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| --- | --- | --- | --- | --- |
| n | Protein name | Enriched GO terms | GO term coverage | GO type |
| 5 | GSC1 YWP1 PMA1 SAP9 ECM33 | Adhesion of symbiont to host  Fungal-type cell wall organisation  Pathogenesis  Cell wall  Plasma membrane  1,3-beta-D-glucan synthase activity | 3/48  3/108  3/350  3/75  4/324  1/4 | BP  BP  BP  CC  CC  MF |
| 35  (36a) | CDR1;CDR2 SUR7 HGT6 orf19.1152 YCP4 VPS21 UBC4 SEC4 orf19.5006.1 GPX2 ACC1 ERO1 VMA5 URA2 orf19.1054  CHC1 VMA13 TPD3 PEP1 FET34  VPH1 MLT1 YKT6 VAC8 orf19.6066  YPT31 ARF3 GAP4 YVC1 orf19.3983  RAC1 MNT1 VMA6 PHR1 NCE102 | Azole transport  ATP hydrolysis coupled proton transport  Pathogenesis  Plasma membrane  Membrane raft  Fungal-type vacuole membrane  Eisosome  Golgi apparatus  Phospholipid transporter activity  GTP binding | 2/2  3/13  8/350  13/324  4/10  3/5  2/4  3/56  2/3  4/83 | BP  BP  BP  CC  CC  CC  CC  CC  MF  MF |
| 17 | GDH3 ATP3 ATP7 QCR2 ATP4  orf19.3859 orf19.2168.3 SEC61 ERV29 SEC18 orf19.1564 orf19.6882.1 SDH12 EMP70 YPT1 orf19.6264.3 VPS1 | ATP synthesis coupled proton transport  Fatty acid elongation  Plasma membrane  Mitochondrial H+-transporting ATP synthase F(0)  Endoplasmic reticulum  H+ transmembrane transporter activity  GTP binding | 3/12  1/1  7/324  2/6  3/93  2/12  2/83 | BP  BP  CC  CC  CC  MF  MF |
| 41 | LHS1 RIP1 SSO2 ERG6 YCK2 CHS3 MYO2 RHO1 MIR1 PET9 QCR7 FAA4 COX5 COX2 MTS1 COX9 ALO1 PHB2 CBR1 GPD2 CYT1 TOM70 orf19.4016 POR1 SEC14 orf19.86 GFA1 NIP1 KAR2 orf19.3799 orf19.1833 TIF orf19.2489 orf19.6883 NOP5 HET1 orf19.1229 CRM1 BGL2 HGT7 PHR2 | Hyphal growth  Cell wall chitin biosynthetic process  Pathogenesis  Plasma membrane  Mitochondrion  Cellular bud tip  1,3-beta-glucanosyltransferase activity  Cytochrome-C oxidase activity  Ran GTPase binding | 5/75  2/7  7/350  17/324  7/175  2/12  2/6  2/7  2/10 | BP  BP  BP  CC  CC  CC  MF  MF  MF |
| 295 | See supplementary file | Translation  Glycolytic process (13/20)  Induction by symbiont of host defence response  Cytoplasm  Cell surface  Ribosome  Nucleotide binding  ATP binding  Aminoacyl ligase activity | 45/128  13/20  12/24  89/393  45/129  33/84  78/490  70/473  16/35 | BP  BP  BP  CC  CC  CC  MF  MF  MF |
| 12 | CDC42 CRH11 ENA21 HGT1 MP65  MSB2 orf19.6741 PGA4 PGA52 PHM7 PLB4.5 RHO3 | Fungal-type cell wall organisation  Establishment of cell polarity  Pathogenesis  Plasma membrane  Extracellular region  Cell wall  Hydrolase activity, O-glycosyl compounds  GTP binding | 4/108  2/8  4/350  6/324  4/134  3/75  2/29  2/83 | BP  BP  BP  CC  CC  CC  MF  MF |