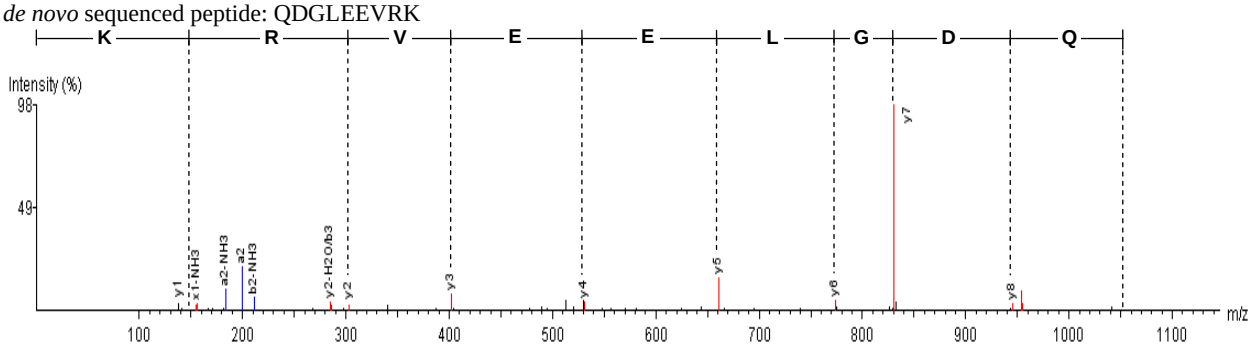
Supporting Information Figure S1. The MS/MS patterns of *de novo* sequenced peptides

Spot number: 7468;

Protein name: porphobilinogen deaminase; gi 309306794;

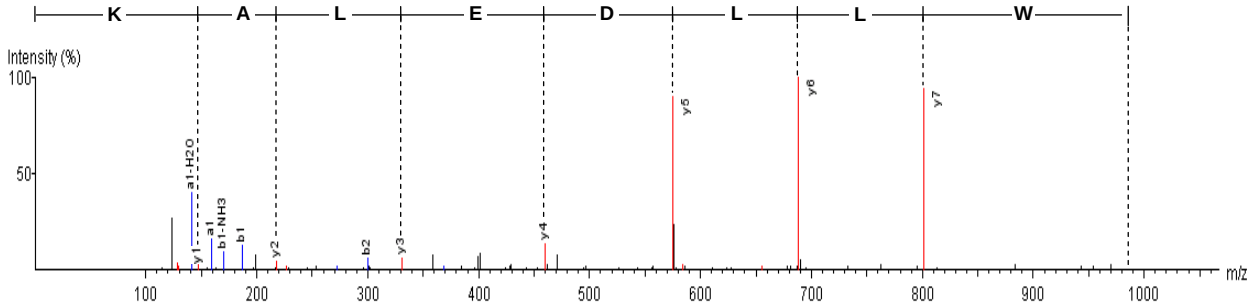
de novo sequenced peptide: QDGLEEVRK



Spot number: 8481;

Protein name: heat shock protein DnaJ domain protein; gi 315185537;

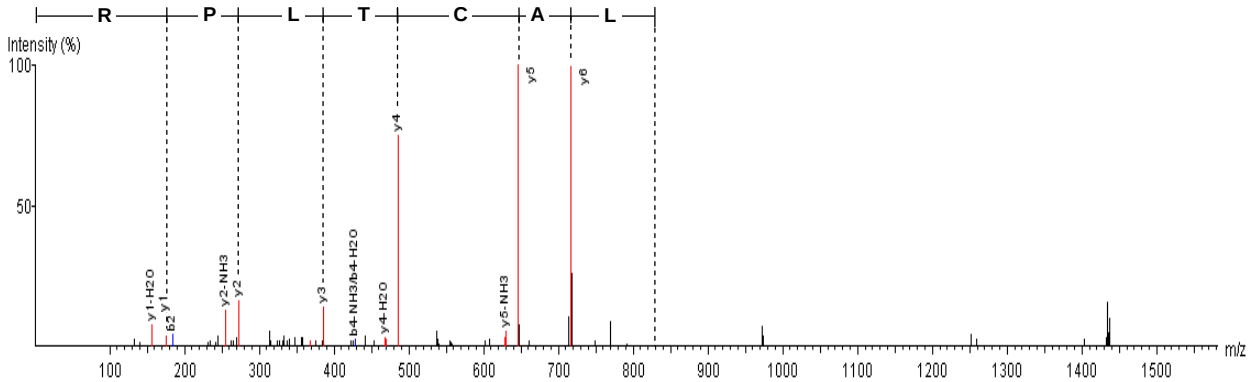
de novo sequenced peptide: WLLDELAK



Spot number: 8883;

Protein name: hypothetical protein Franean1_0062, containing COG2856 predicted Zn peptidase domain; gi 158311928;

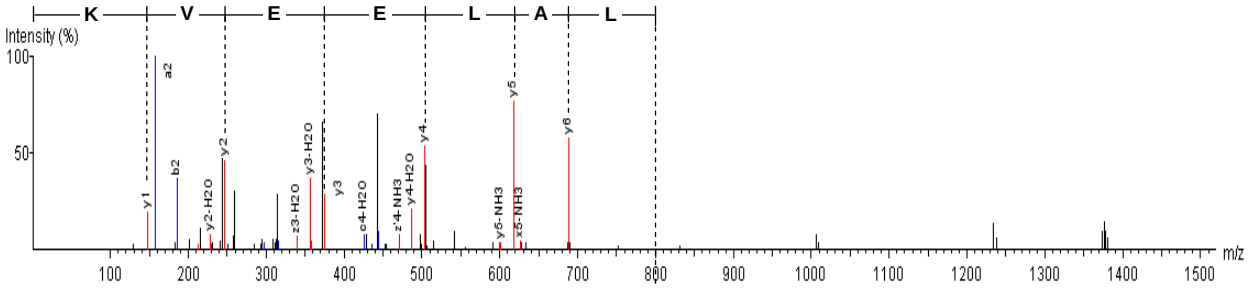
de novo sequenced peptide: LACTLPR



Spot number: 8592;

