

| C | DIP ID | Description of the proteins | Molecular function |
|---|-----------|---|--|
| 1 | DIP:3028N | ATP synthase beta chain, mitochondrial precursor | Components of mitochondrial ATPase complex |
| | DIP:3033N | ATP synthase f chain, mitochondrial precursor | |
| | DIP:3034N | ATP synthase J chain, mitochondrial | |
| | DIP:3038N | ATPase subunit 6 | |
| | DIP:3039N | ATP synthase D chain, mitochondrial | |
| 2 | DIP:1966N | Elp6 protein | RNA polymerase II transcription elongation factor activity |
| | DIP:2384N | IKI3 protein | |
| | DIP:2385N | Elp3 protein | |
| | DIP:2386N | Elp2 protein | |
| | DIP:6718N | Elp4 protein | |
| 3 | DIP:4409N | Vacuolar biogenesis protein END1 | Involved in vacuolar biogenesis, vacuolar protein sorting, endocytosis |
| | DIP:5910N | Vacuolar protein-sorting protein VPS33 | |
| | DIP:5912N | Vacuolar membrane protein PEP3 | |
| | DIP:6298N | Vacuolar protein sorting-associated protein VPS8 | |
| | DIP:6691N | Vacuolar protein sorting-associated protein VPS16 | |
| 4 | DIP:2285N | Origin recognition complex subunit 2 | Components of origin recognition complex (ORC) |
| | DIP:2286N | Origin recognition complex subunit 3 | |
| | DIP:2287N | Origin recognition complex subunit 4 | |
| | DIP:2288N | Origin recognition complex subunit 5 | |
| | DIP:2289N | Origin recognition complex subunit 6 | |
| 5 | DIP:2454N | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase alpha subunit precursor | Subunits of N-oligosaccharyl transferase enzyme |
| | DIP:2456N | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase gamma subunit precursor | |
| | DIP:2457N | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 4 kDa subunit | |
| | DIP:2458N | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase zeta subunit | |
| | DIP:2460N | Dolichyl-diphosphooligosaccharide-protein glycosyltransferase delta subunit precursor | |

Table 1: Annotations of the 5-cliques in *S. cerevisiae* PPI network (1)

| C | DIP ID | Description of the proteins | Molecular function |
|----|-----------|--|--|
| 6 | DIP:939N | Anaphase promoting complex subunit 2 | Components of anaphase promoting complex/cyclosome (APC/C) |
| | DIP:1127N | Anaphase promoting complex subunit 5 | |
| | DIP:1128N | Anaphase promoting complex subunit DOC1 | |
| | DIP:1130N | Anaphase promoting complex subunit 11 | |
| | DIP:1132N | Anaphase promoting complex subunit 4 | |
| 7 | DIP:2096N | Vacuolar protein sorting protein 51 | Involved in retrograde transport from early and late endosomes to late Golgi |
| | DIP:3967N | Vacuolar protein sorting protein 52 | |
| | DIP:5577N | GTP-binding protein YPT6 | |
| | DIP:5902N | Vacuolar protein sorting protein 53 | |
| | DIP:5903N | Vacuolar protein sorting protein 54 | |
| 8 | DIP:2355N | Exosome complex exonuclease RRP44 | Components of the exosome 3'->5' exoribonuclease complex |
| | DIP:5485N | Exosome complex exonuclease RRP43 | |
| | DIP:5888N | Exosome complex exonuclease RRP4 | |
| | DIP:6785N | 3'-5' exoribonuclease CSL4 | |
| | DIP:6838N | Exosome complex exonuclease RRP46 | |
| 9 | DIP:2749N | NAM8 protein | Involved mRNA binding, nuclear mRNA splicing, via spliceosome |
| | DIP:3003N | EXM2 protein | |
| | DIP:5507N | Hypothetical 71.4 kDa protein in SEC9-MSB2 intergenic region | |
| | DIP:6514N | Hypothetical protein | |
| | DIP:6661N | U1 small nuclear ribonucleoprotein C homolog | |
| 10 | DIP:1112N | Pre-mRNA splicing factor PRP19 | Involved in pre-mRNA splicing and cell cycle control |
| | DIP:1682N | Pre-mRNA splicing factor ISY1 | |
| | DIP:1681N | Pre-mRNA splicing factor SYF1 | |
| | DIP:1684N | Pre-mRNA splicing factor SYF2 | |
| | DIP:1685N | Pre-mRNA splicing factor CLF1 | |

