Supplementary Material

Q-clique 1	**Function Annotation**
YLR244C	[F] MAP1 methionine aminopeptidase, isoform 1
YBR283C	[F] SSH1 involved in co-translational pathway of protein transport
YBL091C	[F] MAP2 methionine aminopeptidase, isoform 2
YKL024C	[M] URA6 uridine-monophosphate kinase
YDR226W	[M] ADK1 adenylate kinase, cytosolic
YER170W	[M] ADK2 adenylate kinase, mitochondrial
YLR378C	[O] SEC61 ER protein-translocation complex subunit
YDR117C	[O] YDR117c similarity to mouse ligatin, a trafficking receptor for phosphoglycoproteins
YEL054C	[P] RPL12A 60S large subunit ribosomal protein L12.e
YGL135W	[P] RPL1B 60S large subunit ribosomal protein
YDL202W	[P] MRPL11 ribosomal protein of the large subunit, mitochondrial
YJL177W	[P] RPL17B 60s large subunit ribosomal protein L17.e
YDR041W	[P] RSM10 component of the mitochondrial ribosomal small subunit
YPR166C	[P] MRP2 ribosomal protein S14
YOR063W	[P] RPL3 60S large subunit ribosomal protein L3.e
YPL131W	[P] RPL5 60S large subunit ribosomal protein L5.e
YPR102C	[P] RPL11A ribosomal protein L11.e
YOL040C	[P] RPS15 40S small subunit ribosomal protein
YLR367W	[P] RPS22B ribosomal protein S15a.e.c12
YOL127W	[P] RPL25 ribosomal protein L23a.e
YGL147C	[P] RPL9A ribosomal protein L9.e
YGL103W	[P] RPL28 60S large subunit ribosomal protein L27a.e
YDL136W	[P] RPL35B 60S large subunit ribosomal protein
YDL061C	[P] RPS29B ribosomal protein S29.e.B
YHR147C	[P] MRPL6 ribosomal protein of the large subunit, mitochondrial
YDL191W	[P] RPL35A 60S large subunit ribosomal protein
YIL133C	[P] RPL16A 60S large subunit ribosomal protein
YNL067W	[P] RPL9B ribosomal protein L9.e.c14
YDR237W	[P] MRPL7 ribosomal protein of the large subunit, mitochondrial
YJR145C	[P] RPS4A ribosomal protein S4.e.c10
YBL027W	[P] RPL19B 60S large subunit ribosomal protein L19.e
YDL083C	[P] RPS16B ribosomal protein S16.e
YEL050C	[P] RML2 ribosomal L2 protein, mitochondrial
YMR143W	[P] RPS16A ribosomal protein S16.e
YBR251W	[P] MRPS5 ribosomal protein S5, mitochondrial
YNL069C	[P] RPL16B 60S large subunit ribosomal protein
YBL038W	[P] MRPL16 ribosomal protein of the large subunit, mitochondrial
YLR388W	[P] RPS29A ribosomal protein S29.e.A
YKL170W	[P] MRPL38 ribosomal protein of the large subunit (L14), mitochondrial
YBR146W	[P] MRPS9 ribosomal protein S9 precursor, mitochondrial
YNL185C	[P] MRPL19 ribosomal protein of the large subunit, mitochondrial
YCR031C	[P] RPS14A 40S Ribosomal protein S14.e
YBR048W	[P] RPS11B ribosomal protein S11.e.B
YDR012W	[P] RPL4B ribosomal protein L4.e.B
YIL018W	[P] RPL2B 60S large subunit ribosomal protein L8.e
YJL191W	[P] RPS14B 40S small subunit ribosomal protein S14.e.B
YML025C	[P] YML6 ribosomal protein, mitochondrial
YBL092W	[P] RPL32 60S large subunit ribosomal protein L32.e
YJR123W	[P] RPS5 ribosomal protein S5.e
YMR260C	[P] TIF11 translation initiation factor eIF1a
YNR036C	[P] YNR036c strong similarity to ribosomal protein S12
YJR113C	[P] RSM7 similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7
YDR116C	[P] YDR116c similarity to bacterial ribosomal L1 proteins

YGR085C	[P] RPL11B ribosomal protein
YGR034W	[P] RPL26B 60S large subunit ribosomal protein
YNL244C	[P] SUI1 translation initiation factor 3 (eIF3)
YNL178W	[P] RPS3 ribosomal protein S3.e
YGR118W	[P] RPS23A 40S small subunit ribosomal protein S23.e
YJL063C	[P] MRPL8 ribosomal protein L17, mitochondrial
YGR220C	[P] MRPL9 ribosomal protein YmL9, mitochondrial
YMR188C	[P] YMR188c weak similarity to bacterial ribosomal protein S17
YDR025W	[P] RPS11A ribosomal protein S11.e
YJL190C	[P] RPS22A ribosomal protein S15a.e.c10
YNL284C	[P] MRPL10 ribosomal protein of the large subunit, mitochondrial
YHR203C	[P] RPS4B ribosomal protein S4.e.c8
YML026C	[P] RPS18B ribosomal protein S18.e.c13
YNL306W	[P] MRPS18 ribosomal protein of the small subunit, mitochondrial
YGL068W	[P] YGL068w strong similarity to Cricetus mitochrondial ribosomal L12 protein
YPL220W	[P] RPL1A ribosomal protein
YPR132W	[P] RPS23B 40S small subunit ribosomal protein S23.e
YPL183W-A	[P] YPL183w-a strong similarity to mitochondrial and bacterial ribosomal L36 proteins
YER117W	[P] RPL23B ribosomal protein L23.e
YDR450W	[P] RPS18A ribosomal protein S18.e.c4
YNR037C	[P] RSM19 strong similarity to Mycoplasma ribosomal protein S19
YBR031W	[P] RPL4A ribosomal protein
YDR418W	[P] RPL12B 60S large subunit ribosomal protein L12.e
YNL081C	[P] YNL081c similarity to ribosomal protein S13
YGL123W	[P] RPS2 40S small subunit ribosomal protein
YHL015W	[P] RPS20 ribosomal protein
YBL087C	[P] RPL23A 60S large subunit ribosomal protein L23.e
YLR340W	[P] RPP0 acidic ribosomal protein L10.e
YKL180W	[P] RPL17A ribosomal protein L17.e
YLR075W	[P] RPL10 60S large subunit ribosomal protein
YLR344W	[P] RPL26A 60S large subunit ribosomal protein
YML009C	[P] MRPL39 60S ribosomal protein, mitochondrial
YOR150W	[P] MRPL23 ribosomal protein of the large subunit, mitochondrial
YBR084C-A	[P] RPL19A 60S large subunit ribosomal protein L19.e
YNL292W	[T] PUS4 pseudouridine synthase
YPR010C	[T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit
YOR116C	[T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit
YOR207C	[T] RET1 DNA-directed RNA polymerase III, 130 KD subunit
YPL212C	[T] PUS1 pseudouridine synthase 1
YIL021W	[T] RPB3 DNA-directed RNA-polymerase II, 45 kDa
YGL063W	[T] PUS2 pseudouridine synthase 2
YPR110C	[T] RPC40 DNA-directed RNA polymerase I, III 40 KD subunit
YFL001W	[T] DEG1 pseudouridine synthase
YBR257W	[T] POP4 involved in processing of tRNAs and rRNAs
YLR175W	[T] CBF5 putative rRNA pseuduridine synthase
YML010W	[T] SPT5 transcription elongation protein
YOR151C	[T] RPB2 DNA-directed RNA polymerase II, 140 kDa chain
YOR341W	[T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit
YKL009W	[T] MRT4 mRNA turnover 4
YDL140C	[T] RPO21 DNA-directed RNA polymerase II, 215 KD subunit
YNL177C	[U] YNL177c similarity to hypothetical protein S. pombe
YMR310C	[U] YMR310c similarity to YGR283c
YJR014W	[U] YJR014w strong similarity to S.pombe hypothetical protein SPBC16C6.05
YMR158W	[U] YMR158w weak similarity to E.coli ribosomal S8 protein
YGR283C	[U] YGR283c similarity to hypothetical protein YMR310c

YDR101C	[U] YDR101c weak similarity to proliferation-associated protein
Q-clique 2	**Function Annotation**
YLR244C	[F] MAP1 methionine aminopeptidase, isoform 1
YBR283C	[F] SSH1 involved in co-translational pathway of protein transport
YBL091C	[F] MAP2 methionine aminopeptidase, isoform 2
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YKL024C	[M] URA6 uridine-monophosphate kinase
YDR117C	[O] YDR117c similarity to mouse ligatin, a trafficking receptor for phosphoglycoproteins
YLR378C	[O] SEC61 ER protein-translocation complex subunit
YEL054C	[P] RPL12A 60S large subunit ribosomal protein L12.e
YGL135W	[P] RPL1B 60S large subunit ribosomal protein
YDL202W	[P] MRPL11 ribosomal protein of the large subunit, mitochondrial
YDR041W	[P] RSM10 component of the mitochondrial ribosomal small subunit
YJL177W	[P] RPL17B 60s large subunit ribosomal protein L17.e
YDL136W	[P] RPL35B 60S large subunit ribosomal protein
YNL067W	[P] RPL9B ribosomal protein L9.e.c14
YPR102C	[P] RPL11A ribosomal protein L11.e
YOL040C	[P] RPS15 40S small subunit ribosomal protein
YOL127W	[P] RPL25 ribosomal protein L23a.e
YLR367W	[P] RPS22B ribosomal protein S15a.e.c12
YGL147C	[P] RPL9A ribosomal protein L9.e
YGL103W	[P] RPL28 60S large subunit ribosomal protein L27a.e
YIL133C	[P] RPL16A 60S large subunit ribosomal protein
YHR147C	[P] MRPL6 ribosomal protein of the large subunit, mitochondrial
YDL061C	[P] RPS29B ribosomal protein S29.e.B
YDL191W	[P] RPL35A 60S large subunit ribosomal protein
YEL050C	[P] RML2 ribosomal L2 protein, mitochondrial
YLR388W	[P] RPS29A ribosomal protein S29.e.A
YKL170W	[P] MRPL38 ribosomal protein of the large subunit (L14), mitochondrial
YJR145C	[P] RPS4A ribosomal protein S4.e.c10
YBL027W	[P] RPL19B 60S large subunit ribosomal protein L19.e
YDL083C	[P] RPS16B ribosomal protein S16.e
YDR012W	[P] RPL4B ribosomal protein L4.e.B
YMR143W	[P] RPS16A ribosomal protein S16.e
YBR251W	[P] MRPS5 ribosomal protein S5, mitochondrial
YNL069C	[P] RPL16B 60S large subunit ribosomal protein
YBL038W	[P] MRPL16 ribosomal protein of the large subunit, mitochondrial
YBR146W	[P] MRPS9 ribosomal protein S9 precursor, mitochondrial
YJL191W	[P] RPS14B 40S small subunit ribosomal protein S14.e.B
YNL185C	[P] MRPL19 ribosomal protein of the large subunit, mitochondrial
YCR031C	[P] RPS14A 40S Ribosomal protein S14.e
YBR048W	[P] RPS11B ribosomal protein S11.e.B
YIL018W	[P] RPL2B 60S large subunit ribosomal protein L8.e
YML025C	[P] YML6 ribosomal protein, mitochondrial
YBL092W	[P] RPL32 60S large subunit ribosomal protein L32.e
YJR123W	[P] RPS5 ribosomal protein S5.e
YJR113C	[P] RSM7 similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7
YNR036C	[P] YNR036c strong similarity to ribosomal protein S12
YGR085C	[P] RPL11B ribosomal protein
YGR034W	[P] RPL26B 60S large subunit ribosomal protein
YNL244C	[P] SUI1 translation initiation factor 3 (eIF3)
YNL178W	[P] RPS3 ribosomal protein S3.e
YGR118W	[P] RPS23A 40S small subunit ribosomal protein S23.e
YGR220C	[P] MRPL9 ribosomal protein YmL9, mitochondrial