Protein name: unnamed protein product; gi 313231961;

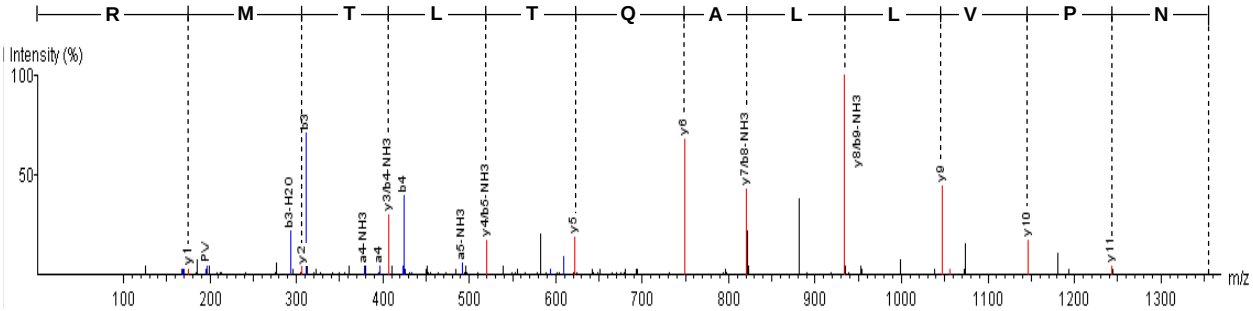
de novo sequenced peptide: LALEEVK



Spot number: 7350;

Protein name: PuDnSP1;

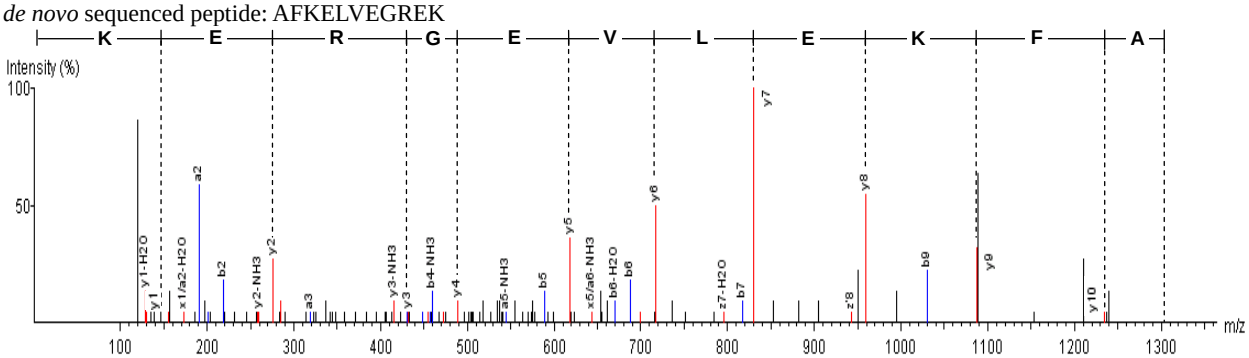
de novo sequenced peptide: NPVLLAQTLTMR



Spot number: 7678;

Protein name: PuDnSP2;

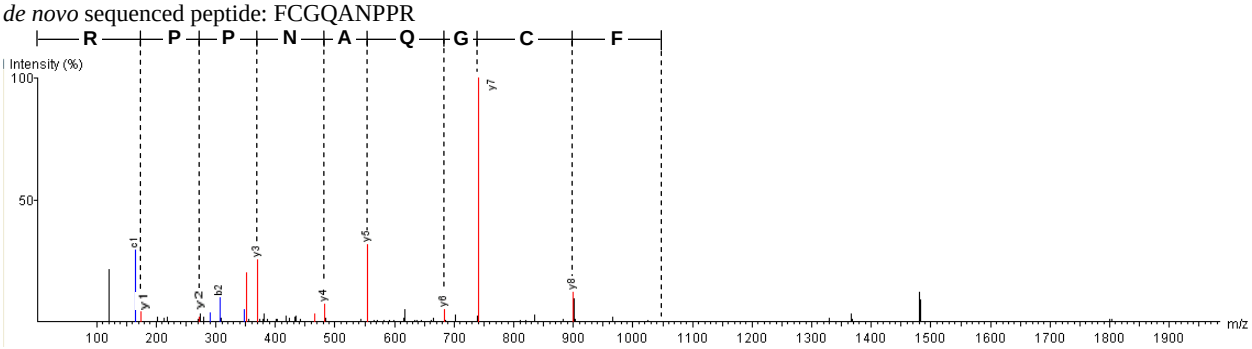
de novo sequenced peptide: AFKELVEGREK



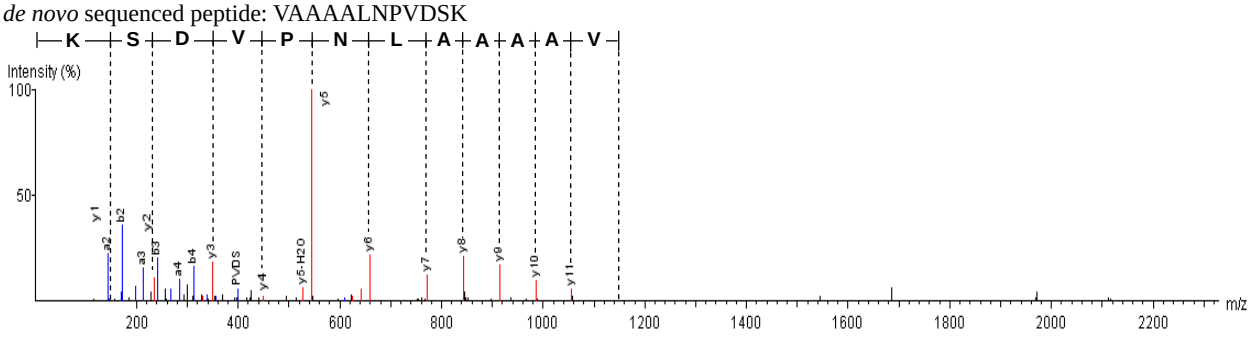
Spot number: 8148;

