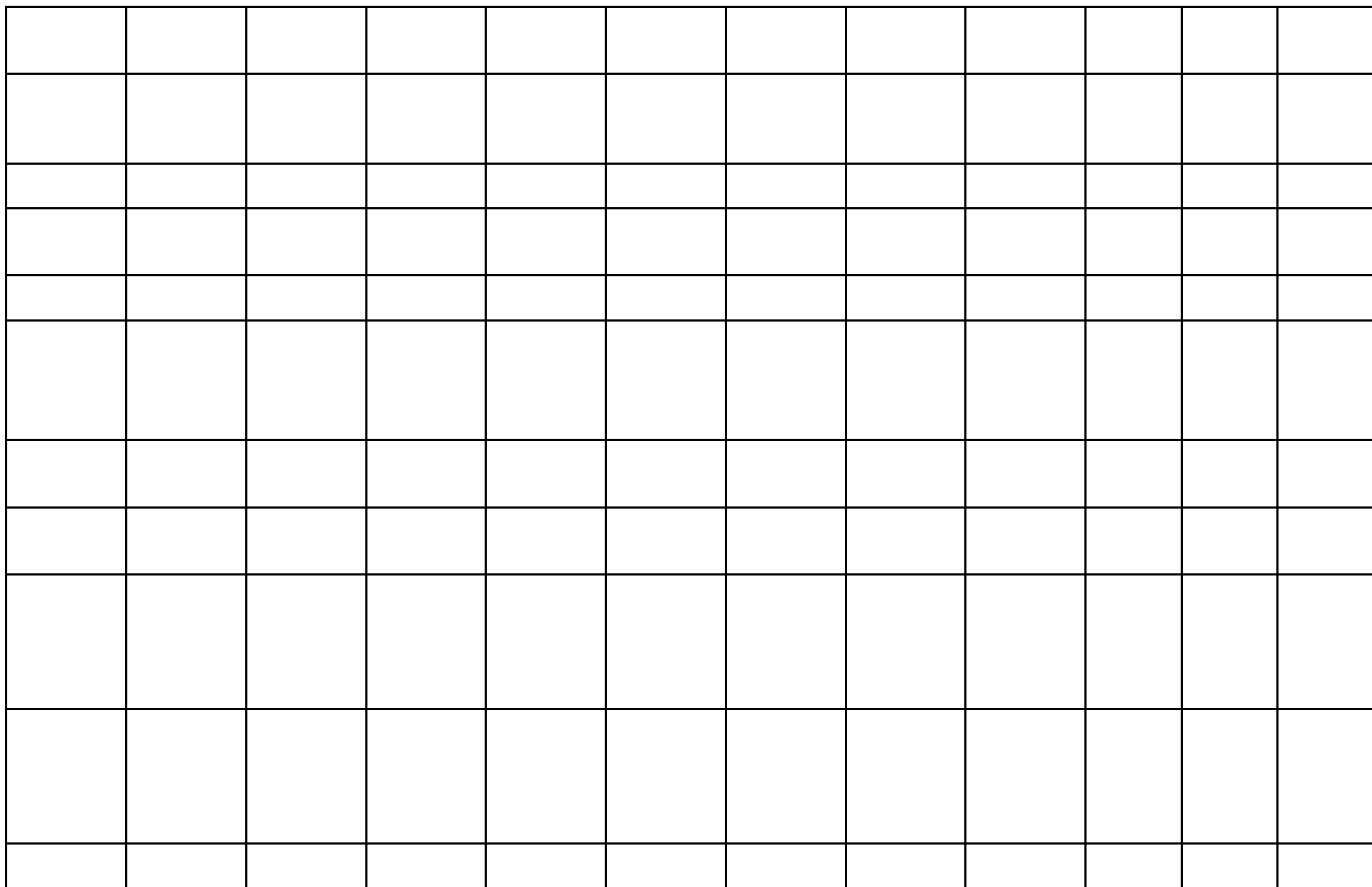
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