Secondary structure and disorder prediction

Sequence: MTKLYRSDRLCGLAELGI DTLRLILLVSI FTTGTTIL IYFLAAALVIPKEPYGP
Secondary structure:
Confidence:
Disorder:

Sequence: DSGPYGP GPGAPYGYGGPGGYYGYGDHP PRGPYNNGGYGDPPGGGYGP
Secondary structure:
Confidence:
Disorder:

Sequence: GAYGGRRPPKHRAQK HGWP PQPGGYYYGYPYGA GA AADSDLDS MKDIEK KVLQKEIEE
Secondary structure:
Confidence:
Disorder:

Sequence: LRAKLA KG E
Secondary structure:
Confidence:
Disorder:

Confidence Key:
- High (9)
- Medium (6)
- Low (0)
- ? Disordered (60%)
- Alpha helix (34%)
- Beta strand (3%)
- TM helix (15%)

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Date: Wed Sep 11 15:44:30 BST 2019
Unique Job ID: a1a798ec058c7191