YMR188C	[P] YMR188c weak similarity to bacterial ribosomal protein S17
YDR025W	[P] RPS11A ribosomal protein S11.e
YJL190C	[P] RPS22A ribosomal protein S15a.e.c10
YNL284C	[P] MRPL10 ribosomal protein of the large subunit, mitochondrial
YHR203C	[P] RPS4B ribosomal protein S4.e.c8
YML026C	[P] RPS18B ribosomal protein S18.e.c13
YNL306W	[P] MRPS18 ribosomal protein of the small subunit, mitochondrial
YPL220W	[P] RPL1A ribosomal protein
YPR132W	[P] RPS23B 40S small subunit ribosomal protein S23.e
YER117W	[P] RPL23B ribosomal protein L23.e
YNR037C	[P] RSM19 strong similarity to Mycoplasma ribosomal protein S19
YBR031W	[P] RPL4A ribosomal protein
YDR450W	[P] RPS18A ribosomal protein S18.e.c4
YNL081C	[P] YNL081c similarity to ribosomal protein S13
YGL123W	[P] RPS2 40S small subunit ribosomal protein
YDR418W	[P] RPL12B 60S large subunit ribosomal protein L12.e
YHL015W	[P] RPS20 ribosomal protein
YBL087C	[P] RPL23A 60S large subunit ribosomal protein L23.e
YKL180W	[P] RPL17A ribosomal protein L17.e
YLR340W	[P] RPP0 acidic ribosomal protein L10.e
YLR075W	[P] RPL10 60S large subunit ribosomal protein
YLR344W	[P] RPL26A 60S large subunit ribosomal protein
YPR166C	[P] MRP2 ribosomal protein S14
YOR150W	[P] MRPL23 ribosomal protein of the large subunit, mitochondrial
YBR084C-A	[P] RPL19A 60S large subunit ribosomal protein L19.e
YOR063W	[P] RPL3 60S large subunit ribosomal protein L3.e
YBR257W	[T] POP4 involved in processing of tRNAs and rRNAs
YOR341W	[T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit
YOR116C	[T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit
YOR207C	[T] RET1 DNA-directed RNA polymerase III, 130 KD subunit
YPL212C	[T] PUS1 pseudouridine synthase 1
YIL021W	[T] RPB3 DNA-directed RNA-polymerase II, 45 kDa
YGL063W	[T] PUS2 pseudouridine synthase 2
YFL001W	[T] DEG1 pseudouridine synthase
YPR110C	[T] RPC40 DNA-directed RNA polymerase I, III 40 KD subunit
YOR151C	[T] RPB2 DNA-directed RNA polymerase II, 140 kDa chain
YML010W	[T] SPT5 transcription elongation protein
YDL140C	[T] RPO21 DNA-directed RNA polymerase II, 215 KD subunit
YNL292W	[T] PUS4 pseudouridine synthase
YNL177C	[U] YNL177c similarity to hypothetical protein S. pombe
YMR310C	[U] YMR310c similarity to YGR283c
YJR014W	[U] YJR014w strong similarity to S.pombe hypothetical protein SPBC16C6.05
YGR283C	[U] YGR283c similarity to hypothetical protein YMR310c
YMR158W	[U] YMR158w weak similarity to E.coli ribosomal S8 protein
Q-clique 3	**Function Annotation**
YNL132W	[C] KRE33 similarity to A.ambisexualis antheridiol steroid receptor
YCR057C	[C] PWP2 periodic tryptophan protein
YMR128W	[C] ECM16 putative DEAH-box RNA helicase
YGR245C	[D] SDA1 required for normal organization of the actin cytoskeleton; required for passage through Start
YMR290C	[D] HAS1 helicase associated with SET1P
YLR129W	[D] DIP2 DOM34P-interacting protein
YPL126W	[D] NAN1 weak similarity to fruit fly TFIID subunit p85
YOR272W	[D] YTM1 microtubule-interacting protein
YLR449W	[F] FPR4 nucleolar peptidylprolyl cis-trans isomerase (PPIase)

YLR002C	[F] NOC3 required for maturation and intranuclear transport of pre-ribosomes
YBR247C	[F] ENP1 effects N-glycosylation
YDR299W	[O] BFR2 involved in protein transport steps at the Brefeldin A blocks
YOR206W	[O] NOC2 crucial for intranuclear movement of ribosomal precursor particles
YER006W	[O] YER006w similarity to P.polycephalum myosin-related protein mlpA
YDR060W	[P] MAK21 protein required for 60S ribosomal subunit biogenesis
YDL148C	[P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis
YCL054W	[P] SPB1 required for ribosome synthesis, putative methylase
YPR016C	[P] TIF6 translation initiation factor 6 (eIF6)
YLR197W	[T] SIK1 involved in pre-rRNA processing
YDL031W	[T] DBP10 putative RNA helicase involved in ribosome biogenesis
YKL172W	[T] EBP2 required for pre-rRNA processing and ribosomal subunit assembly
YPL217C	[T] BMS1 GTP-binding protein, required for distinct steps of 40S ribosome biogenesis
YDR087C	[T] RRP1 involved in processing rRNA precursor species to mature rRNAs
YHR148W	[T] IMP3 component of the U3 small nucleolar ribonucleoprotein
YPL211W	[T] NIP7 required for efficient 60S ribosome subunit biogenesis
YLL011W	[T] SOF1 involved in 18S pre-rRNA production
YPL043W	[T] NOP4 nucleolar protein
YLL008W	[T] DRS1 RNA helicase of the DEAD box family
YJR002W	[T] MPP10 component of the U3 small nucleolar ribonucleoprotein
YGL019W	[T] CKB1 casein kinase II, beta subunit
YDL014W	[T] NOP1 fibrillarin
YNL061W	[T] NOP2 nucleolar protein
YFL002C	[T] SPB4 ATP-dependent RNA helicase of DEAH box family
YKL009W	[T] MRT4 mRNA turnover 4
YGR145W	[U] YGR145w similarity to C.elegans hypothetical protein
YLR222C	[U] CST29 similarity to DIP2P
YER082C	[U] KRE31 similarity to M.sexta steroid regulated MNG10 protein
YGR090W	[U] YGR090w similarity to PIR:T40678 hypothetical protein SPBC776.08c S. pombe
YGR128C	[U] YGR128c hypothetical protein
YDR449C	[U] YDR449c similarity to hypothetical protein S. pombe
YNR053C	[U] NOG2 strong similarity to human breast tumor associated autoantigen
YMR049C	[U] ERB1 weak similarity to A.thaliana PRL1 protein
YHR088W	[U] RPF1 similarity to hypothetical protein YNL075w
YDR496C	[U] PUF6 similarity to hypothetical human and C.elegans proteins
YGL111W	[U] YGL111w weak similarity to hypothetical protein S. pombe
YLR186W	[U] EMG1 strong similarity to S.pombe hypothetical protein C18G6.07C
YMR093W	[U] YMR093w weak similarity to PWP2P
YNL182C	[U] YNL182c weak similarity to S.pombe hypothetical protein
YOL077C	[U] BRX1 strong similarity to C.elegans K12H4.3 protein
YDR101C	[U] YDR101c weak similarity to proliferation-associated protein
YKL014C	[U] YKL014c similarity to hypothetical protein SPCC14G10.02 S. pombe
YPL012W	[U] RRP12 hypothetical protein
YDR324C	[U] YDR324c weak similarity to beta transducin from S. pombe and other WD-40 repeat containing proteins
YPR144C	[U] YPR144c similarity to YDR060w and C.elegans hypothetical protein
YPL093W	[U] NOG1 similarity to M.jannaschii GTP-binding protein
YNL002C	[U] RLP7 strong similarity to mammalian ribosomal L7 proteins
YHR052W	[U] CIC1 adaptor protein specifically linking the 26S proteasome to its substrate, the SCF component CDC4
YOL041C	[U] NOP12 weak similarity to M.sativa NUM1, hnRNP protein from C. tentans and D. melanogaster, murine/bovine poly(A) binding protein II, and NSR1P
YKR060W	[U] YKR060w similarity to hypothetical protein S. pombe
YGR103W	[U] RRP13 similarity to zebrafish essential for embryonic development gene pescadillo
YBL004W	[U] YBL004w weak similarity to Papaya ringspot virus polyprotein

YHR197W	[U] YHR197w weak similarity to PIR:T22172 hypothetical protein F44E5.2 C. elegans
YLR409C	[U] YLR409c strong similarity to S. pombe beta-transducin
YLR276C	[U] DBP9 similarity to YDL031w, MAK5P and RNA helicases
YKR081C	[U] YKR081c strong similarity to hypothetical protein S. pombe
YER126C	[U] KRE32 weak similarity to E.coli colicin N
YJL109C	[U] YJL109c weak similarity to ATPase DRS2P
YNL110C	[U] YNL110c weak similarity to fruit fly RNA-binding protein
Q-clique 4	**Function Annotation**
YHR066W	[C] SSF1 mating protein
YGR245C	[D] SDA1 required for normal organization of the actin cytoskeleton; required for passage through Start
YMR290C	[D] HAS1 helicase associated with SET1P
YOR272W	[D] YTM1 microtubule-interacting protein
YLR449W	[F] FPR4 nucleolar peptidylprolyl cis-trans isomerase (PPIase)
YLR002C	[F] NOC3 required for maturation and intranuclear transport of pre-ribosomes
YOR206W	[O] NOC2 crucial for intranuclear movement of ribosomal precursor particles
YER006W	[O] YER006w similarity to P.polycephalum myosin-related protein mlpA
YPR016C	[P] TIF6 translation initiation factor 6 (eIF6)
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YKL172W	[T] EBP2 required for pre-rRNA processing and ribosomal subunit assembly
YPL043W	[T] NOP4 nucleolar protein
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YFL002C	[T] SPB4 ATP-dependent RNA helicase of DEAH box family
YKL009W	[T] MRT4 mRNA turnover 4
YLL008W	[T] DRS1 RNA helicase of the DEAD box family
YDR087C	[T] RRP1 involved in processing rRNA precursor species to mature rRNAs
YDL051W	[T] LHP1 RNA binding protein
YPL211W	[T] NIP7 required for efficient 60S ribosome subunit biogenesis
YBR142W	[T] MAK5 ATP-dependent RNA helicase
YNL182C	[U] YNL182c weak similarity to S.pombe hypothetical protein
YLR106C	[U] YLR106c similarity to Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene
YFR001W	[U] LOC1 weak similarity to rabbit triadin SPP41P
YKR081C	[U] YKR081c strong similarity to hypothetical protein S. pombe
YNL110C	[U] YNL110c weak similarity to fruit fly RNA-binding protein
YDR496C	[U] PUF6 similarity to hypothetical human and C.elegans proteins
YDR101C	[U] YDR101c weak similarity to proliferation-associated protein
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YHR197W	[U] YHR197w weak similarity to PIR:T22172 hypothetical protein F44E5.2 C. elegans
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YPL012W	[U] RRP12 hypothetical protein
YNR053C	[U] NOG2 strong similarity to human breast tumor associated autoantigen
YLR276C	[U] DBP9 similarity to YDL031w, MAK5P and RNA helicases

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YNL132W	[C] KRE33 similarity to A.ambisexualis antheridiol steroid receptor
YMR128W	[C] ECM16 putative DEAH-box RNA helicase
YCR057C	[C] PWP2 periodic tryptophan protein
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YPL217C	[T] BMS1 GTP-binding protein, required for distinct steps of 40S ribosome biogenesis
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YLL011W	[T] SOF1 involved in 18S pre-rRNA production
YOR061W	[T] CKA2 casein kinase II alpha' chain
YLR197W	[T] SIK1 involved in pre-rRNA processing
YER127W	[T] LCP5 NGG1P interacting protein
YIL035C	[T] CKA1 casein kinase II, catalytic alpha chain
YHR148W	[T] IMP3 component of the U3 small nucleolar ribonucleoprotein
YOR039W	[T] CKB2 casein kinase II beta' chain
YJR002W	[T] MPP10 component of the U3 small nucleolar ribonucleoprotein
YGL019W	[T] CKB1 casein kinase II, beta subunit
YPR144C	[U] YPR144c similarity to YDR060w and C.elegans hypothetical protein
YGR145W	[U] YGR145w similarity to C.elegans hypothetical protein
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YLR409C	[U] YLR409c strong similarity to S. pombe beta-transducin
YGR128C	[U] YGR128c hypothetical protein
YMR093W	[U] YMR093w weak similarity to PWP2P
YDR449C	[U] YDR449c similarity to hypothetical protein S. pombe
YKL099C	[U] YKL099c similarity to C.elegans hypothetical proteins C18G6.06 and C16C10.2
YHR196W	[U] YHR196w weak similarity to YDR398w
YJL109C	[U] YJL109c weak similarity to ATPase DRS2P
YDR324C	[U] YDR324c weak similarity to beta transducin from S. pombe and other WD-40 repeat containing proteins
YOR145C	[U] YOR145c strong similarity to hypothtical S. pombe protein and to hypothetical C. elegans protein
Q-clique 6	**Function Annotation**
YDR117C	[O] YDR117c similarity to mouse ligatin, a trafficking receptor for phosphoglycoproteins
YJL177W	[P] RPL17B 60s large subunit ribosomal protein L17.e
YDR025W	[P] RPS11A ribosomal protein S11.e
YNL244C	[P] SUI1 translation initiation factor 3 (eIF3)
YJL190C	[P] RPS22A ribosomal protein S15a.e.c10
YDR012W	[P] RPL4B ribosomal protein L4.e.B
YHR203C	[P] RPS4B ribosomal protein S4.e.c8
YER117W	[P] RPL23B ribosomal protein L23.e
YPR102C	[P] RPL11A ribosomal protein L11.e
YLR367W	[P] RPS22B ribosomal protein S15a.e.c12
YGL147C	[P] RPL9A ribosomal protein L9.e
YBR031W	[P] RPL4A ribosomal protein
YDL061C	[P] RPS29B ribosomal protein S29.e.B

