Protein catalog

- In silico cleavage at KR and RR sites
  - Less than 4 fragments
    - Cleavage at each KK site
      - Less than 4 fragments
        - Discarded proteins
      - Selection of secreted proteins with SignalP4.0
        - Non-secreted proteins
          - Selection of secreted proteins with SignalP3.0
            - Non-secreted Proteins (discarded)
  - Proteins entering the secretory pathway
    - Detection of transmembrane domains with TMHMM
      - Membrane proteins (discarded)
      - Secreted proteins
        - Proteins cut in at least 4 fragments at KR, RR or KK sites
          - Sequence comparison between the smallest fragment and the other fragments (excepted in the C-terminus), using iupac2meme and FIMO tools
            - Fragment with no match is discarded
            - Similar fragments (N>2) are converted into patterns with FIMO
              - FIMO search in the C-terminal fragment for an additional pattern
                - Pattern alignment and consensus made with CLUSTALW2 and WEBLOGO, protein representation made with the Prosite MyDomains tool.
              - List of KEPS (Table S2)

Figure S1