

ORF	Standard gene name	Feature type	Gene description	Molecular function	Biological process	Cellular compartment	Viability of a deletion strain	Protein localization	Protein-protein interactions
YKR034W	DAL80	Verified	Negative regulator of genes in multiple nitrogen degradation pathways; expression is regulated by nitrogen levels and by Gln3p; member of the GATA-binding family, forms homodimers and heterodimers with Deh1p	Transcription factor activity	Regulation of nitrogen utilization; transcription	Nucleus	Viable	N/A	YJL110C, YER047C, YKR034W, YLR376C, YDR520C, YNL021W, YHR060W
YKR073C	N/A	Dubious	Unlikely to encode a protein	Unknown	Unknown	Unknown	Viable	N/A	YER081W
YKR105C	N/A	Uncharacterized ORF	Hypothetical protein	Unknown	Unknown	Unknown	Viable	N/A	YDR155C, YJR091C
YLR184W	N/A	Dubious	Hypothetical protein	Unknown	Unknown	Unknown	Viable	N/A	N/A
YYLR226W	BUR2	Verified	Cyclin for the Sgv1p (Bur1p) protein kinase; Sgv1p and Bur2p comprise a CDK-cyclin complex involved in transcriptional regulation through its phosphorylation of the carboxy-terminal domain of the largest subunit of RNA polymerase II	Cyclin-dependent protein kinase regulator activity	Mitotic sister chromatid segregation; transcription	Nucleus	Viable	N/A	YPR161C, YBR135W, YMR125W, YJL158C
YLR236C	N/A	Dubious	Hypothetical protein	Unknown	Unknown	Unknown	Viable	N/A	YLR438W, YJR091C
YML009W-B	N/A	Dubious	Hypothetical protein	Unknown	Unknown	Unknown	Viable	N/A	N/A
YML080W	DUS1	Verified	Dihydrouridine synthase, member of a widespread family of conserved proteins including Smm1p, Dus3p, and Dus4p; modifies pre-tRNA (Phe) at U17	tRNA dihydrouridine synthase activity	tRNA modification	Nucleus	Viable	N/A	N/A
YML095C-A	N/A	Dubious	Hypothetical	Unknown	Unknown	Unknown	Viable	N/A	YOR025W,

			protein						YNL298W, YJL030W, YCL029C, YDR332W, YER016W, YFR162C, YBR109C, YJL020C, YNL250W,
YML095C	RAD10	Verified	Single-stranded DNA endonuclease	Single-stranded DNA specific endodeoxyribonuclease activity (TAS)	Double-strand break repair via single-strand annealing, removal of nonhomologous ends (TAS)	Nucleotide-excision repair factor 1 complex (TAS)	Viable	N/A	YPL262W, YJL138C, YEL003W, YGR063C, YER043C, YDL185W, YAL027W, YCR086W, YJL026W, YGL105W, YHR008C, YDR300C, YDR155C, YOR260W, YPL022W
YML123C	PHO84	Verified	High-affinity inorganic phosphate (Pi) transporter and low-affinity manganese transporter	Inorganic phosphate transporter activity (IDA, IMP, ISS), Manganese Ion Transporter activity (IMP)	Manganese ion transporter activity (IMP), phosphate transport (IDA, IMP, ISS)	Integral to plasma membrane (IDA, ISS)	Viable	N/A	YER125W, YDR388W, YDR523C, YLR238W, YNL061W, YNL116W, YJR091C, YDR200C, YGR040W, YOR181W

FIG. 3. Portion of a student's table (from fall 2005) containing information obtained from online databases. The molecular function, biological process, and cellular compartment categories relate to gene ontology. Protein localization information came from the yeast GFP-fusion localization database, and protein-protein interactions information came via BioGRID. As seen in the gene ontology columns, traceable author statement (TAS), inferred from direct assay (IDA), inferred from sequence or structural similarity (ISS), and inferred from mutant phenotype (IMP) are evidence codes for how the annotation was generated.