

# 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:**

### PFAM

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:**