Protein name: PuDnSP3;

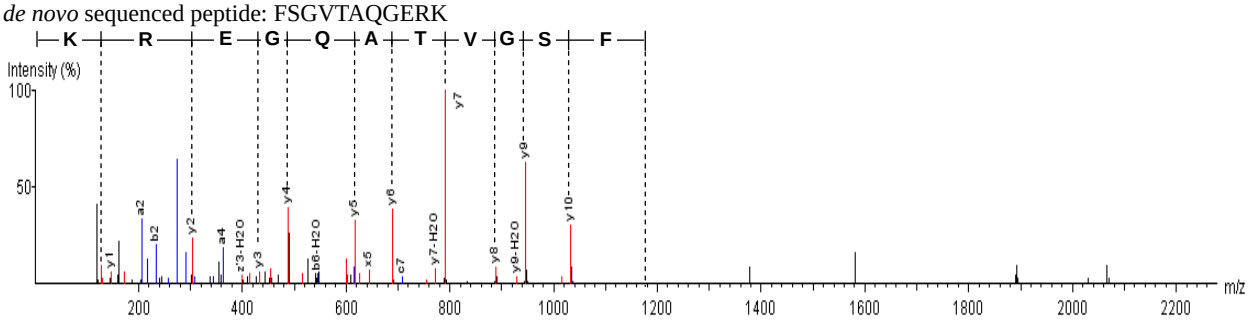
de novo sequenced peptide: FCGQANPPR



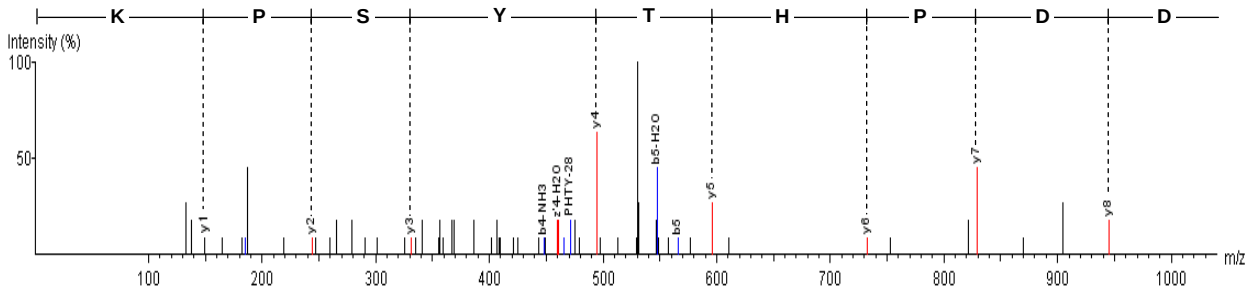
de novo sequenced peptide: VAAAALNPVDSK



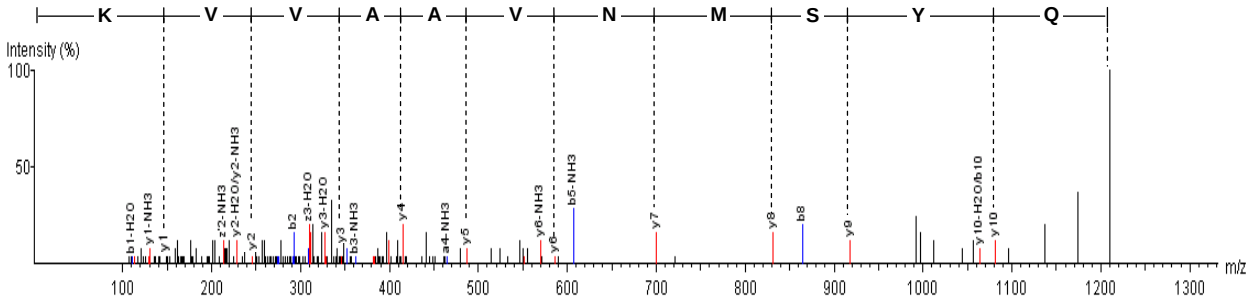
Spot number: 8157;
Protein name: PuDnSP4;
de novo sequenced peptide: FSGVTAQGERK



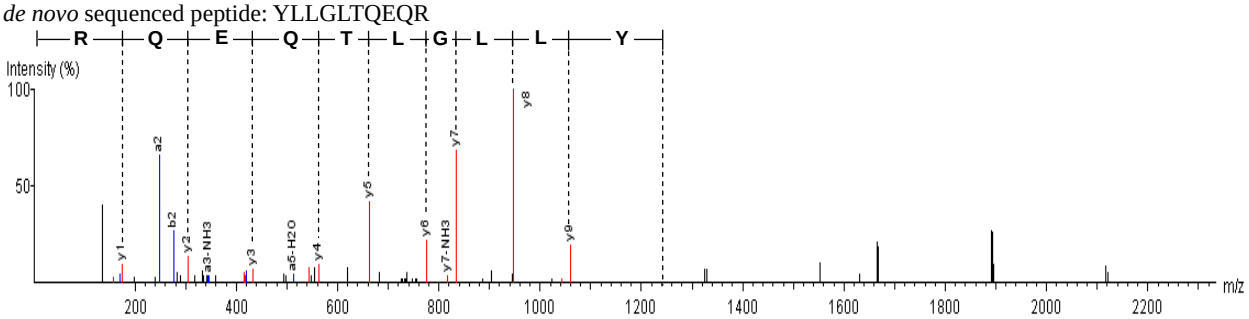
Spot number: 8193;
Protein name: PuDnSP5;
de novo sequenced peptide: DDPHTYSPK



