

**Additional file 10. *Saccharomyces cerevisiae* protein having SILK/PP1 interaction domain**

| S.No. | Accession Number | Protein                                                                                                                                                                                                                                                 | SILK motif    | Protein length | Motif length | Position |
|-------|------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------|----------------|--------------|----------|
| 1     | NP_010383.1      | Hydroperoxide and superoxide-radical responsive glutathione-dependent oxidoreductase; monothiol glutaredoxin subfamily member along with Grx4p and Grx5p; protects cells from oxidative damage; Grx3p                                                   | GILR(1)HQVRF  | 285            | 10           | 219-229  |
| 2     | NP_010188.1      | Protein O-mannosyltransferase, transfers mannanose residues from dolichyl phosphate-D-mannose to protein serine/threonine residues; acts in a complex with Pmt2p, can instead interact with Pmt3p in some conditions; target for new antifungals; Pmt1p | PILK(2)KVVNF  | 817            | 11           | 616-627  |
| 3     | NP_012664.1      | Cystathionine gamma-synthase, converts cysteine into cystathionine; Str2p                                                                                                                                                                               | KTVMF(8)SILR  | 639            | 17           | 339-356  |
| 4     | NP_683715.1      | Protein involved in bud-site selection, nutrient signaling, and gene expression controlled by the TOR kinase; diploid mutants display a random budding pattern instead of the wild-type bipolar pattern; Bud27p                                         | PILK(14)KQVGF | 796            | 23           | 322-345  |
| 5     | NP_014872.1      | Transcriptional repressor involved in regulation of meiosis and silencing; contains WD repeats; Wtm2p                                                                                                                                                   | SILK(23)HSVRF | 467            | 32           | 223-255  |
| 6     | NP_012485.1      | Dead-box family ATP dependent helicase required for mRNA export from the nucleus; co-factor of the exosome complex, required for 3' end formation of 5.8S rRNA;                                                                                         | PILK(29)KTVVF | 1073           | 38           | 481-519  |

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|    |             | Mtr4p                                                                                                                                                                                                                                                   |               |      |    |           |
| 7  | NP_012192.2 | Meiosis-specific protein essential for chromosome synapsis, similar to phospholipase A2, involved in completion of nuclear divisions during meiosis; induced early in meiosis; Spo22p                                                                   | SILR(30)KAVEF | 975  | 39 | 604-643   |
| 8  | NP_009545.1 | Non-essential transcriptional corepressor involved in the cell cycle-regulated transcription of histone H2A, H2B, H3 and H4 genes; contributes to nucleosome formation, heterochromatic gene silencing, and formation of functional kinetochores; Hir1p | KVVKF(41)SILR | 840  | 50 | 2-52      |
| 9  | NP_011422.1 | Protein required for accurate chromosome segregation, localizes to the nuclear side of the spindle pole body; forms a complex with Ydr532cp; Spc105p                                                                                                    | GILK(49)RRVSF | 917  | 58 | 21-79     |
| 10 | NP_010378.1 | Aminophospholipid translocase (flippase) that localizes primarily to the plasma membrane; contributes to endocytosis, protein transport and cell polarity; type 4 P-type ATPase; Dnf2p                                                                  | KNVIF(60)GILR | 1612 | 69 | 1237-1306 |
| 11 | NP_009601.1 | Meiosis-specific regulatory subunit of the Glc7p protein phosphatase, regulates spore wall formation and septin organization, required for expression of some late meiotic genes and for normal localization of Glc7p; Gip1p                            | RCVNF(76)SILK | 573  | 85 | 444-529   |
| 12 | NP_012954.1 | Defining member of the SET3 histone deacetylase                                                                                                                                                                                                         | RRVIF(79)PILK | 751  | 88 | 378-466   |

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|    |             | complex which is a meiosis-specific repressor of sporulation genes; necessary for efficient transcription by RNAPII; one of two yeast proteins that contains both SET and PHD domains; Set3p                                                           |                |      |     |         |
| 13 | NP_012036.1 | Subunit of the anaphase-promoting complex/cyclosome (APC/C), which is a ubiquitin-protein ligase required for degradation of anaphase inhibitors, including mitotic cyclins, during the metaphase/anaphase transition; Cdc23p                          | RCVFF(81)SILK  | 626  | 90  | 103-193 |
| 14 | NP_012160.2 | Component of the mitotic exit network; associates with and is required for the activation and Cdc15p-dependent phosphorylation of the Dbf2p kinase; required for cytokinesis and cell separation; component of the CCR4 transcriptional complex; Mob1p | HCVDF(85)PILR  | 314  | 94  | 160-254 |
| 15 | NP_009385.1 | One of two (see also PSK2) PAS domain containing S/T protein kinases; coordinately regulates protein synthesis and carbohydrate metabolism and storage in response to a unknown metabolite that reflects nutritional status; Psk1p                     | KSVKF(100)SILK | 1356 | 109 | 662-771 |
| 16 | NP_010256.1 | Dual-specificity kinase required for spindle pole body (SPB) duplication and spindle checkpoint function; substrates include SPB proteins Spc42p, Spc110p, and Spc98p, mitotic exit                                                                    | KRVSF(101)GILK | 764  | 110 | 468-578 |

