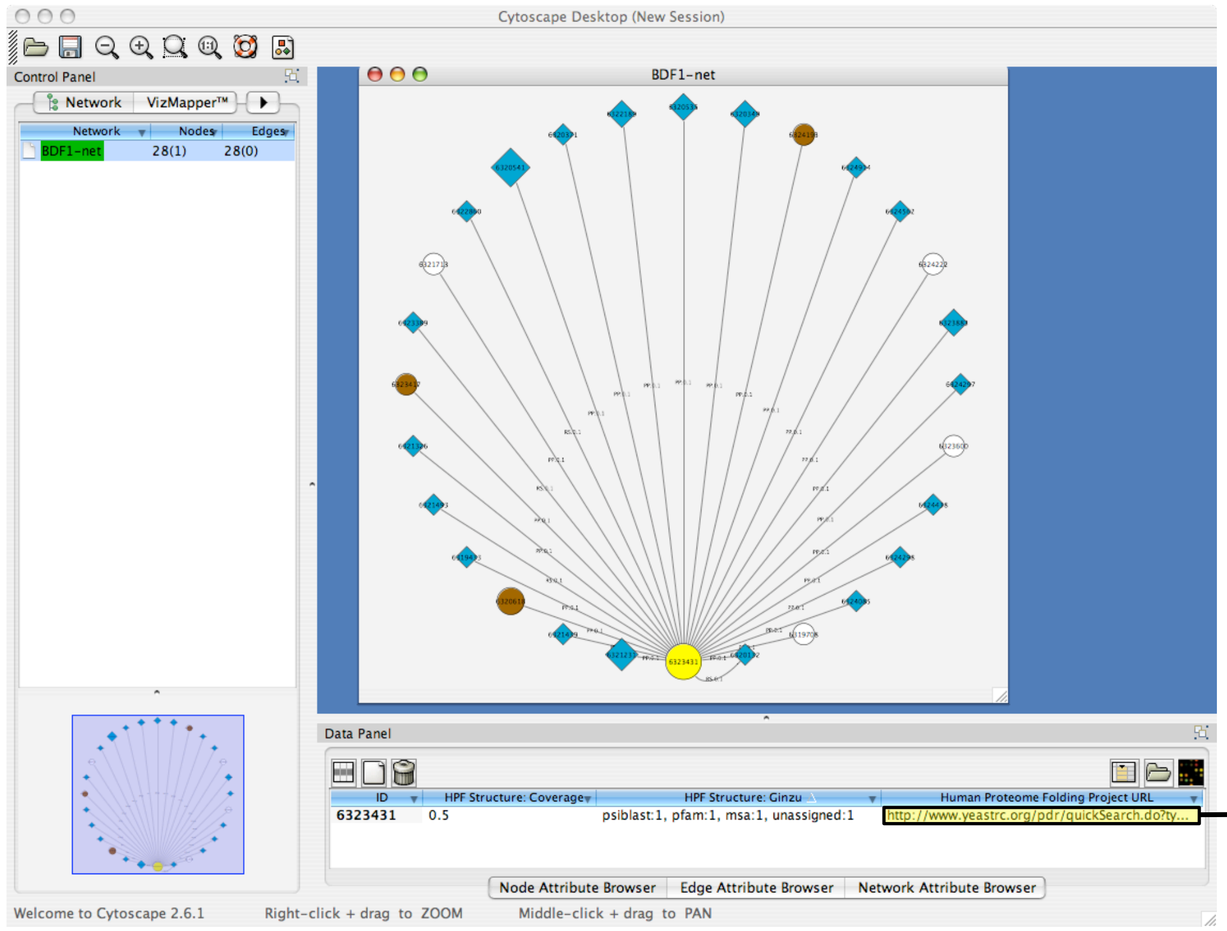
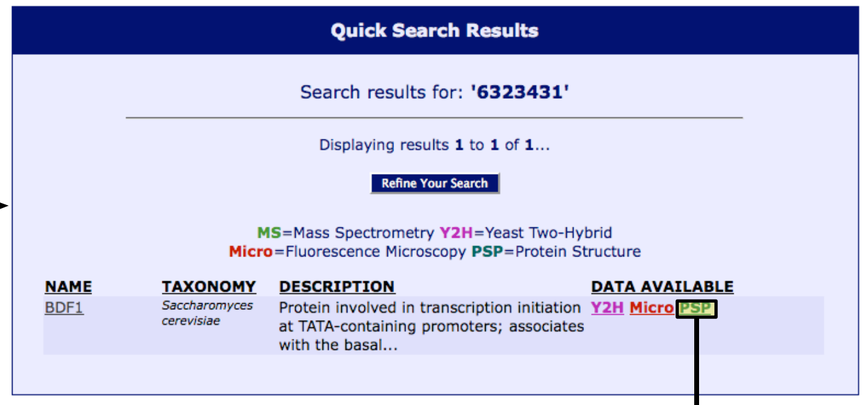
