Cluster K1 Mynx gp81 has both a helix-turn-helix DNA binding domain and a membrane protein. Do I call both of these things?

Membrane domains: gp81 has four transmembrane domains (residues 13 – 136).

TmHmm (Transmembrane prediction) ⟳ Rerun

Last Updated:
4/21/2017, 4:46:52 PM
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```
# WEBSEQUENCE Length: 300
# WEBSEQUENCE Number of predicted TMHs:  4
# WEBSEQUENCE Exp number of AAs in TMHs: 87.60592
# WEBSEQUENCE Exp number, first 60 AAs:  39.49178
# WEBSEQUENCE Total prob of N-in:     0.74462
# WEBSEQUENCE POSSIBLE N-term signal sequence
WEBSEQUENCE    TMHMM2.0    inside       1   12
WEBSEQUENCE    TMHMM2.0    TMhelix     13   32
WEBSEQUENCE    TMHMM2.0    outside     33   41
WEBSEQUENCE    TMHMM2.0    TMhelix     42   64
WEBSEQUENCE    TMHMM2.0    inside      65   76
WEBSEQUENCE    TMHMM2.0    TMhelix     77   99
WEBSEQUENCE    TMHMM2.0    outside    100  113
WEBSEQUENCE    TMHMM2.0    TMhelix    114  136
WEBSEQUENCE    TMHMM2.0    inside     137  300
```

Change Log

At the C-terminus there is a helix-turn-helix DNA binding domain (residues 244 – 280)

Template alignment | Template 3D structure | PDBe
2.   **2M8E_A** SLEEPING BEAUTY TRANSPOSASE; DNA Binding Protein, DNA transposition; NMR {synthetic construct}
Probability: 95.36   E-value: 0.024   Score: 38.64   Aligned Cols: 44   Identities: 18%   Similarity: 0.222

```
Q ss_pred          CcccHHHHHHHHHHhhcCCCHHHHHHHHHCCCHHHHHHHHHHHhh
Q Mynx_81    241    TRIDRVKVAEVLAEHEADVKPSMIARKLGVGYSTVVRILDHHTA   284 (300)
Q Consensus  241    tr~~~~~VA~VL~~~~~g~~~~~Ia~~~gvhhsTV~RIl~aA~~   284 (300)
                    ...+.+....++.....|.+.++|++.+|++++||+++++...+
T Consensus  7      ~~~~~~~~~~i~~~~~~~~~~~ia~~~~~s~~tv~~~~~~~~~   50 (57)
T 2M8E_A     7      KEISQDLRKKIVDLHKSGSSLGAISKRLKVPRSSVQTIVRKYKH   50 (57)
T ss_dssp           CCSCHHHHHHHHHHHHHCTTHHHHHHHTCCCHHHHHHHHHHHHH
T ss_pred           cCCCHHHHHHHHHHHHcCCCHHHHHHHHHCCCHHHHHHHHHHHHH
```

Template alignment | Template 3D structure | PDBe
3.   **5CLV_J** TrfB transcriptional repressor protein/DNA Complex; Helix-turn-helix, complex, transcription; 2.5A {Escherichia coli}; Related PDB entries: 5CLV_M 5CLV_I 5CLV_E 5CLV_F 5CLV_N
Probability: 94.9   E-value: 0.042   Score: 39.78   Aligned Cols: 41   Identities: 12%   Similarity: 0.065

```
Q ss_pred          cHHHHHHHHHHhhcCCCHHHHHHHHHCCCHHHHHHHHHHHhh
Q Mynx_81    244    DRVKVAEVLAEHEADVKPSMIARKLGVGYSTVVRILDHHTA   284 (300)
Q Consensus  244    ~~~~VA~VL~~~~~g~~~~~Ia~~~gvhhsTV~RIl~aA~~   284 (300)
                    ++.....+......|+|..+||+.+|++++||++++..+..
T Consensus  19     ~~~~~~~~~~~~~g~s~~eia~~~gis~~tv~~~~~~~~   59 (65)
T 5CLV_J     19     GQQTIEIARGVLVDGKPQATFATSLGLTRGAVSQAVHRVWA   59 (65)
T ss_dssp           CHHHHHHHCCCCCSCCCTHHHHHHHTCCHHHHHHHHHHHHH
T ss_pred           CHHHHHHHHHHHhCCccHHHHHHHHHCCCHHHHHHHHHHHHH
```