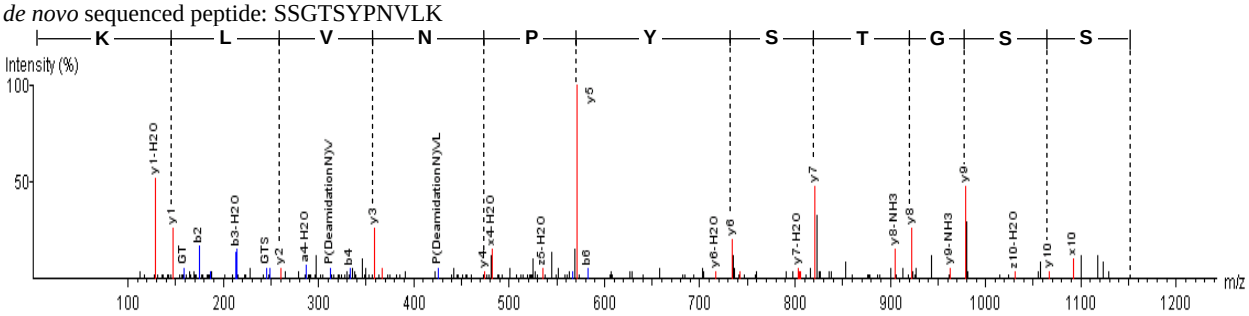
de novo sequenced peptide: QYSMNVAAVVK



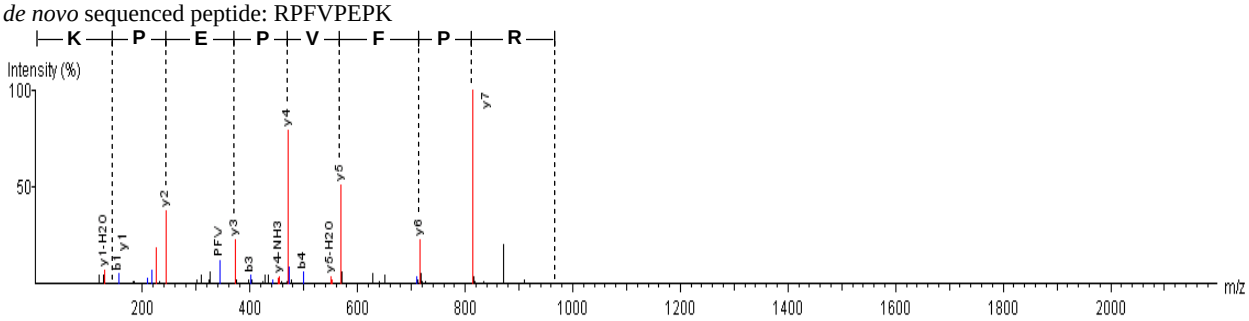
Spot number: 8239;
Protein name: PuDnSP6;
de novo sequenced peptide: YLLGLTQEQR



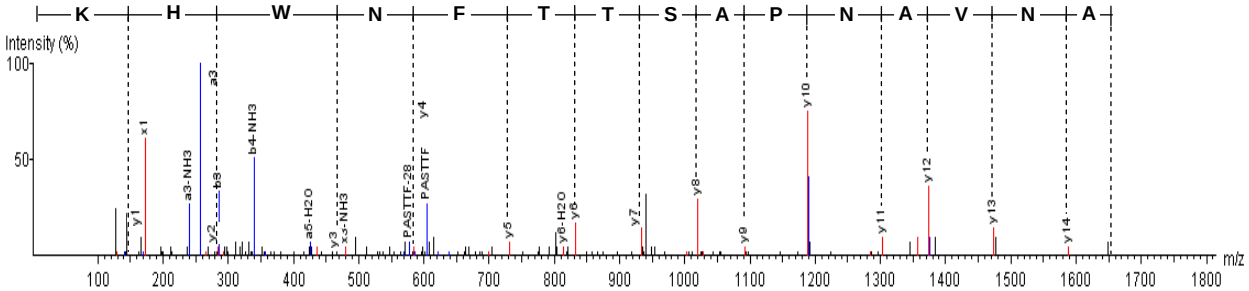
Spot number: 8335;
Protein name: PuDnSP7;
de novo sequenced peptide: SSGTSYPNVLK