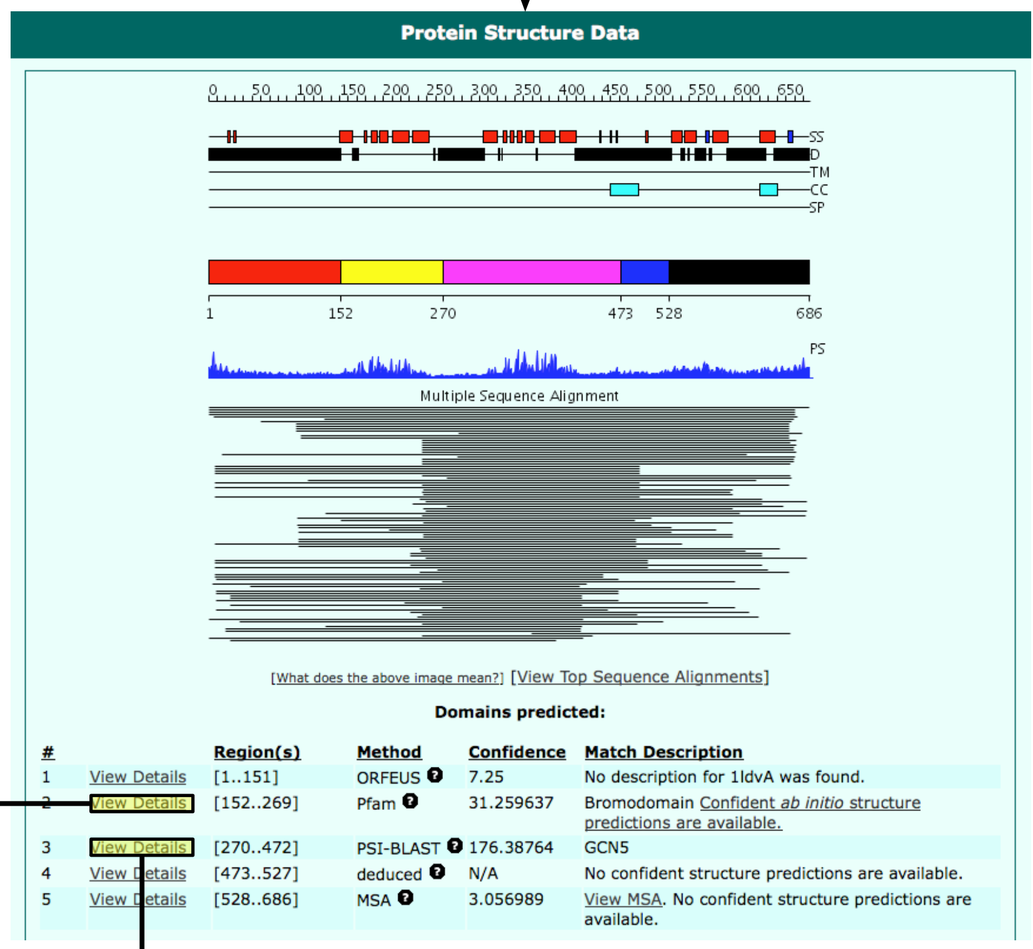
A