YHR147C	[P] MRPL6 ribosomal protein of the large subunit, mitochondrial
YBL087C	[P] RPL23A 60S large subunit ribosomal protein L23.e
YKL180W	[P] RPL17A ribosomal protein L17.e
YBL027W	[P] RPL19B 60S large subunit ribosomal protein L19.e
YJR145C	[P] RPS4A ribosomal protein S4.e.c10
YBR048W	[P] RPS11B ribosomal protein S11.e.B
YML025C	[P] YML6 ribosomal protein, mitochondrial
YBL092W	[P] RPL32 60S large subunit ribosomal protein L32.e
YBR084C-A	[P] RPL19A 60S large subunit ribosomal protein L19.e
YPR166C	[P] MRP2 ribosomal protein S14
YNL067W	[P] RPL9B ribosomal protein L9.e.c14
YDR237W	[P] MRPL7 ribosomal protein of the large subunit, mitochondrial
YGR085C	[P] RPL11B ribosomal protein
YLR388W	[P] RPS29A ribosomal protein S29.e.A
YKL170W	[P] MRPL38 ribosomal protein of the large subunit (L14), mitochondrial
YBR257W	[T] POP4 involved in processing of tRNAs and rRNAs
YNL177C	[U] YNL177c similarity to hypothetical protein S. pombe
YMR310C	[U] YMR310c similarity to YGR283c
YJR014W	[U] YJR014w strong similarity to S.pombe hypothetical protein SPBC16C6.05
YMR158W	[U] YMR158w weak similarity to E.coli ribosomal S8 protein
YGR283C	[U] YGR283c similarity to hypothetical protein YMR310c
Q-clique 7	**Function Annotation**
YGL151W	[B] NUT1 negative transcription regulator from artifical reporters
YHR058C	[B] MED6 RNA polymerase II transcriptional regulation mediator
YOL135C	[B] MED7 member of RNA Polymerase II transcriptional regulation mediator complex
YPR168W	[B] NUT2 negative transcription regulator from artifical reporters
YGL025C	[B] PGD1 mediator complex subunit
YOL148C	[B] SPT20 member of the TBP class of SPT proteins that alter transcription site selection
YNL236W	[B] SIN4 global regulator protein
YML007W	[B] YAP1 transcriptional activator involved in oxidative stress response
YGL127C	[B] SOH1 allows HPR1 null mutant to grow at 37 deg.
YPL042C	[D] SSN3 cyclin-dependent CTD kinase
YMR112C	[T] MED11 mediator complex subunit
YDR443C	[T] SSN2 DNA-directed RNA polymerase II holoenzyme and Srb10 CDK subcomplex subunit
YER022W	[T] SRB4 DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit
YHR041C	[T] SRB2 DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit
YLR071C	[T] RGR1 DNA-directed RNA polymerase II holoenzyme subunit
YPR070W	[T] MED1 component of RNA polymerase II holoenzyme and mediator subcomplex
YCR081W	[T] SRB8 DNA-directed RNA polymerase II holoenzyme and Srb10 CDK subcomplex subunit
YOL051W	[T] GAL11 DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit
YDR308C	[T] SRB7 DNA-directed RNA polymerase II holoenzyme and kornberg's mediator (SRB) subcomplex subunit
YNR010W	[T] CSE2 subunit of RNA polymerase II mediator complex
YOR174W	[T] MED4 transcription regulation mediator
YGR104C	[T] SRB5 DNA-directed RNA polymerase II holoenzyme and Kornberg's mediator (SRB) subcomplex subunit
YBR193C	[T] MED8 transcriptional regulation mediator
YBR253W	[T] SRB6 DNA-directed RNA polymerase II suppressor protein
Q-clique 8	**Function Annotation**
YLR117C	[D] CLF1 strong similarity to Drosophila putative cell cycle control protein crn

YDR364C	[D] CDC40 cell division control protein
YML049C	[O] RSE1 involved in RNA splicing and ER to Golgi transport
YKL173W	[P] SNU114 U5 snRNP-specific protein
YGL128C	[R] YGL128c weak similarity to dnaJ proteins
YLR298C	[T] YHC1 associated with the U1 snRNP complex
YGR074W	[T] SMD1 snRNA-associated protein
YLL036C	[T] PRP19 non-snRNP sliceosome component required for DNA repair
YPL178W	[T] CBC2 small subunit of the nuclear cap-binding protein complex CBC
YJL203W	[T] PRP21 pre-mRNA splicing factor
YBR055C	[T] PRP6 snRNP(U4/U6)-associated splicing factor
YGR013W	[T] SNU71 associated with U1 snRNP, no counterpart in mammalian U1 snRNP
YPL213W	[T] LEA1 U2 A'snRNP protein
YHR086W	[T] NAM8 meiotic recombination protein
YDR416W	[T] SYF1 synthetic lethal with CDC40
YDL043C	[T] PRP11 pre-mRNA splicing factor
YDR240C	[T] SNU56 U1 snRNA protein, no counterpart in mammalian snRNP
YIL061C	[T] SNP1 U1 small nuclear ribonucleoprotein
YMR288W	[T] HSH155 component of a multiprotein splicing factor
YAL032C	[T] PRP45 pre-mRNA splicing factor
YER029C	[T] SMB1 associated with U1 snRNP as part of the Sm-core that is common to all spliceosomal snRNPs
YGL120C	[T] PRP43 involved in spliceosome disassembly
YMR125W	[T] STO1 large subunit of the nuclear cap-binding protein complex CBC
YDL030W	[T] PRP9 pre-mRNA splicing factor (snRNA-associated protein)
YBR119W	[T] MUD1 U1 snRNP-specific A protein
YGR091W	[T] PRP31 pre-mRNA splicing protein
YML046W	[T] PRP39 pre-mRNA splicing factor
YPR178W	[T] PRP4 U4/U6 snRNP 52 KD protein
YKL012W	[T] PRP40 splicing factor
YDL087C	[T] LUC7 yeast U1 snRNP protein with a role in 5'splice site recognition
YMR240C	[T] CUS1 U2 snRNP protein
YLR275W	[T] SMD2 U1 snRNP protein of the Sm class
YOR308C	[T] SNU66 component of U4/U6.U5 snRNP
YLR147C	[T] SMD3 spliceosomal snRNA-associated Sm core protein required for pre-mRNA splicing
YDR235W	[T] PRP42 U1 snRNP associated protein, required for pre-mRNA splicing
YPR101W	[T] SNT309 splicing factor
YGR278W	[U] YGR278w similarity to C.elegans LET-858
YDL209C	[U] YDL209c similarity to hypothetical S. pombe protein
YPL151C	[U] PRP46 strong similarity to A.thaliana PRL1 and PRL2 proteins
YLR424W	[U] YLR424w weak similarity to STU1P
Q-clique 9	**Function Annotation**
YMR128W	[C] ECM16 putative DEAH-box RNA helicase
YNL132W	[C] KRE33 similarity to A.ambisexualis antheridiol steroid receptor
YCR057C	[C] PWP2 periodic tryptophan protein
YPL126W	[D] NAN1 weak similarity to fruit fly TFIID subunit p85
YLR129W	[D] DIP2 DOM34P-interacting protein
YBR247C	[F] ENP1 effects N-glycosylation
YDR299W	[O] BFR2 involved in protein transport steps at the Brefeldin A blocks
YDL148C	[P] NOP14 nuclear and nucleolar protein with possible role in ribosome biogenesis
YHR148W	[T] IMP3 component of the U3 small nucleolar ribonucleoprotein
YLL011W	[T] SOF1 involved in 18S pre-rRNA production
YOR061W	[T] CKA2 casein kinase II alpha'chain
YER127W	[T] LCP5 NGG1P interacting protein
YIL035C	[T] CKA1 casein kinase II, catalytic alpha chain

YOR039W	[T] CKB2 casein kinase II beta' chain
YPL217C	[T] BMS1 GTP-binding protein, required for distinct steps of 40S ribosome biogenesis
YJR002W	[T] MPP10 component of the U3 small nucleolar ribonucleoprotein
YGL019W	[T] CKB1 casein kinase II, beta subunit
YOR145C	[U] YOR145c strong similarity to hypothtical S. pombe protein and to hypothetical C. elegans protein
YPR144C	[U] YPR144c similarity to YDR060w and C.elegans hypothetical protein
YLR222C	[U] CST29 similarity to DIP2P
YOL077C	[U] BRX1 strong similarity to C.elegans K12H4.3 protein
YGR090W	[U] YGR090w similarity to PIR:T40678 hypothetical protein SPBC776.08c S. pombe
YER082C	[U] KRE31 similarity to M.sexta steroid regulated MNG10 protein
YLR186W	[U] EMG1 strong similarity to S.pombe hypothetical protein C18G6.07C
YKR060W	[U] YKR060w similarity to hypothetical protein S. pombe
YLR409C	[U] YLR409c strong similarity to S. pombe beta-transducin
YJL069C	[U] YJL069c similarity to C.elegans hypothetical protein
YGR128C	[U] YGR128c hypothetical protein
YMR093W	[U] YMR093w weak similarity to PWP2P
YDR449C	[U] YDR449c similarity to hypothetical protein S. pombe
YHR196W	[U] YHR196w weak similarity to YDR398w
YJL109C	[U] YJL109c weak similarity to ATPase DRS2P
YKL099C	[U] YKL099c similarity to C.elegans hypothetical proteins C18G6.06 and C16C10.2
YDR324C	[U] YDR324c weak similarity to beta transducin from S. pombe and other WD-40 repeat containing proteins
Q-clique 10	**Function Annotation**
YBR283C	[F] SSH1 involved in co-translational pathway of protein transport
YLR378C	[O] SEC61 ER protein-translocation complex subunit
YDR117C	[O] YDR117c similarity to mouse ligatin, a trafficking receptor for phosphoglycoproteins
YGR220C	[P] MRPL9 ribosomal protein YmL9, mitochondrial
YMR188C	[P] YMR188c weak similarity to bacterial ribosomal protein S17
YJL177W	[P] RPL17B 60s large subunit ribosomal protein L17.e
YDR025W	[P] RPS11A ribosomal protein S11.e
YDR012W	[P] RPL4B ribosomal protein L4.e.B
YJL190C	[P] RPS22A ribosomal protein S15a.e.c10
YNL284C	[P] MRPL10 ribosomal protein of the large subunit, mitochondrial
YHR203C	[P] RPS4B ribosomal protein S4.e.c8
YPL131W	[P] RPL5 60S large subunit ribosomal protein L5.e
YOL040C	[P] RPS15 40S small subunit ribosomal protein
YER117W	[P] RPL23B ribosomal protein L23.e
YPR102C	[P] RPL11A ribosomal protein L11.e
YLR367W	[P] RPS22B ribosomal protein S15a.e.c12
YGL103W	[P] RPL28 60S large subunit ribosomal protein L27a.e
YGL147C	[P] RPL9A ribosomal protein L9.e
YNR037C	[P] RSM19 strong similarity to Mycoplasma ribosomal protein S19
YBR031W	[P] RPL4A ribosomal protein
YDL061C	[P] RPS29B ribosomal protein S29.e.B
YHR147C	[P] MRPL6 ribosomal protein of the large subunit, mitochondrial
YDL191W	[P] RPL35A 60S large subunit ribosomal protein
YGL123W	[P] RPS2 40S small subunit ribosomal protein
YBL087C	[P] RPL23A 60S large subunit ribosomal protein L23.e
YKL180W	[P] RPL17A ribosomal protein L17.e
YBL027W	[P] RPL19B 60S large subunit ribosomal protein L19.e
YJR145C	[P] RPS4A ribosomal protein S4.e.c10
YBR251W	[P] MRPS5 ribosomal protein S5, mitochondrial
YLR344W	[P] RPL26A 60S large subunit ribosomal protein
YBR048W	[P] RPS11B ribosomal protein S11.e.B