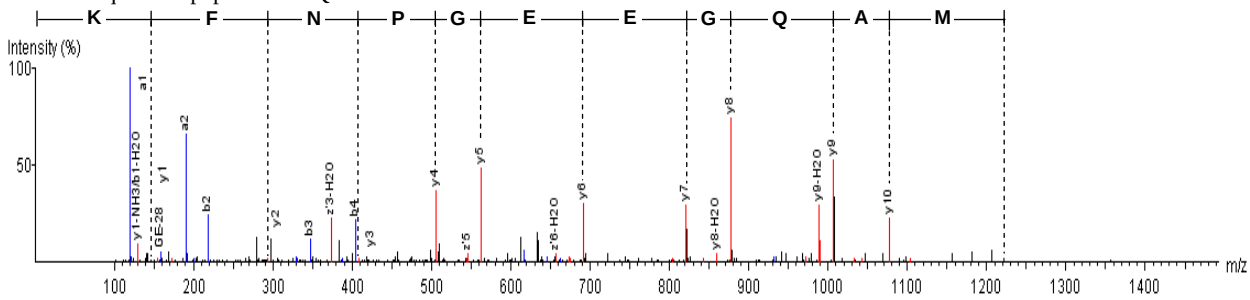
de novo sequenced peptide: RPFVPEPK



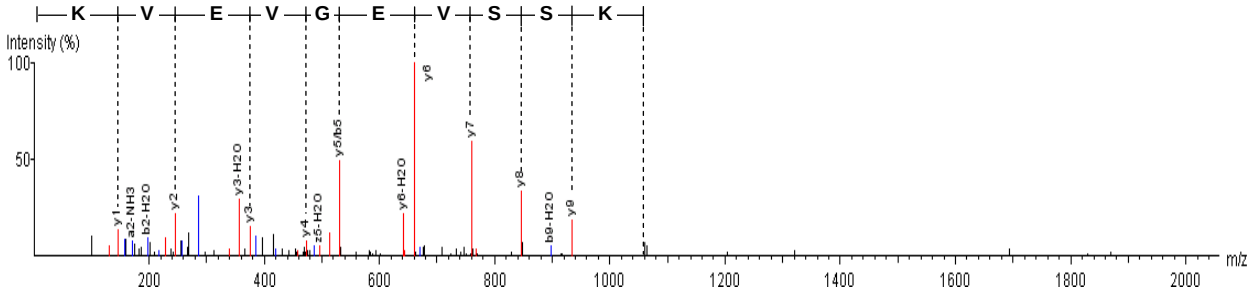
Spot number: 8430;
Protein name: PuDnSP8;
de novo sequenced peptide: ANVANPASTTFNWHK



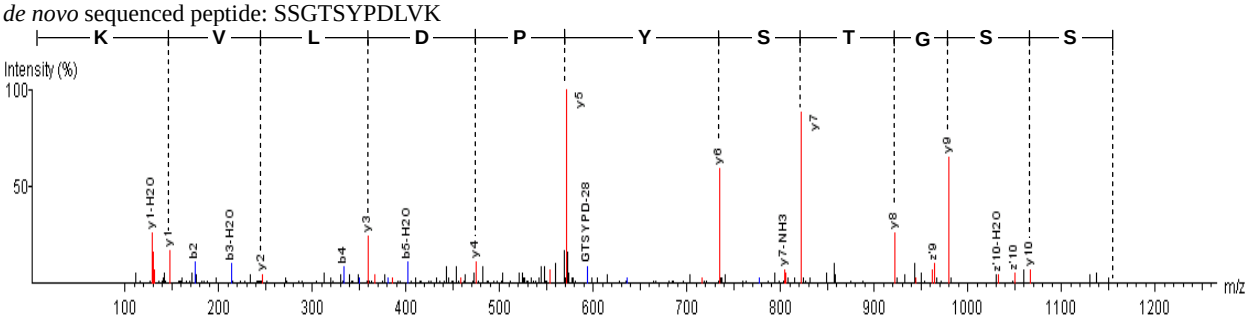
de novo sequenced peptide: MAQGEEGPNFK



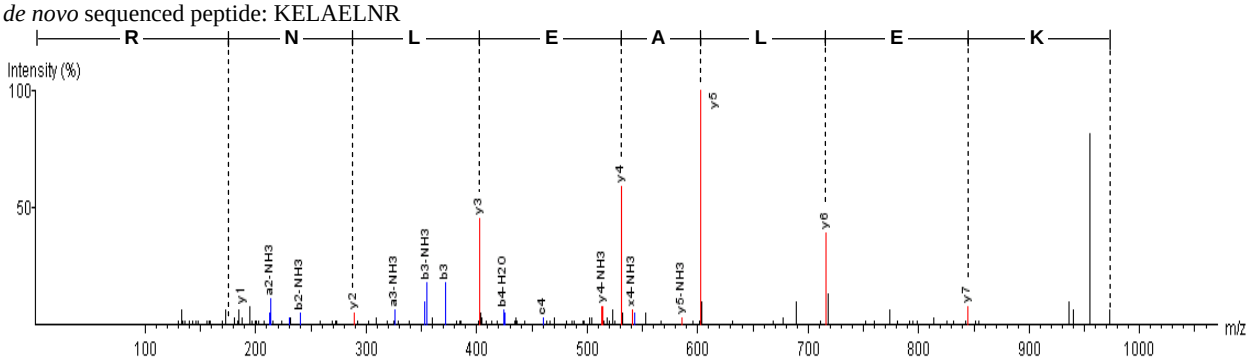
Spot number: 8484;
Protein name: PuDnSP9;
de novo sequenced peptide: KSSVEGVEVK



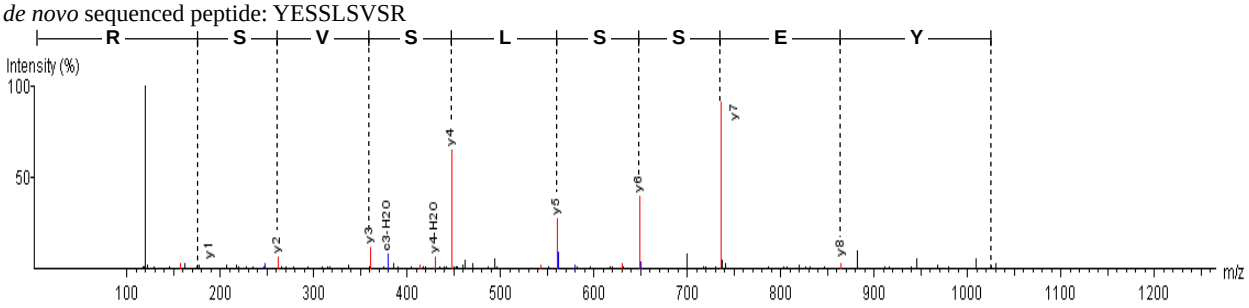
Spot number: 8619;
Protein name: PuDnSP10;
de novo sequenced peptide: SSGTSYPDLVK



Spot number: 7450;
Protein name: hypothetical protein CresD4_00200; gi 300932462;
de novo sequenced peptide: KELAELNR