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|----|-------------|------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------|------|-----|-----------|
|    |             | network protein Mob1p, and checkpoint protein Mad1p; Mps1p                                                                                                                                                                                           |                |      |     |           |
| 17 | NP_009834.1 | Protein that binds to the Rap1p C-terminus and acts synergistically with Rif2p to help control telomere length and establish telomeric silencing; deletion results in telomere elongation; Rif1p                                                     | KSVAF(103)GILR | 1916 | 112 | 114-226   |
| 18 | NP_012906.1 | Alpha subunit of both the farnesyltransferase and type I geranylgeranyltransferase that catalyze prenylation of proteins containing a CAAX consensus motif; essential protein required for membrane localization of Ras proteins and a-factor; Ram2p | PILK(105)KVVDV | 316  | 114 | 131-245   |
| 19 | NP_013534.1 | Presumed helicase required for RNA polymerase II transcription termination and processing of RNAs; homolog of Senataxin which causes Ataxia-Oculomotor Apraxia 2 and a dominant form of amyotrophic lateral sclerosis; Sen1p                         | SILR(125)KHVCF | 2231 | 134 | 1870-2004 |
| 20 | NP_010132.1 | Transmembrane protein involved in formation of Cvt and autophagic vesicles; cycles between the pre-autophagosomal structure and other cytosolic punctate structures, not found in autophagosomes; Atg9p                                              | SILK(135)RSVIF | 997  | 144 | 517-661   |
| 21 | NP_012408.1 | Putative histone acetylase, sequence-specific activator of histone genes, binds specifically and highly cooperatively to pairs of UAS elements in core histone promoters,                                                                            | KNVWF(146)GILK | 640  | 155 | 100-255   |

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|    |             | functions at or near the TATA box; Spt10p                                                                                                                                                                                                              |                 |      |     |         |
| 22 | NP_010950.1 | Protein of unknown function; authentic, non-tagged protein is detected in highly purified mitochondria in high-throughput studies; GFP-fusion protein is localized to the cytoplasm; transcription induced under conditions of zinc deficiency; Zrg8p  | SILR(162)KTVTF  | 1076 | 171 | 800-971 |
| 23 | NP_011733.1 | Voltage-gated high-affinity calcium channel involved in calcium influx in response to some environmental stresses as well as exposure to mating pheromones; interacts and co-localizes with Mid1p, suggesting Cch1p and Mid1p function together; Cch1p | HNVVVF(171)SILR | 2039 | 180 | 369-549 |
| 24 | NP_012379.1 | Probable serine protease of the SPS plasma membrane amino acid sensor system (Ssy1p-Ptr3p-Ssy5p), which senses external amino acid concentration and transmits intracellular signals that regulate expression of amino acid permease genes; Ssy5p      | RAVSF(204)PILR  | 687  | 213 | 121-334 |
| 25 | NP_012030.1 | Peroxin required for targeting of peroxisomal matrix proteins containing PTS2; interacts with Pex7p; partially redundant with Pex21p; Pex18p                                                                                                           | PILK(211)KHVGF  | 283  | 220 | 43-263  |
| 26 | NP_010942.1 | Gamma subunit of the translation initiation factor eIF2, involved in the identification of the start codon; binds GTP when forming the ternary complex with GTP and                                                                                    | KKVAF(213)SILK  | 527  | 222 | 47-269  |

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|    |             | tRNAi-Met; Gcd11p                                                                                                                                                                                                                          |                |      |     |         |
| 27 | NP_010954.1 | Protein of unknown function, expression is induced by low phosphate levels and by inactivation of Pho85p; Phm8p                                                                                                                            | RKVFF(215)SILK | 321  | 224 | 52-276  |
| 28 | NP_010806.1 | Protein disulfide isomerase of the endoplasmic reticulum lumen, function overlaps with that of Pdi1p; may interact with nascent polypeptides in the ER; Eug1p                                                                              | SILK(218)HHVRF | 517  | 227 | 77-304  |
| 29 | NP_012267.1 | Member of the DEAH family of helicases, functions in an error-free DNA damage bypass pathway that involves homologous recombination, mutations confer a mutator phenotype; Mph1p                                                           | KRVFF(223)PILK | 993  | 232 | 179-411 |
| 30 | NP_014759.1 | RNA polymerase III subunit C160, part of core enzyme; similar to bacterial beta-prime subunit; Rpo31p                                                                                                                                      | GILK(228)KRVDF | 1460 | 237 | 139-376 |
| 31 | NP_014579.1 | Mu2-like subunit of the clathrin associated protein complex (AP-2); involved in vesicle transport; Apm4p                                                                                                                                   | SILK(240)RAVKW | 491  | 249 | 229-478 |
| 32 | NP_013529.1 | Guanine nucleotide exchange factor (GEF) that functions to modulate Rho1p activity as part of the cell integrity signaling pathway; multicopy suppressor of tor2 mutation and ypk1 ypk2 double mutation; potential Cdc28p substrate; Tus1p | KAVRF(250)SILK | 1307 | 259 | 370-629 |
| 33 | NP_014864.2 | Predicted malonyl-CoA:ACP transferase, putative component of a type-II mitochondrial fatty acid synthase that                                                                                                                              | SILK(275)RTVQF | 360  | 284 | 16-300  |

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|    |             | produces intermediates for phospholipid remodeling; Mct1p                                                                                                   |                |     |     |         |
| 34 | NP_013496.1 | Putative protein of unknown function; green fluorescent protein (GFP)-fusion protein localizes to the cytoplasm; YLR392C is not an essential gene; Ylr392cp | KTVAF(297)PILR | 518 | 306 | 132-438 |

The NCBI accession Number, protein name, SILK/PP1 interaction domain, protein size, domain length and the position of the motif for the proteins having SILK/PP1 interaction domain are listed in the table. The combination of [SPG]IL[KR] followed by [HKR][ACHKMNRSTV]VX[FW] motif and also the [HKR][ACHKMNRSTV]VX[FW] followed by [SPG]IL[KR] with the occurrence of up to 300 amino acids in between the motifs were searched in the yeast protein sequences.