YIL018W	[P] RPL2B 60S large subunit ribosomal protein L8.e
YML025C	[P] YML6 ribosomal protein, mitochondrial
YBL092W	[P] RPL32 60S large subunit ribosomal protein L32.e
YBR084C-A	[P] RPL19A 60S large subunit ribosomal protein L19.e
YPR166C	[P] MRP2 ribosomal protein S14
YDL136W	[P] RPL35B 60S large subunit ribosomal protein
YOR063W	[P] RPL3 60S large subunit ribosomal protein L3.e
YNL067W	[P] RPL9B ribosomal protein L9.e.c14
YDR237W	[P] MRPL7 ribosomal protein of the large subunit, mitochondrial
YGR085C	[P] RPL11B ribosomal protein
YEL050C	[P] RML2 ribosomal L2 protein, mitochondrial
YGR034W	[P] RPL26B 60S large subunit ribosomal protein
YLR388W	[P] RPS29A ribosomal protein S29.e.A
YKL170W	[P] MRPL38 ribosomal protein of the large subunit (L14), mitochondrial
YNL244C	[P] SUI1 translation initiation factor 3 (eIF3)
YNL292W	[T] PUS4 pseudouridine synthase
YLR175W	[T] CBF5 putative rRNA pseuduridine synthase
YBR257W	[T] POP4 involved in processing of tRNAs and rRNAs
YJR014W	[U] YJR014w strong similarity to S.pombe hypothetical protein SPBC16C6.05
YMR310C	[U] YMR310c similarity to YGR283c
YNL177C	[U] YNL177c similarity to hypothetical protein S. pombe
YGR283C	[U] YGR283c similarity to hypothetical protein YMR310c
YMR158W	[U] YMR158w weak similarity to E.coli ribosomal S8 protein
Q-clique 11	**Function Annotation**
YHL030W	[C] ECM29 involved in cell wall biogenesis and architecture
YBR272C	[D] HSM3 mismatch repair protein
YOR259C	[F] RPT4 26S proteasome regulatory subunit
YOR117W	[F] RPT5 26S proteasome regulatory subunit
YFR052W	[F] RPN12 26S proteasome regulatory subunit
YGL011C	[F] SCL1 20S proteasome subunit YC7ALPHA/Y8 (alpha1)
YDR427W	[F] RPN9 subunit of the regulatory particle of the proteasome
YOR261C	[F] RPN8 26S proteasome regulatory subunit
YER012W	[F] PRE1 20S proteasome subunit C11(beta4)
YMR314W	[F] PRE5 20S proteasome subunit(alpha6)
YER021W	[F] RPN3 26S proteasome regulatory subunit
YDL007W	[F] RPT2 26S proteasome regulatory subunit
YDR394W	[F] RPT3 26S proteasome regulatory subunit
YFR004W	[F] RPN11 26S proteasome regulatory subunit
YGL048C	[F] RPT6 26S proteasome regulatory subunit
YPR108W	[F] RPN7 subunit of the regulatory particle of the proteasome
YDL147W	[F] RPN5 subunit of the regulatory particle of the proteasome
YHR200W	[F] RPN10 26S proteasome regulatory subunit
YDL097C	[F] RPN6 subunit of the regulatory particle of the proteasome
YKL145W	[F] RPT1 26S proteasome regulatory subunit
YGR232W	[F] NAS6 possible homolog of human 26S proteasome regulatory subunit p28
YJR109C	[G] CPA2 arginine-specific carbamoylphosphate synthase, large chain
YKL104C	[M] GFA1 glucosamine--fructose-6-phosphate transaminase
YLR421C	[U] RPN13 weak similarity to human 42K membrane glycoprotein
Q-clique 12	**Function Annotation**
YML054C	[E] CYB2 lactate dehydrogenase cytochrome b2
YMR208W	[M] ERG12 mevalonate kinase
YJL063C	[P] MRPL8 ribosomal protein L17, mitochondrial
YJR113C	[P] RSM7 similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7
YDR041W	[P] RSM10 component of the mitochondrial ribosomal small subunit
YIL133C	[P] RPL16A 60S large subunit ribosomal protein

YPL118W	[P] MRP51 mitochondrial ribosomal protein of the small subunit
YML026C	[P] RPS18B ribosomal protein S18.e.c13
YNL306W	[P] MRPS18 ribosomal protein of the small subunit, mitochondrial
YNL301C	[P] RPL18B 60S large subunit ribosomal protein L18.e
YOL120C	[P] RPL18A 60S large subunit ribosomal protein S18.e
YPL183W-A	[P] YPL183w-a strong similarity to mitochondrial and bacterial ribosomal L36 proteins
YDR337W	[P] MRPS28 ribosomal protein of the small subunit, mitochondrial
YGR084C	[P] MRP13 ribosomal protein of the small subunit, mitochondrial
YDR450W	[P] RPS18A ribosomal protein S18.e.c4
YNL137C	[P] NAM9 ribosomal protein, mitochondrial
YHL004W	[P] MRP4 ribosomal protein of the small subunit, mitochondrial
YNL081C	[P] YNL081c similarity to ribosomal protein S13
YJL191W	[P] RPS14B 40S small subunit ribosomal protein S14.e.B
YDR347W	[P] MRP1 ribosomal protein of the small subunit, mitochondrial
YDL083C	[P] RPS16B ribosomal protein S16.e
YMR143W	[P] RPS16A ribosomal protein S16.e
YNL069C	[P] RPL16B 60S large subunit ribosomal protein
YBL038W	[P] MRPL16 ribosomal protein of the large subunit, mitochondrial
YLR075W	[P] RPL10 60S large subunit ribosomal protein
YBR146W	[P] MRPS9 ribosomal protein S9 precursor, mitochondrial
YCR031C	[P] RPS14A 40S Ribosomal protein S14.e
YOR150W	[P] MRPL23 ribosomal protein of the large subunit, mitochondrial
YMR260C	[P] TIF11 translation initiation factor eIF1a
YIL021W	[T] RPB3 DNA-directed RNA-polymerase II, 45 kDa
YBR154C	[T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit
YPR110C	[T] RPC40 DNA-directed RNA polymerase I, III 40 KD subunit
YPR187W	[T] RPO26 DNA-directed RNA polymerase I, II, III 18 KD subunit
YOR116C	[T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit
YOR207C	[T] RET1 DNA-directed RNA polymerase III, 130 KD subunit
YOR341W	[T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit
YOR210W	[T] RPB10 DNA-directed polymerase I, II, III 8.3 subunit
YDL140C	[T] RPO21 DNA-directed RNA polymerase II, 215 KD subunit
YPR010C	[T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit
YIL093C	[U] RSM25 weak similarity to S.pombe hypothetical protein SPBC16A3
YKL155C	[U] RSM22 similarity to S. pombe SPAC1420.04c putative cytochrome c oxidase assembly protein
YJR008W	[U] YJR008w similarity to S.pombe hypothetical protein
YGL129C	[U] RSM23 similarity to S.pombe hypothetical protein SPBC29A3.15C - putative mitochondrial function
YDR036C	[U] YDR036c similarity to enoyl CoA hydratase
Q-clique 13	**Function Annotation**
YMR208W	[M] ERG12 mevalonate kinase
YJL063C	[P] MRPL8 ribosomal protein L17, mitochondrial
YPL183W-A	[P] YPL183w-a strong similarity to mitochondrial and bacterial ribosomal L36 proteins
YMR260C	[P] TIF11 translation initiation factor eIF1a
YBL038W	[P] MRPL16 ribosomal protein of the large subunit, mitochondrial
YLR075W	[P] RPL10 60S large subunit ribosomal protein
YCR031C	[P] RPS14A 40S Ribosomal protein S14.e
YDR450W	[P] RPS18A ribosomal protein S18.e.c4
YNL081C	[P] YNL081c similarity to ribosomal protein S13
YJR123W	[P] RPS5 ribosomal protein S5.e
YJL191W	[P] RPS14B 40S small subunit ribosomal protein S14.e.B
YML009C	[P] MRPL39 60S ribosomal protein, mitochondrial
YML026C	[P] RPS18B ribosomal protein S18.e.c13
YGL068W	[P] YGL068w strong similarity to Cricetus mitochrondial ribosomal L12 protein

YOL120C	[P] RPL18A 60S large subunit ribosomal protein S18.e
YNL301C	[P] RPL18B 60S large subunit ribosomal protein L18.e
YNR003C	[T] RPC34 DNA-directed RNA polymerase III, 34 KD subunit
YOR210W	[T] RPB10 DNA-directed polymerase I, II, III 8.3 subunit
YPR190C	[T] RPC82 DNA-directed RNA polymerase III, 82 KD subunit
YPR187W	[T] RPO26 DNA-directed RNA polymerase I, II, III 18 KD subunit
YIL021W	[T] RPB3 DNA-directed RNA-polymerase II, 45 kDa
YPR110C	[T] RPC40 DNA-directed RNA polymerase I, III 40 KD subunit
YOR341W	[T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit
YDL140C	[T] RPO21 DNA-directed RNA polymerase II, 215 KD subunit
YBR154C	[T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit
YOR116C	[T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit
YOR151C	[T] RPB2 DNA-directed RNA polymerase II, 140 kDa chain
YPR010C	[T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit
YOR207C	[T] RET1 DNA-directed RNA polymerase III, 130 KD subunit
YOR224C	[T] RPB8 DNA-directed RNA polymerase I, II, III 16 KD subunit
YML010W	[T] SPT5 transcription elongation protein
YJR008W	[U] YJR008w similarity to S.pombe hypothetical protein
Q-clique 14	**Function Annotation**
YIL147C	[C] SLN1 two-component signal transducer
YMR262W	[D] YMR262w similarity to S.pombe scn1 protein
YGL205W	[E] POX1 acyl-CoA oxidase
YAL054C	[E] ACS1 acetyl-CoA synthetase
YER061C	[E] CEM1 beta-keto-acyl-ACP synthase, mitochondrial
YLR153C	[E] ACS2 acetyl-coenzyme A synthetase
YIL160C	[E] POT1 acetyl-CoA C-acyltransferase, peroxisomal
YHR208W	[G] BAT1 branched chain amino acid aminotransferase, mitochondrial
YIL042C	[G] YIL042c similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
YJR148W	[G] BAT2 branched chain amino acid aminotransferase, cytosolic
YBR222C	[M] FAT2 AMP-binding protein, peroxisomal
YBR208C	[M] DUR1,2 urea amidolyase
YOR221C	[M] MCT1 malonyl-CoA:ACP transferase
YPL231W	[M] FAS2 fatty-acyl-CoA synthase, alpha chain
YPL028W	[M] ERG10 acetyl-CoA C-acetyltransferase, cytosolic
YDR272W	[M] GLO2 glyoxalase II (hydroxyacylglutathione hydrolase)
YLR284C	[M] ECI1 delta3-cis-delta2-trans-enoyl-CoA isomerase
YJR057W	[M] CDC8 dTMP kinase
YDL168W	[M] SFA1 long-chain alcohol dehydrogenase
YKL182W	[M] FAS1 fatty-acyl-CoA synthase, beta chain
YNR016C	[M] ACC1 acetyl-CoA carboxylase
YKL192C	[M] ACP1 mitochonrial acyl-carrier protein
YOR180C	[M] DCI1 Enoyl-CoA Hydratase, peroxisomal
YBR041W	[M] FAT1 very long-chain fatty acyl-CoA synthetase
YOR040W	[M] GLO4 glyoxalase II (hydroxyacylglutathione hydrolase)
YKR009C	[M] FOX2 hydratase-dehydrogenase-epimerase, peroxisomal
YCR003W	[P] MRPL32 ribosomal protein YmL32, mitochondrial
YNL168C	[U] YNL168c similarity to C.elegans ZK688.3 protein and E.coli hpcEp
YGL059W	[U] YGL059w similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
YGR263C	[U] YGR263c weak similarity to E.coli lipase like enzyme
YDR036C	[U] YDR036c similarity to enoyl CoA hydratase
YDR428C	[U] YDR428c weak similarity to predicted esterase of proteobacterium
YOR093C	[U] YOR093c similarity to S.pombe hypothetical protein SPAC22F3.04
YBL055C	[U] YBL055c similarity to hypothetical S.pombe protein
Q-clique 15	**Function Annotation**
YOL142W	[D] RRP40 protein involved in ribosomal RNA processing, component of the exosome