Table 2: Annotations of the 5-cliques in *S. cerevisiae* PPI network (2)

| C | DIP ID | Description of the proteins | Molecular function |
|----|-----------|--|--|
| 11 | DIP:1753N | COMPASS component SWD1 | Components of COMPASS (Set1C) complex which specifically methylates Lys-4 of histone H3 and subsequently plays a role in telomere length maintenance |
| | DIP:1935N | COMPASS component BRE2 | |
| | DIP:2946N | COMPASS component SPP1 | |
| | DIP:6843N | COMPASS component SHG1 | |
| | DIP:4616N | Histone-lysine N-methyltransferase, H3 lysine-4 specific | |
| 12 | DIP:1435N | RNA polymerase II mediator complex protein MED7 | Component of the RNA polymerase II holoenzyme and the mediator of activation subcomplex |
| | DIP:1659N | RNA polymerase II mediator complex protein MED8 | |
| | DIP:2335N | MED2 protein | |
| | DIP:1658N | Suppressor of RNA polymerase B SRB5 | Transcription factors |
| | DIP:2334N | Transcription regulatory protein GAL11 | |
| 13 | DIP:774N | Transcriptional adapter 3 | Transcription regulator |
| | DIP:591N | General control protein GCN4 | |
| | DIP:925N | Transcription initiation factor TFIID subunit 9 | Component of the DNA-binding general transcription factor complex TFIID and the regulatory transcription complex SAGA |
| | DIP:981N | Transcription initiation factor TFIID subunit 6 | |
| | DIP:740N | Transcription initiation factor TFIID subunit 5 | |
| 14 | DIP:2101N | ARP2/3 complex 16 kDa subunit | Components of ARP2/3 complex implicated in the control of actin polymerization in cells |
| | DIP:2218N | ARP2/3 complex 21 kDa subunit | |
| | DIP:2219N | Probable ARP2/3 complex 41 kDa subunit | |
| | DIP:2304N | ARP2/3 complex 34 kDa subunit | |
| | DIP:2649N | Actin-like protein 3 | |
| 15 | DIP:2468N | L2946 protein | RNA binding, mRNA cleavage, mRNA polyadenylation |
| | DIP:2469N | Pre-tRNA processing protein PTA1 | |
| | DIP:4402N | Hypothetical 47.0 kDa protein in CYS4-PEM1 intergenic region | |
| | DIP:5816N | Hypothetical 53.1 kDa Trp-Asp repeats containing protein in HXT14-PHA2 intergenic region | |
| | DIP:6650N | Hypothetical 49.6 kDa protein in FBA1-TOA2 intergenic region | |

Table 3: Annotations of the 5-cliques in *S. cerevisiae* PPI network (3)

| C | DIP ID | Description of the proteins | Molecular function |
|----|-----------|--|--|
| 16 | DIP:202N | DNA-directed RNA polymerase III 36 kDa polypeptide | Components of DNA-dependent RNA polymerase |
| | DIP:1003N | DNA-directed RNA polymerase III 47 kDa polypeptide | |
| | DIP:612N | DNA-directed RNA polymerase III largest subunit | |
| | DIP:1414N | DNA-directed RNA polymerase III 25 kDa polypeptide | |
| | DIP:761N | Hypothetical 32.1 kDa protein in DBP7-GCN3 intergenic region | |
| 17 | DIP:1765N | Protein HOS4 | Components of the Set3C complex, which is required to repress early/middle sporulation genes during meiosis |
| | DIP:2082N | Potential DNA-binding protein SNT1 | |
| | DIP:5632N | SET domain protein 3 | |
| | DIP:6757N | NAD-dependent deacetylase HST1 | Histone deacetylase responsible for the deacetylation of lysine residues on the N-terminal part of the core histones (H2A, H2B, H3 and H4) |
| | DIP:6828N | Probable histone deacetylase HOS2 | |
| 18 | DIP:1150N | Transcription regulatory protein SNF2 | Involved in transcriptional activation |
| | DIP:2364N | Transcription regulatory protein SNF5 | |
| | DIP:2471N | Transcription regulatory protein SWI3 | HIR1 and HIR2 are repressors of histone gene transcription |
| | DIP:2365N | Histone transcription regulator 1 | |
| | DIP:2366N | Histone transcription regulator 2 | |
| 19 | DIP:1149N | RNA polymerase-associated protein 1 | Transcription factors |
| | DIP:2814N | CTR9 protein | Transcription initiation factors |
| | DIP:4065N | RTF1 protein | |
| | DIP:6621N | Transcription initiation protein SPT5 | |
| | DIP:4143N | LEO1 protein | RNA polymerase II transcription elongation factor activity |
| 20 | DIP:1704N | Eukaryotic translation initiation factor 3 RNA-binding subunit | Eukaryotic translation initiation factors which bind to the 40S ribosome and promote the binding of methionyl-tRNA _i and mRNA |
| | DIP:2519N | Eukaryotic translation initiation factor 3 90 kDa subunit | |
| | DIP:5870N | Eukaryotic translation initiation factor 3 110 kDa subunit | |
| | DIP:4532N | Possible eukaryotic translation initiation factor 3 30 kDa subunit | |
| | DIP:2303N | Eukaryotic translation initiation factor 5 | |

