

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: List of the 100 most abundant proteins identified in the proteomics of the crop fluids from *Thermobia* grown on Avicel. The table includes the best blastX hits against NCBI nr, E-value, top blastX species and accession, predicted CAZy family and molar percentage abundance calculated from emPAI values obtained from shotgun proteomics. In order to increase the stringency of the analysis, only contigs with 2 or more significant peptide matches were considered.

File Name: Supplementary Data 2

Description: List of the 100 most abundant proteins identified in the proteomics of the crop fluids from *Thermobia* grown on wheat straw. The table includes the best blastX hits against NCBI nr, E-value, top blastX species and accession, predicted CAZy family and molar percentage abundance calculated from emPAI values obtained from shotgun proteomics. In order to increase the stringency of the analysis, only contigs with 2 or more significant peptide matches were considered.

File Name: Supplementary Data 3

Description: List of the 100 most abundant proteins identified in the proteomics of the crop fluids from *Thermobia* grown on filter paper. The table includes the best blastX hits against NCBI nr, E-value, top blastX species and accession, predicted CAZy family and molar percentage abundance calculated from emPAI values obtained from shotgun proteomics. In order to increase the stringency of the analysis, only contigs with 2 or more significant peptide matches were considered.

File Name: Supplementary Data 4

Description: List of the 100 most abundant proteins identified in the proteomics of the crop fluids from *Thermobia* grown on oats. The table includes the best blastX hits against NCBI nr, E-value, top blastX species and accession, predicted CAZy family and molar percentage abundance calculated from emPAI values obtained from shotgun proteomics. In order to increase the stringency of the analysis, only contigs with 2 or more significant peptide matches were considered.

File Name: Supplementary Data 5

Description: Hit values obtained by searching LPMO protein sequences against the hidden Markov model (HMM) created from the multiple sequence alignment of AA15s.