Cytoscape Desktop (New Session)
Control Panel
Network
VizMapper™
Network
Nodes
Edges
BDF1-net
28(1)
28(0)
BDF1-net
Data Panel
ID
HPF Structure: Coverage
HPF Structure: Ginzu
Human Proteome Folding Project URL
6323431
0.5
psiblast:1, pfam:1, msa:1, unassigned:1
http://www.yeastrc.org/pdr/quickSearch.do?ty...
Node Attribute Browser
Edge Attribute Browser
Network Attribute Browser
Welcome to Cytoscape 2.6.1
Right-click + drag to ZOOM
Middle-click + drag to PAN

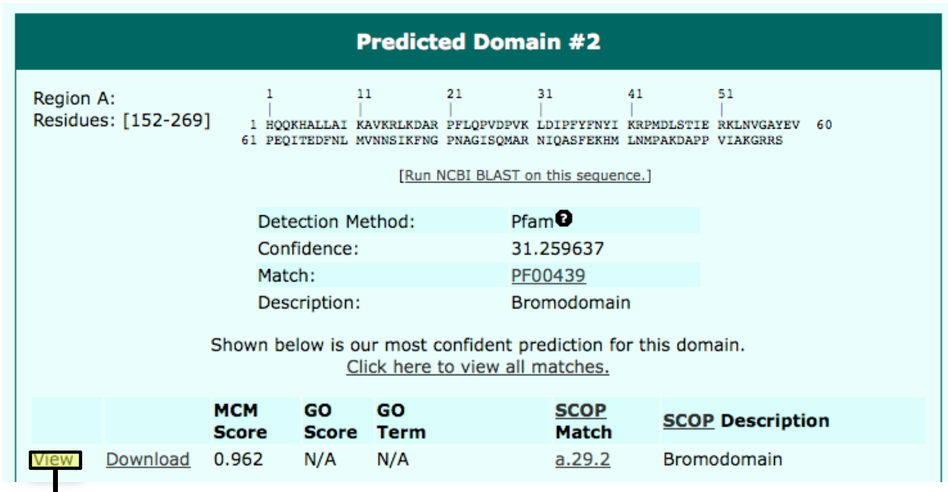
B


Quick Search Results
Search results for: '6323431'
Displaying results 1 to 1 of 1...
Refine Your Search
MS=Mass Spectrometry Y2H=Yeast Two-Hybrid
Micro=Fluorescence Microscopy PSP=Protein Structure
NAME
TAXONOMY
DESCRIPTION
DATA AVAILABLE
BDF1
Saccharomyces cerevisiae
Protein involved in transcription initiation at TATA-containing promoters; associates with the basal...
Y2H Micro PSP

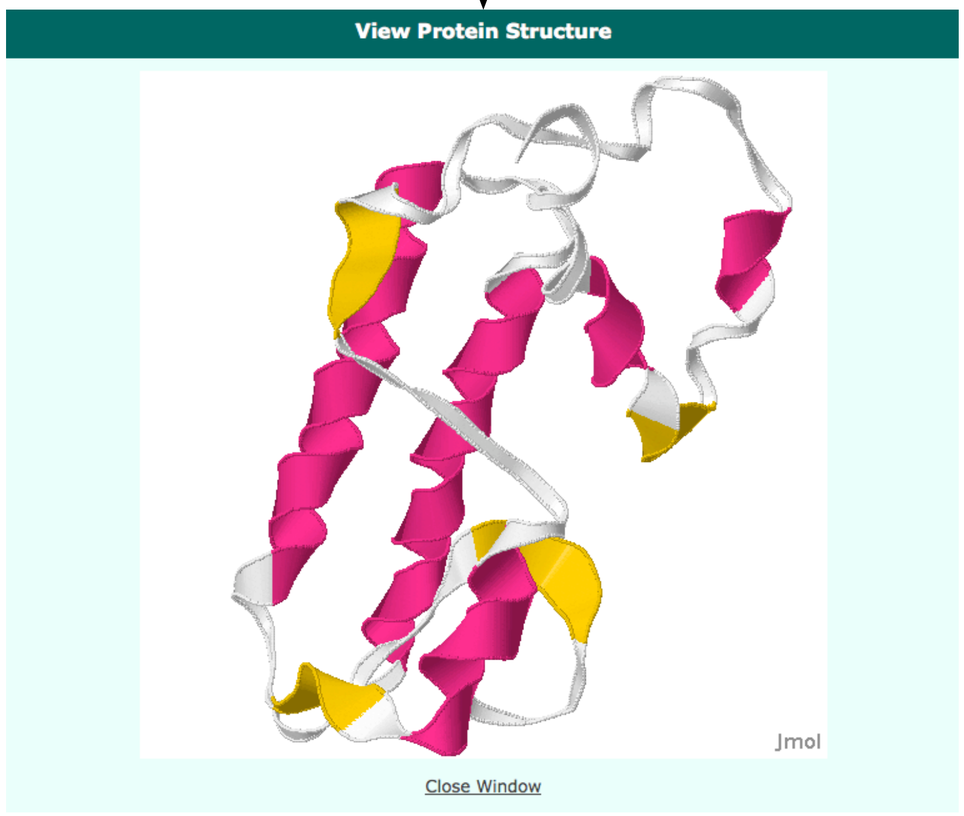
C


Protein Structure Data
0 50 100 150 200 250 300 350 400 450 500 550 600 650
SS
D
TM
CC
SP
1 152 270 473 528 686
PS
Multiple Sequence Alignment
[What does the above image mean?] [View Top Sequence Alignments]
Domains predicted:
Region(s) Method Confidence Match Description
1 View Details [1..151] ORFEUS 7.25 No description for 1IdvA was found.
2 View Details [152..269] Pfam 31.259637 Bromodomain Confident ab initio structure predictions are available.
3 View Details [270..472] PSI-BLAST 176.38764 GCN5
4 View Details [473..527] deduced N/A No confident structure predictions are available.
5 View Details [528..686] MSA 3.056989 View MSA. No confident structure predictions are available.