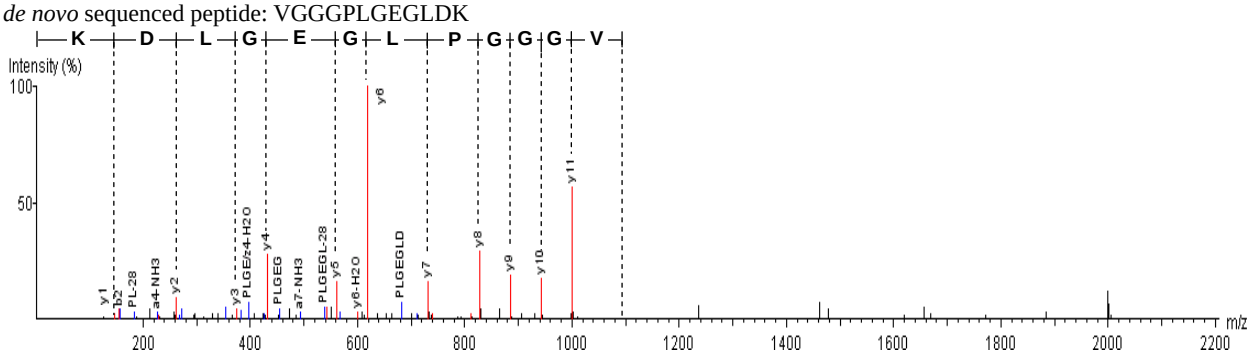
Spot number: 7450;
Protein name: PuDnSP11;
de novo sequenced peptide: YESSLSVSR



Spot number: 8404; gi 302810440;

Protein name: light-harvesting complex;

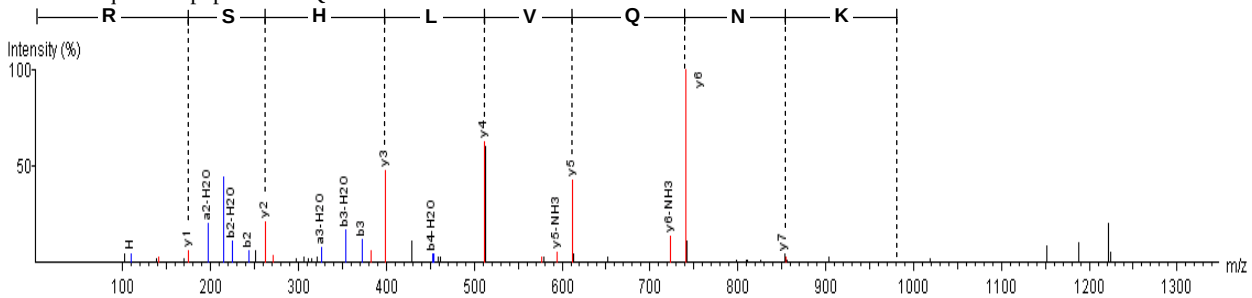
de novo sequenced peptide: VGGGPLGEGLDK



Spot number: 8404;

Protein name: PuDnSP12;

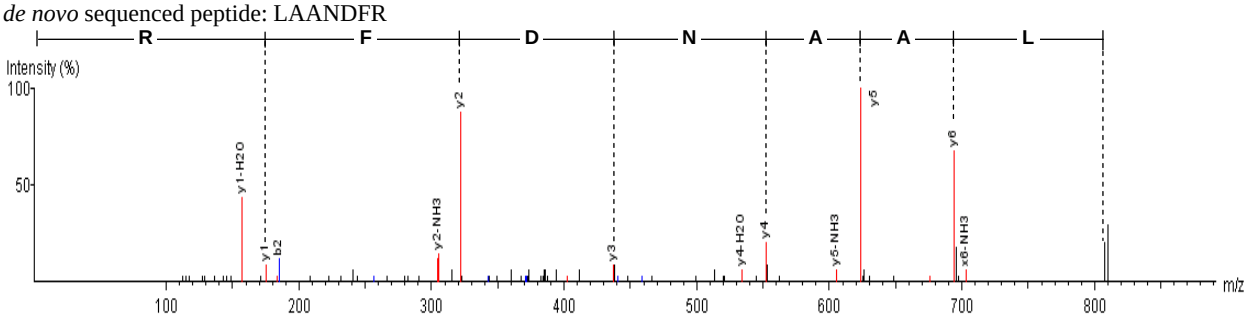
de novo sequenced peptide: KNQVLHSR



Spot number: 8567; gi 317126495;

Protein name: oxidoreductase molybdopterin binding protein;

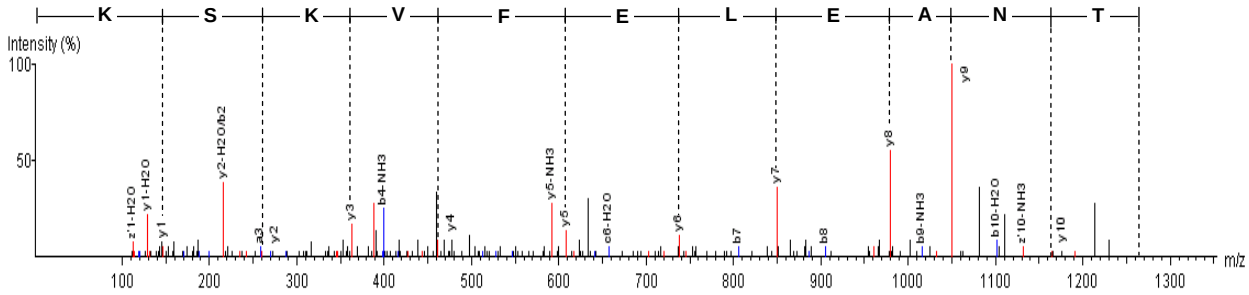
de novo sequenced peptide: LAANDFR



Spot number: 8567;

Protein name: PuDnSP13;