Table 4: Annotations of the 5-cliques in *S. cerevisiae* PPI network (4)

| C | DIP ID | Description of the proteins | Molecular function |
|----|-----------|---|---|
| 21 | DIP:5398N | U3 small nucleolar RNA-associated protein 7 | Involved in nucleolar processing of ribosomal RNA |
| | DIP:6479N | U3 small nucleolar RNA-associated protein 6 | |
| | DIP:1868N | Periodic tryptophan protein 2 | |
| | DIP:6612N | Protein ENPI | |
| | DIP:5304N | Nucleolar protein UTP22 | |
| 22 | DIP:5395N | Eukaryotic translation initiation factor 6 | Binds to the 60S ribosomal subunit and prevents its association with the 40S ribosomal subunit to form the 80S initiation complex |
| | DIP:6326N | Nucleolar protein 7 | Involved in biogenesis of the 60S ribosomal subunit |
| | DIP:6488N | Nucleolar protein NOP2 | |
| | DIP:6602N | Ribosome biogenesis protein RPF2 | |
| | DIP:6484N | Microtubule-associated protein YTM1 | |
| 23 | DIP:2529N | Replication factor C subunit 3 | Involved in DNA replication |
| | DIP:2530N | Replication factor C subunit 4 | |
| | DIP:2531N | Replication factor C subunit 5 | |
| | DIP:2727N | Kinetochore protein CTF8 | |
| | DIP:5868N | CHL12 protein | |
| 24 | DIP:1587N | 26S protease regulatory subunit 6B homolog | Components of 26S protease complex |
| | DIP:2883N | 26S protease regulatory subunit 7 homolog | |
| | DIP:2100N | 26S proteasome regulatory subunit RPN10 | |
| | DIP:5261N | 26S proteasome regulatory subunit RPN9 | |
| | DIP:2808N | Proteasome component C11 | |
| 25 | DIP:673N | Cell division control protein 10 | Septins, involved in cytokinesis that assemble into filaments and form a ring at the cleavage site |
| | DIP:1656N | Cell division control protein 11 | |
| | DIP:3010N | Cell division control protein 3 | |
| | DIP:5596N | Septation protein 7 | |
| | DIP:2260N | Serine/threonine-protein kinase GIN4 | May play a role in septin assembly |

Table 5: Annotations of the 5-cliques in *S. cerevisiae* PPI network (5)

| C | DIP ID | Description of the proteins | Molecular function |
|----|-----------|--|---|
| 26 | DIP:866N | Nucleoporin NUP57 | Components of the nuclear pore complex (NPC) |
| | DIP:709N | Nucleoporin NUP49/NSP49 | |
| | DIP:2074N | Nucleoporin NUP145 precursor | |
| | DIP:2430N | Nucleoporin NUP84 | |
| | DIP:2721N | Nucleoporin NUP120 | |
| 27 | DIP:681N | Histone deacetylase RPD3 | Transcription factors with roles in meiotic regulation and silencing |
| | DIP:597N | Paired amphipathic helix protein SIN3 | |
| | DIP:5290N | Meiosis negative regulator UME1 | |
| | DIP:1797N | <i>S.cerevisiae</i> chromosome IV reading frame ORF YDL076c | |
| | DIP:2958N | ORF YPL181w | |
| 28 | DIP:1722N | Vacuolar morphogenesis protein VAM7 | Involved in morphogenesis of the vacuole, vacuolar assembly, vesicle transportation, vesicle fusion and docking |
| | DIP:1726N | Syntaxin VAM3 | |
| | DIP:2145N | Vesicle transport v-SNARE protein VTI1 | |
| | DIP:2247N | Synaptobrevin homolog YKT6 | |
| | DIP:2248N | Vacuolar v-SNARE NYV1 | |
| 29 | DIP:1957N | POP2 protein | Transcription factors |
| | DIP:2255N | General negative regulator of transcription subunit 4 | |
| | DIP:2522N | Glucose-repressible alcohol dehydrogenase transcriptional effector | Catalytic component of the cytoplasmic mRNA deadenylase complex |
| | DIP:1995N | Hypothetical 41.2 kDa protein in PLC1-SEC21 intergenic region | Protein binding, regulation of transcription from RNA polymerase II promoter |
| | DIP:2683N | Hypothetical 128.8 kDa protein in PAS2-PRS5 intergenic region | |

Table 6: Annotations of the 5-cliques in *S. cerevisiae* PPI network (6)