<table>
<thead>
<tr>
<th>Protein Name/Gene/Sequence ID</th>
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<tbody>
<tr>
<td>PAB-dependent poly(A)-specific ribonuclease subunit PAN2 (PAN2_PICGU) A5DAD0</td>
<td>H</td>
<td></td>
<td>Catalytic subunit of the poly(A)-nuclease (PAN) deadenylation complex involved in cytoplasmic mRNA turnover. PAN specifically shortens poly(A) tails of RNA when the poly(A) stretch is bound by polyadenylate-binding protein PAB1. Deadenylation of the 3'-tail to a length that is too short to bind PAB1 induces mRNA decay. May also be involved in post-transcriptional maturation of mRNA poly(A) tails</td>
<td>Candida guilliermondii</td>
</tr>
<tr>
<td>pH-responsive protein 2 (PPHR2_CANAL) O13318</td>
<td>H</td>
<td></td>
<td>Required for apical cell growth and plays an essential role in morphogenesis. May be integral to the pathogenic ability of the organism</td>
<td>Candida albicans</td>
</tr>
<tr>
<td>Palmitoyltransferase PFA4 (PFA4_YARLI) Q6C7Q0</td>
<td>H</td>
<td></td>
<td>Involves fatty acid transport and synthesis</td>
<td>Candida lipolytica</td>
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## Nonhuman-originating proteins exhibiting higher expression

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<tr>
<td>Mediator of RNA polymerase II transcription subunit 14 (MED14_CANAL) Q5AG31</td>
<td>SII</td>
<td></td>
<td>Component of the Mediator complex, a coactivator involved in the regulated transcription of nearly all RNA polymerase II-dependent genes. Mediator functions as a bridge to convey information from gene-specific regulatory proteins to the basal RNA polymerase II transcription machinery. Mediator is recruited to promoters by direct interactions with regulatory proteins and serves as a scaffold for the assembly of a functional preinitiation complex with RNA polymerase II and the general transcription factors</td>
<td>Candida albicans</td>
</tr>
<tr>
<td>Pre-mRNA-splicing factor SLU7 (SLU7_CANGA) Q6FRY5</td>
<td>SII</td>
<td></td>
<td>Involved in pre-mRNA splicing</td>
<td>Candida glabrata</td>
</tr>
<tr>
<td>Acyl-coenzyme A oxidase 4 (ACOX4_CANTR) P06598</td>
<td>SII, SIII</td>
<td></td>
<td>Involved in lipid metabolism and beta oxidation.</td>
<td>Candida tropicalis</td>
</tr>
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<tr>
<td>Myosin-1 (MYO1_PICGU A5DKH0)</td>
<td>SIII</td>
<td></td>
<td>Type-I myosin implicated in the organization of the actin cytoskeleton. Required for proper actin cytoskeleton polarization. At the cell cortex, assembles in patch-like structures together with proteins from the actin-polymerizing machinery and promotes actin assembly. Functions as actin nucleation-promoting factor (NPF) for the Arp2/3 complex</td>
<td>Candida guilliermondii</td>
</tr>
<tr>
<td>Helicase SWR1 (SWR1_YARLI Q6CA87)</td>
<td>SIII</td>
<td></td>
<td>Catalytic component of the SWR1 complex which mediates the ATP-dependent exchange of histone H2A for the H2A variant HZT1 leading to transcriptional regulation of selected genes by chromatin remodeling</td>
<td>Candida lipolytica</td>
</tr>
<tr>
<td>Protein CGI121 (CG121_CANG A) Q6FV72</td>
<td>SIII</td>
<td></td>
<td>Component of the EKC/KEOPS complex which promotes both telomere uncapping and telomere elongation By similarity. The complex is required for efficient recruitment of transcriptional coactivators</td>
<td>Candida glabrata</td>
</tr>
<tr>
<td>Stress response protein NST1 (NST1_LODEL A5DXA0)</td>
<td>H, SII</td>
<td></td>
<td>May act as a negative regulator of salt tolerance</td>
<td>Saccharomyces elongisporous</td>
</tr>
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<tr>
<td>Ubiquitin-conjugating enzyme E2 2 (UBC2_CANGA) Q6FR76</td>
<td>H, SII</td>
<td>Catalyzes the covalent attachment of ubiquitin to other proteins. Plays a role in transcription regulation by catalyzing the monoubiquitination of histone H2B to form H2BK123ub1. H2BK123ub1 gives a specific tag for epigenetic transcriptional activation and is also a prerequisite for H3K4me and H3K79me formation. Also involved in postreplication repair of UV-damaged DNA, in N-end rule-dependent protein degradation and in sporulation</td>