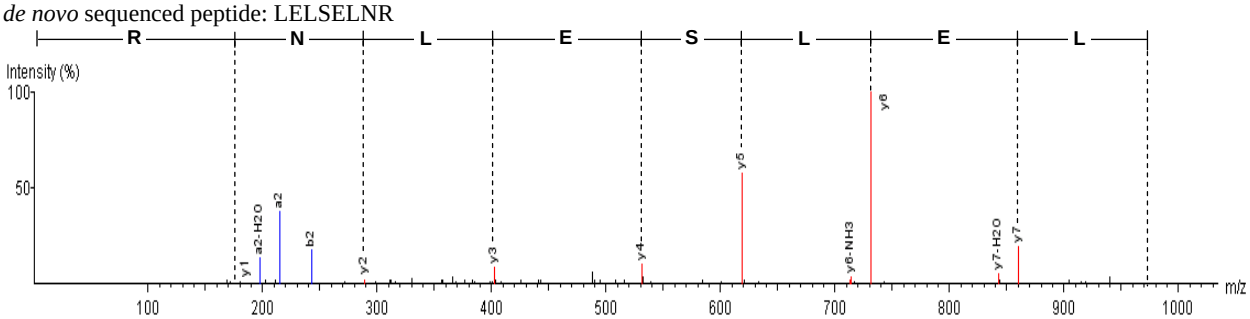
de novo sequenced peptide: TNAELEFVKSK



Spot number: 8626;
gi 158702302;

Protein name: oxysterol-binding protein-like protein 7;

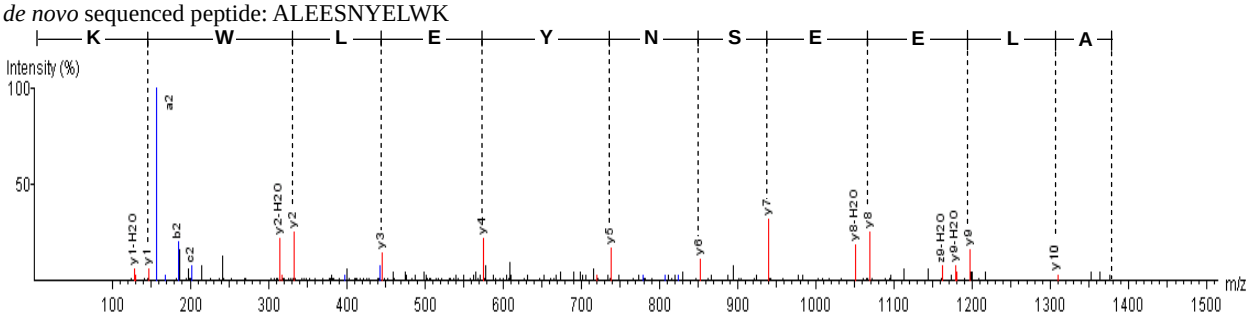
de novo sequenced peptide: LELSELNR



Spot number: 8626;

Protein name: PuDnSP14;

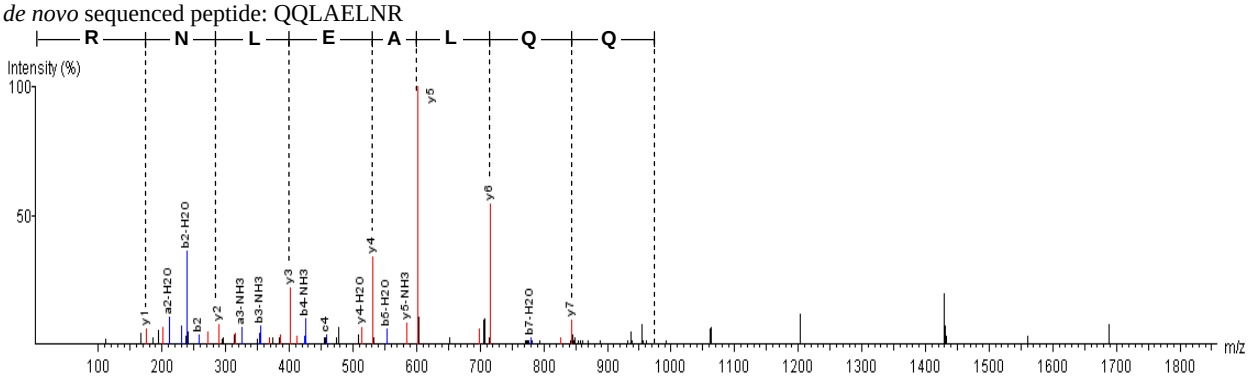
de novo sequenced peptide: ALEESNYELWK



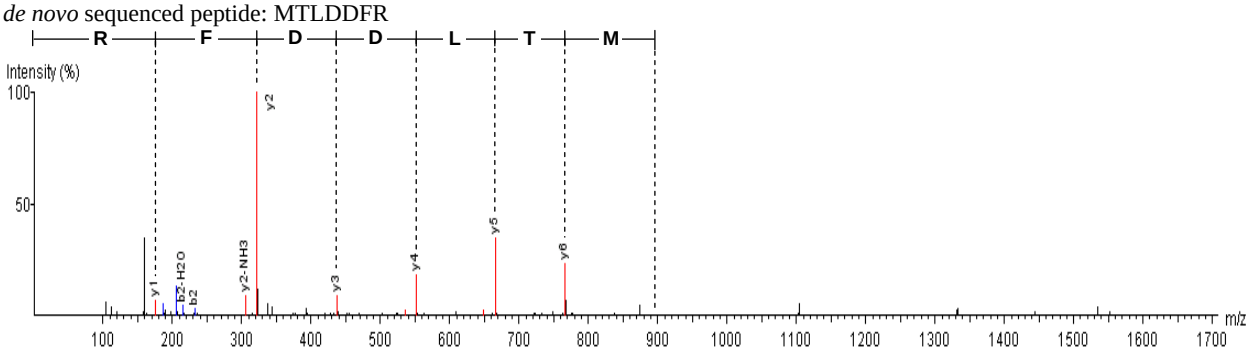
Spot number: 8732;
gi 154497814;

Protein name: hypothetical protein BACCAP_01792;