	complex responsible for 3’end processing and degradation of many RNA species
YNL232W	[M] CSL4 core component of the 3’-5’exosome
YOR076C	[M] SKI7 GTPase with function in 3’-to-5’degradation of mRNA
YNL189W	[O] SRP1 karyopherin-alpha or importin
YLR029C	[P] RPL15A 60s large subunit ribosomal protein L15.e.c12
YPR043W	[P] RPL43A ribosomal protein L37a.e
YMR121C	[P] RPL15B 60S large subunit ribosomal protein L15.e.c13
YDL111C	[T] RRP42 rRNA processing protein
YOL021C	[T] DIS3 3’->5’exoribonuclease required for 3’end formation of 5.8S rRNA
YCR035C	[T] RRP43 rRNA processing protein
YHR062C	[T] RPP1 required for processing of tRNA and 35S rRNA
YGR195W	[T] SKI6 3’->5’exoribonuclease required for 3’end formation of 5.8S rRNA
YNL075W	[T] IMP4 component of the U3 small nucleolar ribonucleoprotein
YAL033W	[T] POP5 required for processing of tRNAs and rRNAs
YGR158C	[T] MTR3 involved in mRNA transport
YDR280W	[T] RRP45 rRNA processing protein
YGR095C	[T] RRP46 involved in rRNA processing
YHR069C	[T] RRP4 3’->5’exoribonuclease required for 3’end formation of 5.8S rRNA
YOR001W	[U] RRP6 similarity to human nucleolar 100K polymyositis-scleroderma protein
YLR022C	[U] YLR022c similarity to C.elegans and M.jannaschii hypothetical proteins
YHR088W	[U] RPF1 similarity to hypothetical protein YNL075w
Q-clique 16	**Function Annotation**
YIL147C	[C] SLN1 two-component signal transducer
YMR262W	[D] YMR262w similarity to S.pombe scn1 protein
YLR153C	[E] ACS2 acetyl-coenzyme A synthetase
YIL160C	[E] POT1 acetyl-CoA C-acyltransferase, peroxisomal
YGL205W	[E] POX1 acyl-CoA oxidase
YER061C	[E] CEM1 beta-keto-acyl-ACP synthase, mitochondrial
YIL042C	[G] YIL042c similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
YJR148W	[G] BAT2 branched chain amino acid aminotransferase, cytosolic
YHR208W	[G] BAT1 branched chain amino acid aminotransferase, mitochondrial
YOR180C	[M] DCI1 Enoyl-CoA Hydratase, peroxisomal
YKR009C	[M] FOX2 hydratase-dehydrogenase-epimerase, peroxisomal
YBR222C	[M] FAT2 AMP-binding protein, peroxisomal
YBR208C	[M] DUR1,2 urea amidolyase
YOR221C	[M] MCT1 malonyl-CoA:ACP transferase
YPL231W	[M] FAS2 fatty-acyl-CoA synthase, alpha chain
YPL028W	[M] ERG10 acetyl-CoA C-acetyltransferase, cytosolic
YJR057W	[M] CDC8 dTMP kinase
YDL168W	[M] SFA1 long-chain alcohol dehydrogenase
YLR284C	[M] ECI1 delta3-cis-delta2-trans-enoyl-CoA isomerase
YKL182W	[M] FAS1 fatty-acyl-CoA synthase, beta chain
YNR016C	[M] ACC1 acetyl-CoA carboxylase
YKL192C	[M] ACP1 mitochonrial acyl-carrier protein
YBR041W	[M] FAT1 very long-chain fatty acyl-CoA synthetase
YJR149W	[M] YJR149w similarity to 2-nitropropane dioxygenase
YCR003W	[P] MRPL32 ribosomal protein YmL32, mitochondrial
YGR263C	[U] YGR263c weak similarity to E.coli lipase like enzyme
YDR036C	[U] YDR036c similarity to enoyl CoA hydratase
YGL059W	[U] YGL059w similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
YDR428C	[U] YDR428c weak similarity to predicted esterase of proteobacterium
YBL055C	[U] YBL055c similarity to hypothetical S.pombe protein
YOR093C	[U] YOR093c similarity to S.pombe hypothetical protein SPAC22F3.04
Q-clique 17	**Function Annotation**
YGR245C	[D] SDA1 required for normal organization of the actin cytoskeleton; required for passage

	through Start
YER006W	[O] YER006w similarity to P.polycephalum myosin-related protein mlpA
YOR206W	[O] NOC2 crucial for intranuclear movement of ribosomal precursor particles
YPR016C	[P] TIF6 translation initiation factor 6 (eIF6)
YNL061W	[T] NOP2 nucleolar protein
YKL009W	[T] MRT4 mRNA turnover 4
YLL008W	[T] DRS1 RNA helicase of the DEAD box family
YDL051W	[T] LHP1 RNA binding protein
YDL031W	[T] DBP10 putative RNA helicase involved in ribosome biogenesis
YNL182C	[U] YNL182c weak similarity to S.pombe hypothetical protein
YLR106C	[U] YLR106c similarity to Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene
YHR052W	[U] CIC1 adaptor protein specifically linking the 26S proteasome to its substrate, the SCF component CDC4
YPL093W	[U] NOG1 similarity to M.jannaschii GTP-binding protein
YGR090W	[U] YGR090w similarity to PIR:T40678 hypothetical protein SPBC776.08c S. pombe
YFR001W	[U] LOC1 weak similarity to rabbit triadin SPP41P
YNL002C	[U] RLP7 strong similarity to mammalian ribosomal L7 proteins
YLR074C	[U] BUD20 weak similarity to human zinc finger protein
YGR103W	[U] RRP13 similarity to zebrafish essential for embryonic development gene pescadillo
YNL110C	[U] YNL110c weak similarity to fruit fly RNA-binding protein
YGL111W	[U] YGL111w weak similarity to hypothetical protein S. pombe
YOL077C	[U] BRX1 strong similarity to C.elegans K12H4.3 protein
YMR049C	[U] ERB1 weak similarity to A.thaliana PRL1 protein
YDR101C	[U] YDR101c weak similarity to proliferation-associated protein
YDR496C	[U] PUF6 similarity to hypothetical human and C.elegans proteins
YKR081C	[U] YKR081c strong similarity to hypothetical protein S. pombe
YHR197W	[U] YHR197w weak similarity to PIR:T22172 hypothetical protein F44E5.2 C. elegans
YER126C	[U] KRE32 weak similarity to E.coli colicin N
Q-clique 18	**Function Annotation**
YNL222W	[B] SSU72 suppressor of cs mutant of SUA7
YER133W	[C] GLC7 ser/thr phosphoprotein phosphatase 1, catalytic chain
YDR195W	[T] REF2 RNA 3'-end formation protein
YMR061W	[T] RNA14 component of pre-mRNA 3'-end processing factor CF I
YDR301W	[T] CFT1 pre-mRNA 3'-end processing factor CF II
YAL043C	[T] PTA1 pre-tRNA processing protein / PF I subunit
YKR002W	[T] PAP1 poly(A) polymerase
YJR093C	[T] FIP1 component of pre-mRNA polyadenylation factor PF I
YDR228C	[T] PCF11 component of pre-mRNA 3'-end processing factor CF I
YNL317W	[T] PFS2 polyadenylation factor I subunit 2 required for mRNA 3'-end processing, bridges two mRNA 3'-end processing factors
YLR115W	[T] CFT2 cleavage and polyadenylation specificity factor, part of CF II
YPR107C	[T] YTH1 protein of the 3' processing complex
YLR277C	[T] YSH1 component of pre-mRNA polyadenylation factor PF I
YGR156W	[U] PTI1 weak similarity to PIR:A40220 cleavage stimulation factor 64K chain - human
YKL059C	[U] YKL059c similarity to C.elegans hypothetical protein
YKL018W	[U] SWD2 similarity to C.elegans hypothetical protein
Q-clique 19	**Function Annotation**
YML054C	[E] CYB2 lactate dehydrogenase cytochrome b2
YMR208W	[M] ERG12 mevalonate kinase
YLR048W	[P] RPS0B 40S ribosomal protein p40 homolog B
YPL118W	[P] MRP51 mitochondrial ribosomal protein of the small subunit
YDR337W	[P] MRPS28 ribosomal protein of the small subunit, mitochondrial
YBR146W	[P] MRPS9 ribosomal protein S9 precursor, mitochondrial
YNL137C	[P] NAM9 ribosomal protein, mitochondrial

YGR214W	[P] RPS0A 40S ribosomal protein p40 homolog A
YDR347W	[P] MRP1 ribosomal protein of the small subunit, mitochondrial
YNL306W	[P] MRPS18 ribosomal protein of the small subunit, mitochondrial
YOL120C	[P] RPL18A 60S large subunit ribosomal protein S18.e
YNL301C	[P] RPL18B 60S large subunit ribosomal protein L18.e
YGR084C	[P] MRP13 ribosomal protein of the small subunit, mitochondrial
YHL004W	[P] MRP4 ribosomal protein of the small subunit, mitochondrial
YPR187W	[T] RPO26 DNA-directed RNA polymerase I, II, III 18 KD subunit
YOR210W	[T] RPB10 DNA-directed polymerase I, II, III 8.3 subunit
YIL093C	[U] RSM25 weak similarity to S.pombe hypothetical protein SPBC16A3
YKL155C	[U] RSM22 similarity to S. pombe SPAC1420.04c putative cytochrome c oxidase assembly protein
YJR008W	[U] YJR008w similarity to S.pombe hypothetical protein
YGL129C	[U] RSM23 similarity to S.pombe hypothetical protein SPBC29A3.15C - putative mitochondrial function
YDR036C	[U] YDR036c similarity to enoyl CoA hydratase
Q-clique 20	**Function Annotation**
YLR244C	[F] MAP1 methionine aminopeptidase, isoform 1
YBL091C	[F] MAP2 methionine aminopeptidase, isoform 2
YDR226W	[M] ADK1 adenylate kinase, cytosolic
YJL063C	[P] MRPL8 ribosomal protein L17, mitochondrial
YGR118W	[P] RPS23A 40S small subunit ribosomal protein S23.e
YGL135W	[P] RPL1B 60S large subunit ribosomal protein
YEL054C	[P] RPL12A 60S large subunit ribosomal protein L12.e
YOR335C	[P] ALA1 alanyl-tRNA synthetase, cytosolic
YDL202W	[P] MRPL11 ribosomal protein of the large subunit, mitochondrial
YGL068W	[P] YGL068w strong similarity to Cricetus mitochrondial ribosomal L12 protein
YPL220W	[P] RPL1A ribosomal protein
YPR132W	[P] RPS23B 40S small subunit ribosomal protein S23.e
YPL183W-A	[P] YPL183w-a strong similarity to mitochondrial and bacterial ribosomal L36 proteins
YGL030W	[P] RPL30 60S large subunit ribosomal protein L30.e
YDR418W	[P] RPL12B 60S large subunit ribosomal protein L12.e
YHL015W	[P] RPS20 ribosomal protein
YLR340W	[P] RPP0 acidic ribosomal protein L10.e
YBL038W	[P] MRPL16 ribosomal protein of the large subunit, mitochondrial
YLR075W	[P] RPL10 60S large subunit ribosomal protein
YNL185C	[P] MRPL19 ribosomal protein of the large subunit, mitochondrial
YJR123W	[P] RPS5 ribosomal protein S5.e
YML009C	[P] MRPL39 60S ribosomal protein, mitochondrial
YMR260C	[P] TIF11 translation initiation factor eIF1a
YNR036C	[P] YNR036c strong similarity to ribosomal protein S12
YDR116C	[P] YDR116c similarity to bacterial ribosomal L1 proteins
YML010W	[T] SPT5 transcription elongation protein
YBR154C	[T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit
YOR151C	[T] RPB2 DNA-directed RNA polymerase II, 140 kDa chain
YOR341W	[T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit
YPR010C	[T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit
YDL140C	[T] RPO21 DNA-directed RNA polymerase II, 215 KD subunit
YKL009W	[T] MRT4 mRNA turnover 4
YOR207C	[T] RET1 DNA-directed RNA polymerase III, 130 KD subunit
YOR116C	[T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit
YDR101C	[U] YDR101c weak similarity to proliferation-associated protein
Q-clique 21	**Function Annotation**
YLR153C	[E] ACS2 acetyl-coenzyme A synthetase
YER061C	[E] CEM1 beta-keto-acyl-ACP synthase, mitochondrial