<td>Candida glabrata</td>
<td></td>
</tr>
<tr>
<td>Transcription elongation factor SPT5 (SPT5_CANGA) Q6FRZ5</td>
<td>H, SII</td>
<td>The SPT4-SPT5 complex mediates both activation and inhibition of transcription elongation, and plays a role in pre-mRNA processing. This complex seems to be important for the stability of the RNA polymerase II elongation machinery on the chromatin template but not for the inherent ability of this machinery to translocate down the gene</td>
<td>Candida glabrata</td>
<td></td>
</tr>
<tr>
<td>Golgi apparatus membrane protein TVP38 (TVP38_CANGA) Q6FTI0</td>
<td>H, SII</td>
<td>Golgi membrane protein involved in vesicular trafficking and spindle migration.</td>
<td>Candida glabrata</td>
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<tr>
<td>Enolase (ENO2_CANGA) Q6FQYA, (ENO_KRULA) Q70CP7</td>
<td>H, SIII</td>
<td>Involved in glycolysis.</td>
<td>Candida glabrata, Candida sphaerica</td>
<td></td>
</tr>
<tr>
<td>SWR1-complex protein 4 (SWC4_CANGA) Q6FTV1</td>
<td>H, SIII</td>
<td>Component of the SWR1 complex which mediates the ATP-dependent exchange of histone H2A for the H2A variant HZT1 leading to transcriptional regulation of selected genes by chromatin remodeling. Component of the NuA4 histone acetyltransferase complex which is involved in transcriptional activation of selected genes principally by acetylation of nucleosomal histone H4 and H2A. The NuA4 complex is also involved in DNA repair</td>
<td>Candida glabrata</td>
<td></td>
</tr>
<tr>
<td>ATP-dependent RNA helicase DRS1 (DRS1_KRULA) Q6CJV1</td>
<td>SII</td>
<td>ATP-binding RNA helicase involved in ribosome assembly</td>
<td>Candida sphaerica</td>
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<tr>
<td>Bud site selection protein BUD4 (BUD4_CANAL) P53705</td>
<td></td>
<td>SIII</td>
<td>Required for establishment of the axial budding pattern in yeast cells. May be involved in the selection of future sites of septation in hyphal cells. Contributes to morphogenesis and is important for induction of hyphal growth. Also plays a role in epithelial adherence, and is involved in intestinal colonization and systemic infection. The role in adhesion is probably minor compared with its role in morphogenesis.</td>
<td>Candida albicans</td>
</tr>
<tr>
<td>Ubiquitin-conjugating enzyme E2 2 (UBC2_KRULA) Q6CUD9</td>
<td></td>
<td>SIII</td>
<td>Catalyzes the covalent attachment of ubiquitin to other proteins. Plays a role in transcription regulation by catalyzing the monoubiquitination of histone H2B to form H2BK123ub1. H2BK123ub1 gives a specific tag for epigenetic transcriptional activation and is also a prerequisite for H3K4me and H3K79me formation. Also involved in postreplication repair of UV-damaged DNA, in N-end rule-dependent protein degradation and in sporulation</td>
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<td>Myosin-1 (MYO1_KRULA) Q6CVE9</td>
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<td>SIII</td>
<td>Type-I myosin implicated in the organization of the actin cytoskeleton. Required for proper actin cytoskeleton polarization. At the cell cortex, assembles in patch-like structures together with proteins from the actin-polymerizing machinery and promotes actin assembly. Functions as actin nucleation-promoting factor (NPF) for the Arp2/3 complex</td>
<td>Candida sphaerica</td>
</tr>
<tr>
<td>Serine/threonine-e-protein kinase PTK2 (PTK2_CANGA) Q6FRE7</td>
<td></td>
<td>SIII</td>
<td>ATP binding protein</td>
<td>Candida glabrata</td>
</tr>
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H = healthy; SII = Stomatitis type II; SIII = Stomatitis type III  
W = Waters Synapt System; T = Thermo Orbi System  
ANOVA cutoff range p < 0.01. All function information presented is obtained from UniProt Protein Database, except for protein information indicated as referenced from an additional source.