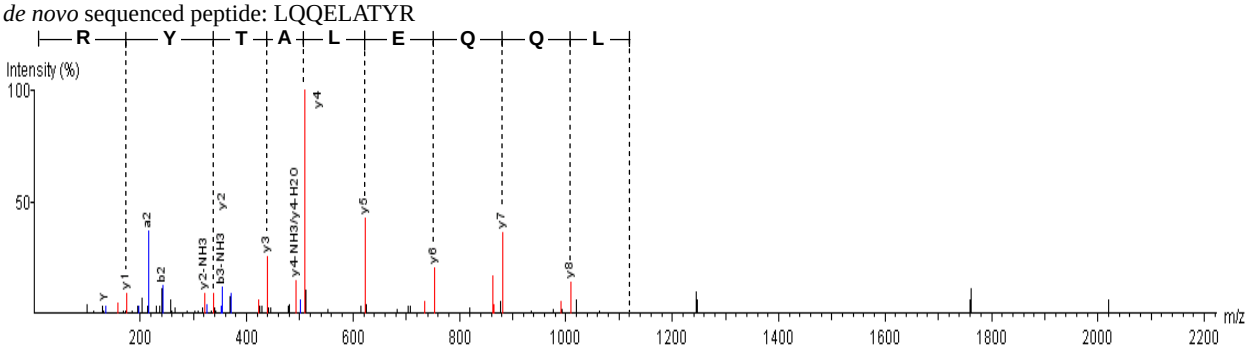
de novo sequenced peptide: QQLAELNR

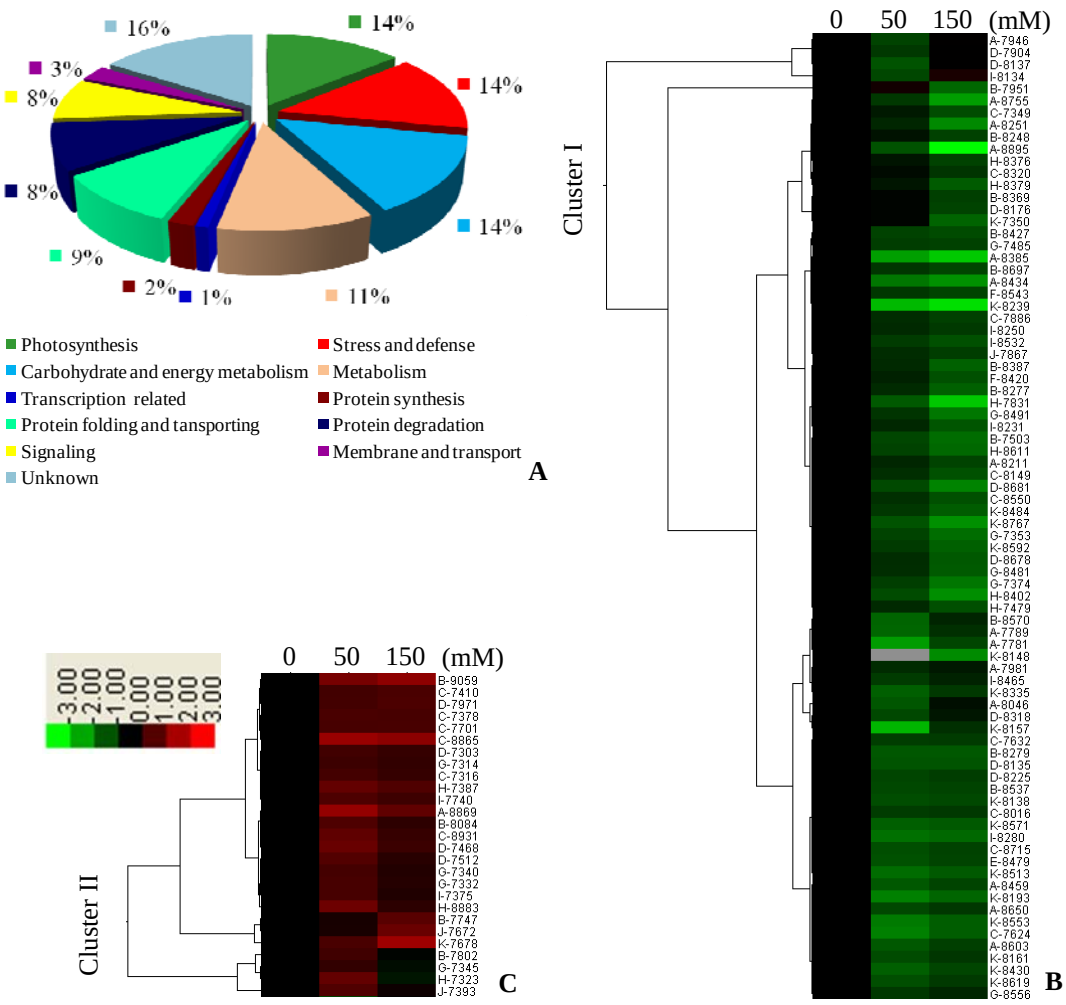


Spot number: 8732;
gi 309362239;
Protein name: CBR-MLK-1 protein;
de novo sequenced peptide: MTLDDFR



Spot number: 8732;
Protein name: PuDnSP15;
de novo sequenced peptide: LQQELATYR





Supporting Information Figure S2. Functional categorization and Hierarchical clustering analysis of the 107 identified proteins in leaves of *P. tenuiflora*. (A) Functional categorization of identified proteins. A total of 107 proteins identified by ESI-Q-TOF MS were classified into 11 groups based on BLAST alignments and information from literatures; (B, C) Hierarchical clustering analysis of the proteins. The columns represent different treatments, including 0 mM, 50 mM, and 150 mM NaCl. The rows represent individual proteins. The protein cluster is on the left side, and the treatment cluster is on the top. The up- and down-regulated proteins are indicated in red or green, respectively. The color intensity increases with increasing expression differences, as showed in the scale bar. Protein spot numbers are listed on the right, and the letters before the spot numbers represent various functional categories of the proteins. A. Photosynthesis; B. Stress and defense; C. Carbohydrate and energy metabolism; D. Metabolism; E. Transcription related; F. Protein synthesis; G. Protein folding and transport; H. Protein degradation; I. Signaling; J. Membrane and transport; K. Unknown. Detailed information can be found in Supporting information Table S1.