Fig. S1:

1. Disorder Filtering
   A. DDDDDDDDDDDNNN_NNNDDDDDDDDDDDDDDDDD
      29 residues 29 residues
   B. DDDDDDDDDDDNNNDDNNNNDDNNDDDDDDDDDD
      8 residues 10 residues 6 residues

2. Search not disordered region with length ≥ 30 consecutive residues
   A. DDDDDDDDDDDDDNNN_NNNDDDDDDDDDDDDDDDDDDDD
      62 residues
   B. DDDDDDDDDDDNNNDDNNNNDDNNDDDDDDDDDDDDDDDDDDDD
      27 residues

3. Search disordered region with length ≥ 30 consecutive residues
   B. DDDDDDDDDDDNNNDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
      45 residues 27 residues 15 residues

Fig. S1: Processing steps for “completely disordered” approach: This method was considered in order to capture proteins without a single region that we could perceive as a “nucleation site” for adopting regular structure. Operationally, we first removed any prediction of disorder that spanned over fewer than five residues (step 1), next we searched any region without predicted disorder over 30 consecutive residues (step 2). If we found no such region, and if we also found at least one region with ≥30 consecutive residues predicted as disordered, we considered the protein as “completely disordered” (step 3).