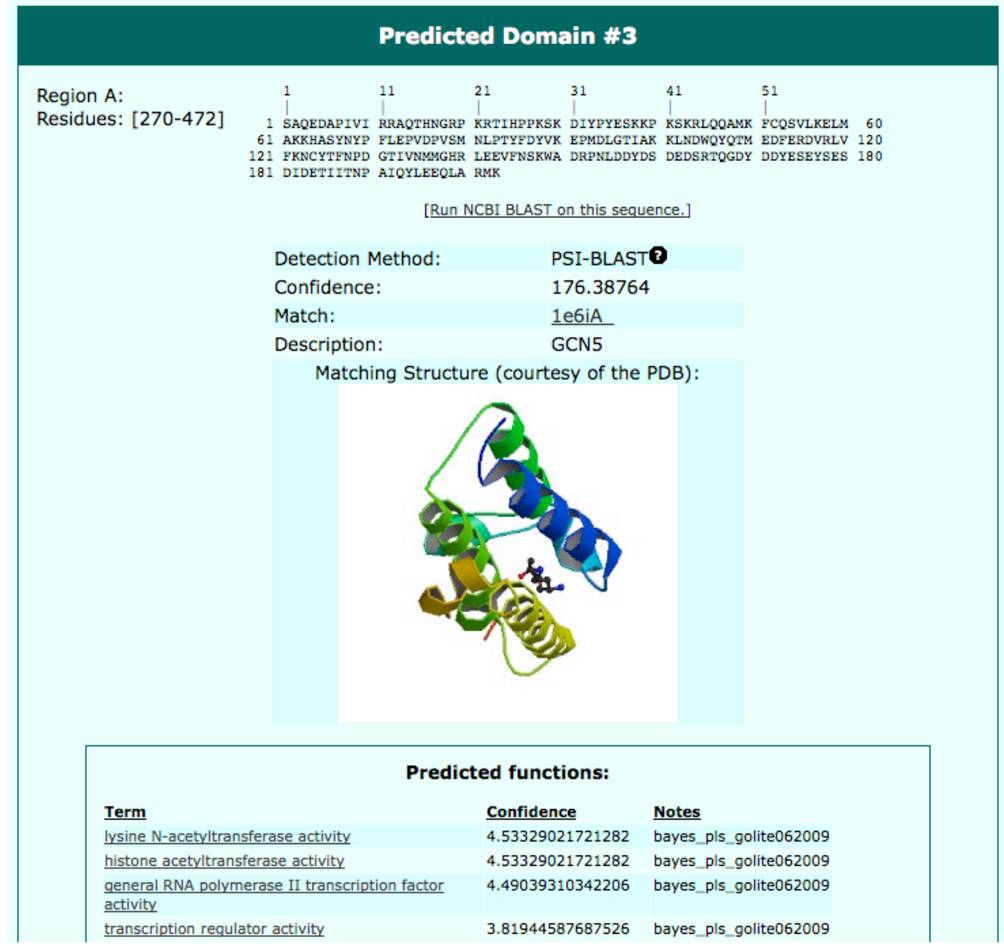
D


Predicted Domain #2
Region A:
Residues: [152-269]
1 11 21 31 41 51
1 HQQKHALLAI KAVKRLKDAR PFLQPVDPVK LDIPFYFNYI KRPMDLSTIE RKLNVGAYEV 60
61 PEQITEDFNL MVNNSIKFNG PNAGISQMAR NIQASFEKHM LNMPAKDAPP VIAKGRRS
[Run NCBI BLAST on this sequence.]
Detection Method: Pfam
Confidence: 31.259637
Match: PF00439
Description: Bromodomain
Shown below is our most confident prediction for this domain.
Click here to view all matches.
View Download 0.962 N/A N/A a.29.2 Bromodomain

E


View Protein Structure
Jmol
Close Window

F


Predicted Domain #3
Region A:
Residues: [270-472]
1 11 21 31 41 51
1 SAQEDAPIVI RRAQTHNGRP KRTIHPPKSK DIYPYESKKP KSKRLQQAMK FCQSVLKELM 60
61 AKKHASYNYP FLEPVDPVSM NLPTYFDYVK EPMDLGTIAK KLNDWQYQTM EDFERDVRLV 120
121 FKNCYTFNPD GTIVNMMGHR LEEVFNSKWA DRPNLDDYDS DEDSRTQGDY DDYESEYSES 180
181 DIDETIITNP AIQYLEEQLA RMK
[Run NCBI BLAST on this sequence.]
Detection Method: PSI-BLAST
Confidence: 176.38764
Match: 1e6iA
Description: GCN5
Matching Structure (courtesy of the PDB):
Predicted functions:
Term Confidence Notes
lysine N-acetyltransferase activity 4.53329021721282 bayes_pls_golite062009
histone acetyltransferase activity 4.53329021721282 bayes_pls_golite062009
general RNA polymerase II transcription factor activity 4.49039310342206 bayes_pls_golite062009
transcription regulator activity 3.81944587687526 bayes_pls_golite062009