YAL054C	[E] ACS1 acetyl-CoA synthetase
YKL182W	[M] FAS1 fatty-acyl-CoA synthase, beta chain
YKL192C	[M] ACP1 mitochonrial acyl-carrier protein
YPL231W	[M] FAS2 fatty-acyl-CoA synthase, alpha chain
YBR041W	[M] FAT1 very long-chain fatty acyl-CoA synthetase
YBR222C	[M] FAT2 AMP-binding protein, peroxisomal
YKR009C	[M] FOX2 hydratase-dehydrogenase-epimerase, peroxisomal
YNR016C	[M] ACC1 acetyl-CoA carboxylase
YBR208C	[M] DUR1,2 urea amidolyase
YNL137C	[P] NAM9 ribosomal protein, mitochondrial
YDR041W	[P] RSM10 component of the mitochondrial ribosomal small subunit
YNL306W	[P] MRPS18 ribosomal protein of the small subunit, mitochondrial
YDR347W	[P] MRP1 ribosomal protein of the small subunit, mitochondrial
YGR084C	[P] MRP13 ribosomal protein of the small subunit, mitochondrial
YPL118W	[P] MRP51 mitochondrial ribosomal protein of the small subunit
YJR113C	[P] RSM7 similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7
YDR337W	[P] MRPS28 ribosomal protein of the small subunit, mitochondrial
YIL093C	[U] RSM25 weak similarity to S.pombe hypothetical protein SPBC16A3
YOR093C	[U] YOR093c similarity to S.pombe hypothetical protein SPAC22F3.04
YKL155C	[U] RSM22 similarity to S. pombe SPAC1420.04c putative cytochrome c oxidase assembly protein
YDR036C	[U] YDR036c similarity to enoyl CoA hydratase
YGL129C	[U] RSM23 similarity to S.pombe hypothetical protein SPBC29A3.15C - putative mitochondrial function
Q-clique 22	**Function Annotation**
YLR006C	[A] SSK1 two-component signal transducer
YDL235C	[A] YPD1 phosphorelay intermediate between SLN1P and SSK1P
YHR206W	[B] SKN7 transcription factor with similarity to HSF1P
YIL147C	[C] SLN1 two-component signal transducer
YFL033C	[C] RIM15 protein kinase involved in expression of meiotic genes
YDR076W	[D] RAD55 DNA repair protein
Q0250	[E] COX2 cytochrome-c oxidase subunit II
Q0275	[E] COX3 cytochrome-c oxidase chain III
Q0045	[E] COX1 cytochrome-c oxidase subunit I
YGR112W	[E] SHY1 SURF homologue protein
YDR292C	[F] SRP101 signal recognition particle receptor, alpha chain
YDR127W	[G] ARO1 arom pentafunctional enzyme
YIL042C	[G] YIL042c similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
YKL104C	[M] GFA1 glucosamine--fructose-6-phosphate transaminase
YNL123W	[U] YNL123w weak similarity to C.jejuni serine protease
YGL059W	[U] YGL059w similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
Q-clique 23	**Function Annotation**
YNL306W	[P] MRPS18 ribosomal protein of the small subunit, mitochondrial
YJR113C	[P] RSM7 similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7
YDR347W	[P] MRP1 ribosomal protein of the small subunit, mitochondrial
YGR084C	[P] MRP13 ribosomal protein of the small subunit, mitochondrial
YDR041W	[P] RSM10 component of the mitochondrial ribosomal small subunit
YBR146W	[P] MRPS9 ribosomal protein S9 precursor, mitochondrial
YPL118W	[P] MRP51 mitochondrial ribosomal protein of the small subunit
YDR337W	[P] MRPS28 ribosomal protein of the small subunit, mitochondrial
YNL137C	[P] NAM9 ribosomal protein, mitochondrial
YGL129C	[U] RSM23 similarity to S.pombe hypothetical protein SPBC29A3.15C - putative mitochondrial function
YIL093C	[U] RSM25 weak similarity to S.pombe hypothetical protein SPBC16A3
YDR036C	[U] YDR036c similarity to enoyl CoA hydratase

YKL155C	[U] RSM22 similarity to S. pombe SPAC1420.04c putative cytochrome c oxidase assembly protein
Q-clique 24	**Function Annotation**
YMR208W	[M] ERG12 mevalonate kinase
YDL083C	[P] RPS16B ribosomal protein S16.e
YMR143W	[P] RPS16A ribosomal protein S16.e
YLR048W	[P] RPS0B 40S ribosomal protein p40 homolog B
YOR150W	[P] MRPL23 ribosomal protein of the large subunit, mitochondrial
YNL069C	[P] RPL16B 60S large subunit ribosomal protein
YNL301C	[P] RPL18B 60S large subunit ribosomal protein L18.e
YOL120C	[P] RPL18A 60S large subunit ribosomal protein S18.e
YIL133C	[P] RPL16A 60S large subunit ribosomal protein
YGR214W	[P] RPS0A 40S ribosomal protein p40 homolog A
YKL144C	[T] RPC25 DNA-direcred RNA polymerase III, 25 KD subunit
YPR190C	[T] RPC82 DNA-directed RNA polymerase III, 82 KD subunit
YPR187W	[T] RPO26 DNA-directed RNA polymerase I, II, III 18 KD subunit
YDL150W	[T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit
YPR010C	[T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit
YNL113W	[T] RPC19 DNA-directed RNA polymerase I,III 16 KD subunit
YNL248C	[T] RPA49 DNA-directed RNA polymerase A (I) chain, 46 kDa
YKR025W	[T] RPC37 Pol III transcription
YPR110C	[T] RPC40 DNA-directed RNA polymerase I, III 40 KD subunit
YBR154C	[T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit
YNL151C	[T] RPC31 DNA-directed RNA polymerase III, 31 KD subunit
YNR003C	[T] RPC34 DNA-directed RNA polymerase III, 34 KD subunit
YOR116C	[T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit
YOR207C	[T] RET1 DNA-directed RNA polymerase III, 130 KD subunit
YOR224C	[T] RPB8 DNA-directed RNA polymerase I, II, III 16 KD subunit
YOR210W	[T] RPB10 DNA-directed polymerase I, II, III 8.3 subunit
YJR008W	[U] YJR008w similarity to S.pombe hypothetical protein
Q-clique 25	**Function Annotation**
YLR006C	[A] SSK1 two-component signal transducer
YHR206W	[B] SKN7 transcription factor with similarity to HSF1P
YIL147C	[C] SLN1 two-component signal transducer
YFL033C	[C] RIM15 protein kinase involved in expression of meiotic genes
YML054C	[E] CYB2 lactate dehydrogenase cytochrome b2
YGR112W	[E] SHY1 SURF homologue protein
Q0275	[E] COX3 cytochrome-c oxidase chain III
Q0045	[E] COX1 cytochrome-c oxidase subunit I
Q0250	[E] COX2 cytochrome-c oxidase subunit II
YDR292C	[F] SRP101 signal recognition particle receptor, alpha chain
YIL042C	[G] YIL042c similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
YER069W	[G] ARG5,6 acetylglutamate kinase and acetylglutamyl-phosphate reductase
YDR127W	[G] ARO1 arom pentafunctional enzyme
YGL059W	[U] YGL059w similarity to rat branched-chain alpha-ketoacid dehydrogenase kinase
Q-clique 26	**Function Annotation**
YLR447C	[A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar
YGR020C	[A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar
YHR026W	[A] PPA1 H+-ATPase 23 KD subunit, vacuolar
YMR054W	[A] STV1 H+-ATPase V0 domain 102 KD subunit, not vacuolar
YEL051W	[A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar
YDL227C	[C] HO homothallic switching endonuclease
Q0130	[E] OLI1 F1F0-ATPase complex, F0 subunit 9
YBR127C	[O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar
YEL027W	[O] CUP5 H+-ATPase V0 domain 17 KD subunit, vacuolar

YOR332W	[O] VMA4 H+-ATPase V1 domain 27 KD subunit, vacuolar
YPL234C	[O] TFP3 H+-ATPase V0 domain 17 KD subunit, vacuolar
YOR270C	[O] VPH1 H+-ATPase V0 domain 95K subunit, vacuolar
YDL185W	[O] TFP1 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar
YPR010C	[T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit
YDL150W	[T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit
YNL113W	[T] RPC19 DNA-directed RNA polymerase I,III 16 KD subunit
YKR025W	[T] RPC37 Pol III transcription
YBR154C	[T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit
YNL248C	[T] RPA49 DNA-directed RNA polymerase A (I) chain, 46 kDa
YNR003C	[T] RPC34 DNA-directed RNA polymerase III, 34 KD subunit
YOR341W	[T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit
YNL151C	[T] RPC31 DNA-directed RNA polymerase III, 31 KD subunit
YOR116C	[T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit
YOR207C	[T] RET1 DNA-directed RNA polymerase III, 130 KD subunit
YKL144C	[T] RPC25 DNA-direcred RNA polymerase III, 25 KD subunit
YOR224C	[T] RPB8 DNA-directed RNA polymerase I, II, III 16 KD subunit
YPR187W	[T] RPO26 DNA-directed RNA polymerase I, II, III 18 KD subunit
YPR190C	[T] RPC82 DNA-directed RNA polymerase III, 82 KD subunit
Q-clique 27	**Function Annotation**
YNL189W	[O] SRP1 karyopherin-alpha or importin
YDR432W	[O] NPL3 nucleolar protein
YLR347C	[O] KAP95 karyopherin-beta
YGR162W	[P] TIF4631 mRNA cap-binding protein (eIF4F), 150K subunit
YGL049C	[P] TIF4632 mRNA cap-binding protein (eIF4F), 130K subunit
YLR298C	[T] YHC1 associated with the U1 snRNP complex
YGR074W	[T] SMD1 snRNA-associated protein
YML046W	[T] PRP39 pre-mRNA splicing factor
YKL012W	[T] PRP40 splicing factor
YPL178W	[T] CBC2 small subunit of the nuclear cap-binding protein complex CBC
YDL087C	[T] LUC7 yeast U1 snRNP protein with a role in 5'splice site recognition
YLR275W	[T] SMD2 U1 snRNP protein of the Sm class
YLR147C	[T] SMD3 spliceosomal snRNA-associated Sm core protein required for pre-mRNA splicing
YGR013W	[T] SNU71 associated with U1 snRNP, no counterpart in mammalian U1 snRNP
YDR235W	[T] PRP42 U1 snRNP associated protein, required for pre-mRNA splicing
YER029C	[T] SMB1 associated with U1 snRNP as part of the Sm-core that is common to all spliceosomal snRNPs
YHR086W	[T] NAM8 meiotic recombination protein
YMR125W	[T] STO1 large subunit of the nuclear cap-binding protein complex CBC
YIL061C	[T] SNP1 U1 small nuclear ribonucleoprotein
YDR240C	[T] SNU56 U1 snRNA protein, no counterpart in mammalian snRNP
YBR119W	[T] MUD1 U1 snRNP-specific A protein
Q-clique 28	**Function Annotation**
YLR117C	[D] CLF1 strong similarity to Drosophila putative cell cycle control protein crn
YDR364C	[D] CDC40 cell division control protein
YMR213W	[D] CEF1 required during G2/M transition
YML049C	[O] RSE1 involved in RNA splicing and ER to Golgi transport
YKL173W	[P] SNU114 U5 snRNP-specific protein
YGL128C	[R] YGL128c weak similarity to dnaJ proteins
YDL030W	[T] PRP9 pre-mRNA splicing factor (snRNA-associated protein)
YPR101W	[T] SNT309 splicing factor
YGR091W	[T] PRP31 pre-mRNA splicing protein
YPR178W	[T] PRP4 U4/U6 snRNP 52 KD protein
YLL036C	[T] PRP19 non-snRNP sliceosome component required for DNA repair

