

Additional Figure 1

Secondary structure prediction of *LmLeuRS* showing the first 300 residues which includes the CP1 domain. The 35 residue N-terminal insertion in the CP1 domain is highlighted in yellow. The numerical values corresponds to the confidence levels (ranging from 0-9). H refers to Helix; C refers to Coil and E refers to Sheet.

```
Conf: 983012346999999999998959983159999999999549957899888754400002
Pred: CCCCCCCHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCCEEECCCCCCCCCCCCCCCCC
AA:  MSTARRDALVAIEQEKQAYWAAEKLHEFDAPAGEARPAKYLTTFPPYMNGKLHLGHGF
      10      20      30      40      50      60
```

```
Conf: 246989999986408970024576787790189999999998864199999963323589
Pred: HHHHHHHHHHHHHCCCCCECCCCCCCCCHHHHHHHHHHHHHHHCCCCCCCCCCCCCCCCC
AA:  SLTKAEFASRFQRMGRRSLWPFGFHVTGTPIAACAKIAKEMQQYGNPPQFPAELLEDK
      70      80      90     100     110     120
```

```
Conf: 999887887210123322246779980488999952999233302489578997285358
Pred: CCCCCCCCCCCCCCCCCCCCCCCCCCHHHHHHHHHCCCCCHHHHCCCCCHHHHHHHHCCHHH
AA:  PKTPVVKEPTEALGQHKSKRGKSGPAKPQWLIMRSMGIPDSEIAKFADPQYWLDYFPPIA
      130     140     150     160     170     180
```

```
Conf: 999976157754444323115784200110044201238999999996551898425999
Pred: HHHHHHHCCCCCCCCCEEECCCCCCCCCCCCCHHHHHHCCHHHHHHHHHHHHHCCCCCCCCC
AA:  MEDLKHFGCHIDWRRAFMTTERNPYFDRFMSTARRDALVAIEQEKQAYWAAEKLHEFDAP
      190     200     210     220     230     240
```

```
Conf: 999999995499488998886554000023579999999876089700355667877903
Pred: CCCCCCCCCCEEECCCCCCCCCCCCCCCCCHHHHHHHHHHHHHHHCCCCCCCCCCCCCHH
AA:  APGEARPAKYLTTFPPYMNGKLHLGHGFSLTAEFASRFQRMGRRSLWPFGFHVTGTP
      250     260     270     280     290     300
```