

# Yeast ORFan Gene Project: Module 2 Worksheet

## Structure-Based Evidence

### Conserved Domain Database Search

Hit #1

**Name:**

**Accession:**

**Description:**

**Interval:**

**E-value:**

Hit #2

**Name:**

**Accession:**

**Description:**

**Interval:**

**E-value:**

**TIGRFA**

**M**

For each significant TIGRFAM hit, record:

**TIGRFAM**

**Model:**

**TIGRFAM**

**Description:**

**Score:**

**E-value:**

**GO**

**#:**

**EC**

**#:**

**PFA**

**M**

For each significant PFAM hit, record:

**PFAM**

**Family:**

**PFAM Name (Description):**

**E-value:**

**Predicted Active Sites:**

**HMM From: HMM To: Is the entire domain  
included in your protein?**

**PAIRWISE**

**ALIGNEMENT**

**Pairwise Alignment:**

**Record the identities and positions of residues in your query sequence that are identical to those in the consensus:**

**Comment on the pairwise alignment, including percentage of alignment matches, E-value, etc and how you will use this information to predicted function for your gene product:**

**DOMAIN**

**SUMMARY**

**PFAM Family Descriptor and Number:**

**Clan Name:**

**Clan Number:**

**Notes on text from Domain Summary page:**

**GO**

**#:**

**EC**

**#:**

**HMM  
LOGO**

**HMM Logo  
File:**

**Comment on which residues are most highly conserved: (make sure to consider families of amino acids, such as those that are polar or negatively charged)**

**CURATED  
ALIGNMENT**

**Report the key functional or structural amino acid residues or patterns from the Curated  
Alignment:**

**PROTEIN DATA  
BANK**

**PDB  
Code:**

**PDB Name:**

**PDB Alignment:**

**Alignment Length:**

**E-value:**

**Identities:**

**Notes on information given in PDB about the function of this protein domain:**