YJL203W	[T] PRP21 pre-mRNA splicing factor
YMR240C	[T] CUS1 U2 snRNP protein
YBR055C	[T] PRP6 snRNP(U4/U6)-associated splicing factor
YPL213W	[T] LEA1 U2 A'snRNP protein
YDR416W	[T] SYF1 synthetic lethal with CDC40
YMR288W	[T] HSH155 component of a multiprotein splicing factor
YGL120C	[T] PRP43 involved in spliceosome disassembly
YAL032C	[T] PRP45 pre-mRNA splicing factor
YGR278W	[U] YGR278w similarity to C.elegans LET-858
YLR424W	[U] YLR424w weak similarity to STU1P
YPL151C	[U] PRP46 strong similarity to A.thaliana PRL1 and PRL2 proteins
YDL209C	[U] YDL209c similarity to hypothetical S. pombe protein
Q-clique 29	**Function Annotation**
YJR113C	[P] RSM7 similarity to bacterial, chloroplast and mitochondrial ribosomal protein S7
YGL030W	[P] RPL30 60S large subunit ribosomal protein L30.e
YNL113W	[T] RPC19 DNA-directed RNA polymerase I,III 16 KD subunit
YKR025W	[T] RPC37 Pol III transcription
YBR154C	[T] RPB5 DNA-directed RNA polymerase I, II, III 25 KD subunit
YJR063W	[T] RPA12 DNA-directed RNA polymerase I, 13.7 KD subunit
YOR341W	[T] RPA190 DNA-directed RNA polymerase I, 190 KD alpha subunit
YNL248C	[T] RPA49 DNA-directed RNA polymerase A (I) chain, 46 kDa
YNR003C	[T] RPC34 DNA-directed RNA polymerase III, 34 KD subunit
YNL151C	[T] RPC31 DNA-directed RNA polymerase III, 31 KD subunit
YKL144C	[T] RPC25 DNA-direcred RNA polymerase III, 25 KD subunit
YOR116C	[T] RPO31 DNA-directed RNA polymerase III, 160 KD subunit
YPR190C	[T] RPC82 DNA-directed RNA polymerase III, 82 KD subunit
YOR207C	[T] RET1 DNA-directed RNA polymerase III, 130 KD subunit
YOR224C	[T] RPB8 DNA-directed RNA polymerase I, II, III 16 KD subunit
YDL150W	[T] RPC53 DNA-directed RNA polymerase III, 47 KD subunit
YPR010C	[T] RPA135 DNA-directed RNA polymerase I, 135 KD subunit
Q-clique 30	**Function Annotation**
YEL051W	[A] VMA8 H+-ATPsynthase V1 domain 32 KD subunit, vacuolar
YHR026W	[A] PPA1 H+-ATPase 23 KD subunit, vacuolar
YGR020C	[A] VMA7 H+-ATPase V1 domain 14 kDa subunit, vacuolar
YLR447C	[A] VMA6 H+-ATPase V0 domain 36 KD subunit, vacuolar
Q0130	[E] OLI1 F1F0-ATPase complex, F0 subunit 9
YJR121W	[E] ATP2 F1F0-ATPase complex, F1 beta subunit
Q0085	[E] ATP6 F1F0-ATPase complex, FO A subunit
YDR298C	[E] ATP5 F1F0-ATPase complex, OSCP subunit
YBL099W	[E] ATP1 F1F0-ATPase complex, F1 alpha subunit
YDL004W	[E] ATP16 F1F0-ATPase complex, F1 delta subunit
YBR039W	[E] ATP3 F1F0-ATPase complex, F1 gamma subunit
YBR127C	[O] VMA2 H+-ATPase V1 domain 60 KD subunit, vacuolar
YEL027W	[O] CUP5 H+-ATPase V0 domain 17 KD subunit, vacuolar
YOR332W	[O] VMA4 H+-ATPase V1 domain 27 KD subunit, vacuolar
YPL234C	[O] TFP3 H+-ATPase V0 domain 17 KD subunit, vacuolar
YDL185W	[O] TFP1 H+-ATPase V1 domain 69 KD catalytic subunit, vacuolar
YGL236C	[P] MTO1 strong similarity to gidA E.coli protein
YLR289W	[P] GUF1 strong similarity to E. coli elongation factor-type GTP-binding protein lepa
Q-clique 31	**Function Annotation**
YMR118C	[E] YMR118c strong similarity to succinate dehydrogenase
YLL041C	[E] SDH2 succinate dehydrogenase iron-sulfur protein subunit
YDR148C	[E] KGD2 2-oxoglutarate dehydrogenase complex E2 component
YOR142W	[E] LSC1 succinate-CoA ligase alpha subunit
YER178W	[E] PDA1 pyruvate dehydrogenase (lipoamide) alpha chain precursor

YBR221C	[E] PDB1 pyruvate dehydrogenase (lipoamide) beta chain precursor
YIL125W	[E] KGD1 2-oxoglutarate dehydrogenase complex E1 component
YNL071W	[E] LAT1 dihydrolipoamide S-acetyltransferase
YGR244C	[E] LSC2 succinate-CoA ligase beta subunit
YKL141W	[E] SDH3 cytochrome b560 subunit of respiratory complex II
YGR193C	[E] PDX1 pyruvate dehydrogenase complex protein X
YOR375C	[G] GDH1 glutamate dehydrogenase (NADP+)
YFL018C	[G] LPD1 dihydrolipoamide dehydrogenase precursor
YAL062W	[G] GDH3 NADP-glutamate dehydrogenase
YML022W	[M] APT1 adenine phosphoribosyltransferase
YOR196C	[M] LIP5 lipoic acid synthase
YDR441C	[M] APT2 adenine phosphoribosyltransferase
YPL017C	[M] YPL017c strong similarity to LPD1P and other dihydrolipoamide dehydrogenases
YJL046W	[U] YJL046w similarity to E.coli lipoate-protein ligase A
Q-clique 30	**Function Annotation**
YMR262W	[D] YMR262w similarity to S.pombe scn1 protein
YER061C	[E] CEM1 beta-keto-acyl-ACP synthase, mitochondrial
YPL148C	[F] PPT2 phosphopantetheine protein transferase
YHR208W	[G] BAT1 branched chain amino acid aminotransferase, mitochondrial
YJR148W	[G] BAT2 branched chain amino acid aminotransferase, cytosolic
YKL192C	[M] ACP1 mitochonrial acyl-carrier protein
YPL231W	[M] FAS2 fatty-acyl-CoA synthase, alpha chain
YOR221C	[M] MCT1 malonyl-CoA:ACP transferase
YJR057W	[M] CDC8 dTMP kinase
YKL182W	[M] FAS1 fatty-acyl-CoA synthase, beta chain
YDR454C	[M] GUK1 guanylate kinase
YMR024W	[P] MRPL3 ribosomal protein of the large subunit, mitochondrial
YCR003W	[P] MRPL32 ribosomal protein YmL32, mitochondrial
YMR239C	[T] RNT1 double-stranded ribonuclease
YBL055C	[U] YBL055c similarity to hypothetical S.pombe protein
Q-clique 33	**Function Annotation**
YCL017C	[A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution
YPR067W	[A] ISA2 mitochondrial protein required for iron metabolism
YLL027W	[A] ISA1 mitochondrial protein required for normal iron metabolism
YGL018C	[F] JAC1 molecular chaperone
YPL135W	[M] ISU1 strong similarity to nitrogen fixation protein (nifU)
YOR226C	[M] ISU2 strong similarity to nitrogen fixation proteins
YLR231C	[M] YLR231c strong similarity to rat kynureninase
YKL067W	[M] YNK1 nucleoside diphosphate kinase
YDR283C	[P] GCN2 ser/thr protein kinase
YPR033C	[P] HTS1 histidine--tRNA ligase, mitochondrial
YPL252C	[U] YAH1 similarity to adrenodoxin and ferrodoxin
Q-clique 34	**Function Annotation**
YLL027W	[A] ISA1 mitochondrial protein required for normal iron metabolism
YCL017C	[A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution
YPR067W	[A] ISA2 mitochondrial protein required for iron metabolism
YGL018C	[F] JAC1 molecular chaperone
YLR231C	[M] YLR231c strong similarity to rat kynureninase
YPL135W	[M] ISU1 strong similarity to nitrogen fixation protein (nifU)
YKL040C	[M] NFU1 iron homeostasis
YOR226C	[M] ISU2 strong similarity to nitrogen fixation proteins
YKL067W	[M] YNK1 nucleoside diphosphate kinase
YPR033C	[P] HTS1 histidine--tRNA ligase, mitochondrial
YDR283C	[P] GCN2 ser/thr protein kinase
YPL252C	[U] YAH1 similarity to adrenodoxin and ferrodoxin

Q-clique 35	**Function Annotation**
YMR118C	[E] YMR118c strong similarity to succinate dehydrogenase
YLL041C	[E] SDH2 succinate dehydrogenase iron-sulfur protein subunit
YDR148C	[E] KGD2 2-oxoglutarate dehydrogenase complex E2 component
YOR142W	[E] LSC1 succinate-CoA ligase alpha subunit
YER178W	[E] PDA1 pyruvate dehydrogenase (lipoamide) alpha chain precursor
YBR221C	[E] PDB1 pyruvate dehydrogenase (lipoamide) beta chain precursor
YIL125W	[E] KGD1 2-oxoglutarate dehydrogenase complex E1 component
YNL071W	[E] LAT1 dihydrolipoamide S-acetyltransferase
YGR244C	[E] LSC2 succinate-CoA ligase beta subunit
YKL141W	[E] SDH3 cytochrome b560 subunit of respiratory complex II
YGR193C	[E] PDX1 pyruvate dehydrogenase complex protein X
YOR375C	[G] GDH1 glutamate dehydrogenase (NADP+)
YFL018C	[G] LPD1 dihydrolipoamide dehydrogenase precursor
YAL062W	[G] GDH3 NADP-glutamate dehydrogenase
YML022W	[M] APT1 adenine phosphoribosyltransferase
YOR196C	[M] LIP5 lipoic acid synthase
YDR441C	[M] APT2 adenine phosphoribosyltransferase
YPL017C	[M] YPL017c strong similarity to LPD1P and other dihydrolipoamide dehydrogenases
YPL091W	[R] GLR1 glutathione reductase (NADPH)
YJL046W	[U] YJL046w similarity to E.coli lipoate-protein ligase A
Q-clique 36	**Function Annotation**
YGL211W	[U] YGL211w similarity to M.jannaschii hypothetical proteins MJ1157 and MJ1478
YNR016C	[M] ACC1 acetyl-CoA carboxylase
YNL026W	[U] YNL026w similarity to S.pombe hypothetical protein
YLR048W	[P] RPS0B 40S ribosomal protein p40 homolog B
YGR214W	[P] RPS0A 40S ribosomal protein p40 homolog A
YNL072W	[M] RNH35 RNase H(35), a 35 kDa ribonuclease H
YHR038W	[P] FIL1 Killed in Mutagen, sensitive to Diepoxybutane and/or Mitomycin C
YDL193W	[U] YDL193w similarity to N.crassa hypothetical 32 kDa protein
YMR101C	[M] SRT1 cis-prenyltransferase homologue
YBR029C	[M] CDS1 CDP-diacylglycerol synthase
YBR002C	[F] RER2 cis-prenyltransferase, a key enzyme in dolichol synthesis
Q-clique 37	**Function Annotation**
YGL018C	[F] JAC1 molecular chaperone
YOR226C	[M] ISU2 strong similarity to nitrogen fixation proteins
YPR067W	[A] ISA2 mitochondrial protein required for iron metabolism
YPR033C	[P] HTS1 histidine--tRNA ligase, mitochondrial
YPL252C	[U] YAH1 similarity to adrenodoxin and ferrodoxin
YLR231C	[M] YLR231c strong similarity to rat kynureninase
YPL135W	[M] ISU1 strong similarity to nitrogen fixation protein (nifU)
YCL017C	[A] NFS1 regulates Iron-Sulfur cluster proteins, cellular Iron uptake, andIron distribution
YKL067W	[M] YNK1 nucleoside diphosphate kinase
YDR283C	[P] GCN2 ser/thr protein kinase
YLL027W	[A] ISA1 mitochondrial protein required for normal iron metabolism
Q-clique 38	**Function Annotation**
YBR272C	[D] HSM3 mismatch repair protein
YOR261C	[F] RPN8 26S proteasome regulatory subunit
YER021W	[F] RPN3 26S proteasome regulatory subunit
YDR394W	[F] RPT3 26S proteasome regulatory subunit
YDL007W	[F] RPT2 26S proteasome regulatory subunit
YFR004W	[F] RPN11 26S proteasome regulatory subunit
YOR259C	[F] RPT4 26S proteasome regulatory subunit
YDL097C	[F] RPN6 subunit of the regulatory particle of the proteasome
YOR117W	[F] RPT5 26S proteasome regulatory subunit

