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| --- | --- | --- | --- | --- |
| n | Protein name | Enriched GO terms | GO term coverage | GO type |
| 17  (18a) | CDR1;CDR2 SUR7 FET34 HGT6 PMA1 GSC1 PHR1 RAC1 NCE102 ARF3 YKT6 GAP4 VAC8 RHO1 MNT1 VPH1 PEP1 | Azole transport  Fungal-type cell wall organisation  Small GTPase mediated signal transduction  Pathogenesis  Plasma membrane  Eisosome  Cell surface  Golgi apparatus  Phospholipid transporter activity  GTP binding | 2/2  5/108  3/37  6/350  13/324  2/4  4/129  3/56  2/3  3/83 | BP  BP  BP  BP  CC  CC  CC  CC  MF  MF |
| 21 | MLT1 YCP4 orf19.5006.1 VMA5 CBR1 ERV29 COX2 COX5 FAA4 ALO1 ERV25 ATP4 QCR2 ATP3 ATP7 GDH3 EMP70 URA6 VPS1 SAH1 GPD1 | ATP synthesis coupled proton transport  Oxidation-reduction process  Hydrogen ion transmembrane transport  Plasma membrane  Mitochondrion  Cytochrome-c oxidase activity  Oxidoreductase activity | 3/12  7/407  2/11  10/324  4/175  2/7  6/309 | BP  BP  BP  CC  CC  MF  MF |
| 20 | BGL2 ECM33 PHR2 HGT7 CHS3 MIR1 PHB2 YCK2 MYO2 ERG6 PET9 POR1 CYT1 orf19.4016 SSO2 COX9 TOM70 QCR7 RIP1 LHS1 | Fungal-type cell wall organisation  Hyphal growth  Cell morphogenesis  Transmembrane transport  Plasma membrane  Yeast-form cell wall  Mitochondrion  1,3-beta-glucanosyltransferase activity  Transporter activity | 4/108  3/75  2/20  4/232  13/324  3/44  4/175  2/6  2/46 | BP  BP  BP  BP  CC  CC  CC  MF  MF |
| 38 | YWP1 orf19.3859 orf19.1054 ERO1 orf19.2168.3 SEC61 MTS1 SEC4 YPT31  UBC4 GPD2 orf19.3335 VPS21 NOP5  HET1 CRM1 orf19.1229 orf19.6264.3  orf19.2489 TIF orf19.1833 orf19.3799  NIP1 GFA1 KAR2 orf19.6883 orf19.86  SEC14 DHH1 ACC1 CHC1 VMA13 YPT1 SEC21 URA2 TPD3 SEC18 orf19.1564 | Protein transport  Small GTPase mediated signal transduction  ER to Golgi vesicle-mediated transport  Cytoplasmic vesicle  Plasma membrane  Cytoplasm  Endoplasmic reticulum  Structural molecule activity  GTP binding | 6/113  3/37  2/17  3/18  6/324  6/393  3/93  2/11  3/83 | BP  BP  BP  CC  CC  CC  CC  MF  MF |
| 287  (293a) | See supplemental Table S5 | Translation  Glycolytic process  Induction by symbiont of host defen response  Cytoplasm  Cell surface  Ribosome  Nucleotide binding  Aminoacyl-tRNA ligase activity | 47/128  15/20  12/24  87/393  48/129  33/84  80/490  16/35 | BP  BP  BP  CC  CC  CC  MF  MF |
| 13 | CDC42 CRH11 ENA21 HGT1 MP65 MSB2 orf19.6741 PGA4 PGA52 PHM7  PLB4.5 RHO3 SAP9 | Fungal-type cell wall organisation  Establishment of cell polarity  Pathogenesis  Plasma membrane  Extracellular region  Cell wall  Hydrolase activity, O-glycosyl compounds  GTP binding | 5/108  2/8  5/350  7/324  5/134  4/75  2/29  2/83 | BP  BP  BP  CC  CC  CC  MF  MF |