YGL048C	[F] RPT6 26S proteasome regulatory subunit
YPR108W	[F] RPN7 subunit of the regulatory particle of the proteasome
YDL147W	[F] RPN5 subunit of the regulatory particle of the proteasome
YHR200W	[F] RPN10 26S proteasome regulatory subunit
YDR427W	[F] RPN9 subunit of the regulatory particle of the proteasome
YKL145W	[F] RPT1 26S proteasome regulatory subunit
YGR232W	[F] NAS6 possible homolog of human 26S proteasome regulatory subunit p28
YJR109C	[G] CPA2 arginine-specific carbamoylphosphate synthase, large chain
YKL104C	[M] GFA1 glucosamine--fructose-6-phosphate transaminase
YLR421C	[U] RPN13 weak similarity to human 42K membrane glycoprotein
Q-clique 39	**Function Annotation**
YGR135W	[F] PRE9 20S proteasome subunit Y13 (alpha3)
YER012W	[F] PRE1 20S proteasome subunit C11(beta4)
YMR314W	[F] PRE5 20S proteasome subunit(alpha6)
YOR362C	[F] PRE10 20S proteasome subunit C1 (alpha7)
YPR103W	[F] PRE2 20S proteasome subunit (beta5)
YER094C	[F] PUP3 20S proteasome subunit (beta3)
YGR253C	[F] PUP2 20S proteasome subunit(alpha5)
YOL038W	[F] PRE6 20S proteasome subunit (alpha4)
YML092C	[F] PRE8 20S proteasome subunit Y7 (alpha2)
YBL041W	[F] PRE7 20S proteasome subunit(beta6)
YGL011C	[F] SCL1 20S proteasome subunit YC7ALPHA/Y8 (alpha1)
YFR050C	[F] PRE4 20S proteasome subunit(beta7)
YJL001W	[F] PRE3 20S proteasome subunit (beta1)
Q-clique 40	**Function Annotation**
YBR002C	[F] RER2 cis-prenyltransferase, a key enzyme in dolichol synthesis
YBR029C	[M] CDS1 CDP-diacylglycerol synthase
YNL072W	[M] RNH35 RNase H(35), a 35 kDa ribonuclease H
YMR101C	[M] SRT1 cis-prenyltransferase homologue
YNR016C	[M] ACC1 acetyl-CoA carboxylase
YER087W	[P] YER087w similarity to E.coli prolyl-tRNA synthetase
YLR048W	[P] RPS0B 40S ribosomal protein p40 homolog B
YHR020W	[P] YHR020w strong similarity to human glutamyl-prolyl-tRNA synthetase and fruit fly multifunctional aminoacyl-tRNA synthetase
YHR038W	[P] FIL1 Killed in Mutagen, sensitive to Diepoxybutane and/or Mitomycin C
YHL004W	[P] MRP4 ribosomal protein of the small subunit, mitochondrial
YGR214W	[P] RPS0A 40S ribosomal protein p40 homolog A
YNL026W	[U] YNL026w similarity to S.pombe hypothetical protein
YDL193W	[U] YDL193w similarity to N.crassa hypothetical 32 kDa protein
YGL211W	[U] YGL211w similarity to M.jannaschii hypothetical proteins MJ1157 and MJ1478
Q-clique 41	**Function Annotation**
YJL046W	[U] YJL046w similarity to E.coli lipoate-protein ligase A
YMR118C	[E] YMR118c strong similarity to succinate dehydrogenase
YIL125W	[E] KGD1 2-oxoglutarate dehydrogenase complex E1 component
YOR142W	[E] LSC1 succinate-CoA ligase alpha subunit
YLL041C	[E] SDH2 succinate dehydrogenase iron-sulfur protein subunit
YGR244C	[E] LSC2 succinate-CoA ligase beta subunit
YGR193C	[E] PDX1 pyruvate dehydrogenase complex protein X
YNL071W	[E] LAT1 dihydrolipoamide S-acetyltransferase
YER178W	[E] PDA1 pyruvate dehydrogenase (lipoamide) alpha chain precursor
YDR148C	[E] KGD2 2-oxoglutarate dehydrogenase complex E2 component
YOR196C	[M] LIP5 lipoic acid synthase
YFL018C	[G] LPD1 dihydrolipoamide dehydrogenase precursor
YKL141W	[E] SDH3 cytochrome b560 subunit of respiratory complex II
Q-clique 42	**Function Annotation**

YCR003W	[P] MRPL32 ribosomal protein YmL32, mitochondrial
YPL231W	[M] FAS2 fatty-acyl-CoA synthase, alpha chain
YKL182W	[M] FAS1 fatty-acyl-CoA synthase, beta chain
YJR057W	[M] CDC8 dTMP kinase
YMR262W	[D] YMR262w similarity to S.pombe scn1 protein
YOR221C	[M] MCT1 malonyl-CoA:ACP transferase
YJR148W	[G] BAT2 branched chain amino acid aminotransferase, cytosolic
YHR208W	[G] BAT1 branched chain amino acid aminotransferase, mitochondrial
YER061C	[E] CEM1 beta-keto-acyl-ACP synthase, mitochondrial
YDR454C	[M] GUK1 guanylate kinase
YKL192C	[M] ACP1 mitochonrial acyl-carrier protein
YBL055C	[U] YBL055c similarity to hypothetical S.pombe protein
Q-clique 43	**Function Annotation**
YNL262W	[D] POL2 DNA-directed DNA polymerase epsilon, catalytic subunit A
YMR290C	[D] HAS1 helicase associated with SET1P
YAL035W	[P] FUN12 general translation factor eIF2 homolog
YGR162W	[P] TIF4631 mRNA cap-binding protein (eIF4F), 150K subunit
YOL139C	[P] CDC33 translation initiation factor eIF4E
YGL049C	[P] TIF4632 mRNA cap-binding protein (eIF4F), 130K subunit
YDL051W	[T] LHP1 RNA binding protein
YLR175W	[T] CBF5 putative rRNA pseuduridine synthase
YOR310C	[T] NOP58 required for pre-18S rRNA processing
YPL043W	[T] NOP4 nucleolar protein
YLR197W	[T] SIK1 involved in pre-rRNA processing
YGL120C	[T] PRP43 involved in spliceosome disassembly
YOL041C	[U] NOP12 weak similarity to M.sativa NUM1, hnRNP protein from C. tentans and D. melanogaster, murine/bovine poly(A) binding protein II, and NSR1P
YBL004W	[U] YBL004w weak similarity to Papaya ringspot virus polyprotein
YDL213C	[U] FYV14 weak similarity to potato small nuclear ribonucleoprotein U2B and human splicing factor homolog
YGR145W	[U] YGR145w similarity to C.elegans hypothetical protein
YDR496C	[U] PUF6 similarity to hypothetical human and C.elegans proteins
YKL014C	[U] YKL014c similarity to hypothetical protein SPCC14G10.02 S. pombe
YPL012W	[U] RRP12 hypothetical protein
Q-clique 44	**Function Annotation**
YDR292C	[F] SRP101 signal recognition particle receptor, alpha chain
YML094W	[F] GIM5 Gim complex component
YJL189W	[P] RPL39 60S large subunit ribosomal protein L39.e
YLR406C	[P] RPL31B 60S large subunit ribosomal protein L31.e.c12
YMR242C	[P] RPL20A 60s large subunit ribosomal protein
YOL121C	[P] RPS19A 40S small subunit ribosomal protein S19.e
YNL302C	[P] RPS19B 40S small subunit ribosomal protein S19.e
YDL075W	[P] RPL31A 60S large subunit ribosomal protein L31.e
YOR312C	[P] RPL20B 60S large subunit ribosomal protein
YPR016C	[P] TIF6 translation initiation factor 6 (eIF6)
YMR074C	[U] YMR074c strong similarity to hypothetical S. pombe protein
Q-clique 45	**Function Annotation**
YGR240C	[E] PFK1 6-phosphofructokinase, alpha subunit
YJR109C	[G] CPA2 arginine-specific carbamoylphosphate synthase, large chain
YDR007W	[G] TRP1 phosphoribosylanthranilate isomerase
YDR127W	[G] ARO1 arom pentafunctional enzyme
YER090W	[G] TRP2 anthranilate synthase component I
YKL211C	[G] TRP3 anthranilate synthase component II
YNR033W	[M] ABZ1 para-aminobenzoate synthase
YKL104C	[M] GFA1 glucosamine--fructose-6-phosphate transaminase

YMR012W	[P] CLU1 translation initiation factor eIF3 (p135 subunit)
YGL245W	[P] YGL245w strong similarity to glutamine--tRNA ligase
Q-clique 46	**Function Annotation**
YML094W	[F] GIM5 Gim complex component
YDR292C	[F] SRP101 signal recognition particle receptor, alpha chain
YMR242C	[P] RPL20A 60s large subunit ribosomal protein
YOL121C	[P] RPS19A 40S small subunit ribosomal protein S19.e
YOR312C	[P] RPL20B 60S large subunit ribosomal protein
YDL075W	[P] RPL31A 60S large subunit ribosomal protein L31.e
YPR016C	[P] TIF6 translation initiation factor 6 (eIF6)
YNL302C	[P] RPS19B 40S small subunit ribosomal protein S19.e
YJL189W	[P] RPL39 60S large subunit ribosomal protein L39.e
YLR406C	[P] RPL31B 60S large subunit ribosomal protein L31.e.c12
YMR074C	[U] YMR074c strong similarity to hypothetical S. pombe protein
Q-clique 47	**Function Annotation**
YMR089C	[F] YTA12 protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)
YER017C	[F] AFG3 protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)
YPR024W	[F] YME1 protease of the SEC18/CDC48/PAS1 family of ATPases (AAA)
YER090W	[G] TRP2 anthranilate synthase component I
YDR007W	[G] TRP1 phosphoribosylanthranilate isomerase
YGL026C	[G] TRP5 tryptophan synthase
YKL211C	[G] TRP3 anthranilate synthase component II
YNR033W	[M] ABZ1 para-aminobenzoate synthase
YOR241W	[M] MET7 tetrahydrofolylpolyglutamate synthase
YMR113W	[M] FOL3 dihydrofolate synthetase
YMR278W	[M] YMR278w similarity to phosphomannomutases
YNL256W	[M] FOL1 Dihydroneopterin aldolase, dihydro-6-hydroxymethylpterin pyrophosphokinase, dihydropteroate synthetase
YGR267C	[M] FOL2 GTP cyclohydrolase I
YEL058W	[M] PCM1 phosphoacetylglucosamine mutase
YKL132C	[M] RMA1 similarity to B.subtilis folC protein and strong similarity to YMR113w
Q-clique 48	**Function Annotation**
YBR002C	[F] RER2 cis-prenyltransferase, a key enzyme in dolichol synthesis
YDL142C	[M] CRD1 cardiolipin synthase
YBR042C	[M] CST26 weak similarity to 1-acyl-sn-glycerol-3-phosphate acyltransferase from Brassica napus
YMR101C	[M] SRT1 cis-prenyltransferase homologue
YPR113W	[M] PIS1 CDP diacylglycerol--inositol 3-phosphatidyltransferase
YNR016C	[M] ACC1 acetyl-CoA carboxylase
YNL072W	[M] RNH35 RNase H(35), a 35 kDa ribonuclease H
YBR029C	[M] CDS1 CDP-diacylglycerol synthase
YDL052C	[M] SLC1 fatty acyltransferase
YLR048W	[P] RPS0B 40S ribosomal protein p40 homolog B
YHR038W	[P] FIL1 Killed in Mutagen, sensitive to Diepoxybutane and/or Mitomycin C
YGR214W	[P] RPS0A 40S ribosomal protein p40 homolog A
YNL026W	[U] YNL026w similarity to S.pombe hypothetical protein
YDL193W	[U] YDL193w similarity to N.crassa hypothetical 32 kDa protein
YDR018C	[U] YDR018c strong similarity to hypothetical protein YBR042c

Note: All quasi-cliques and their members along with function annotation (48 quasi-cliques and 511 proteins in total) are listed above. Q-clique N: the No. of quasi-cliques.