**Supplementary data to the paper "Lack of A-factor production induces the expression of nutrient scavenging and stress-related proteins in *Streptomyces griseus*". PSD and CID-spectra confirming the protein identifications.**

Peptide fragments are labeled according to [Biemann, K. (1990). Nomenclature for peptide fragment ions (positive-ions) *Meth. Enzymol.* **193**, 886-887.]; NH_3 loss from certain fragments is indicated by asterisks.
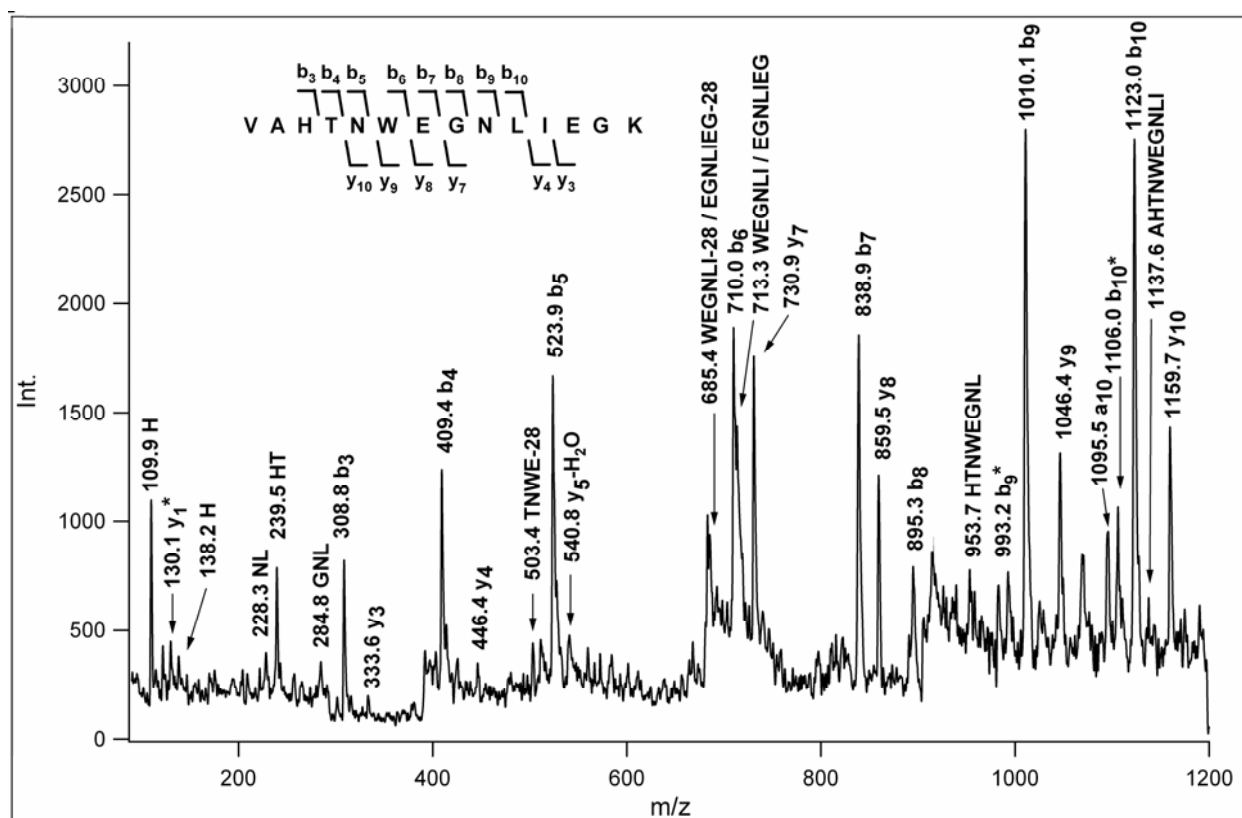
S1a
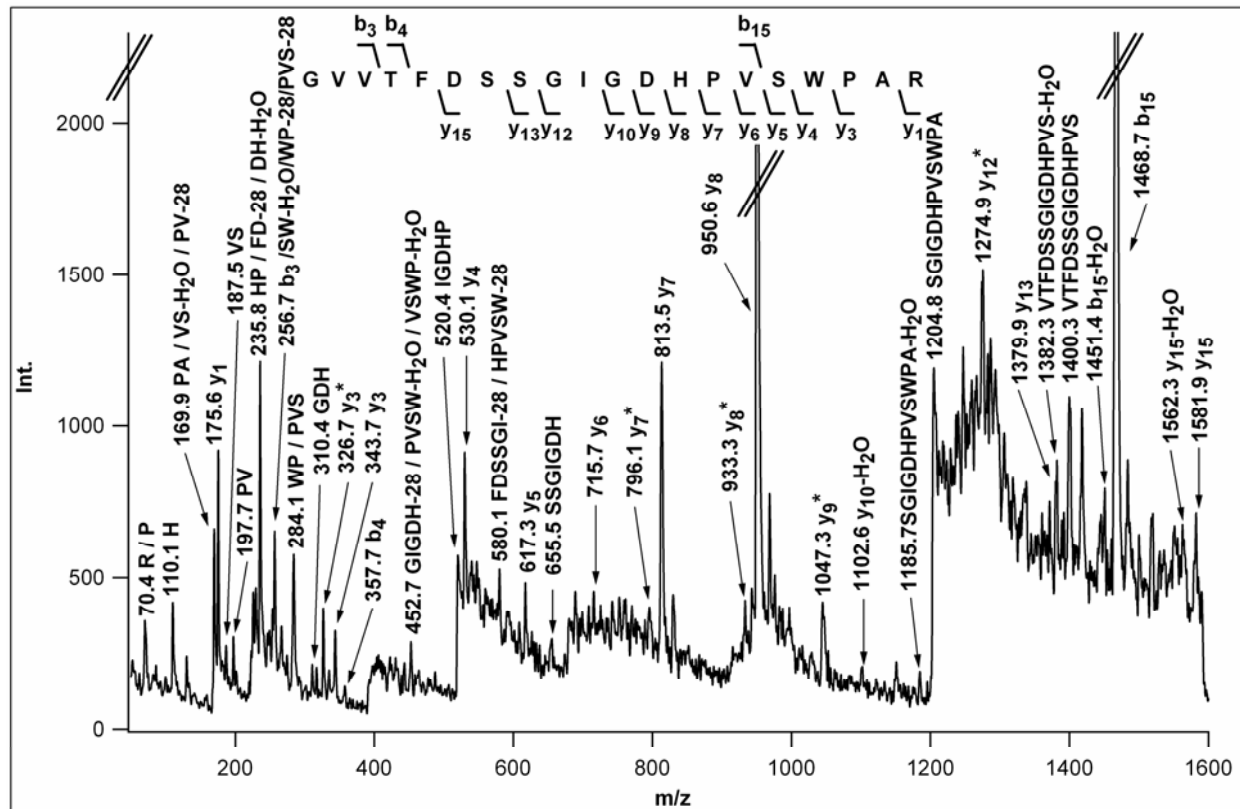
S1b

Figure S1 PSD-spectra of $MH^+ = 1567.79$ (S1a) and $MH^+ = 2084.02$ (S1b) peptides corresponding to VAHTNWEGNLIEGK [6-19] and GVVTFDSSGIGDHPVSWPAR [20-39] of putative ATP/GTP-binding protein (# 1).
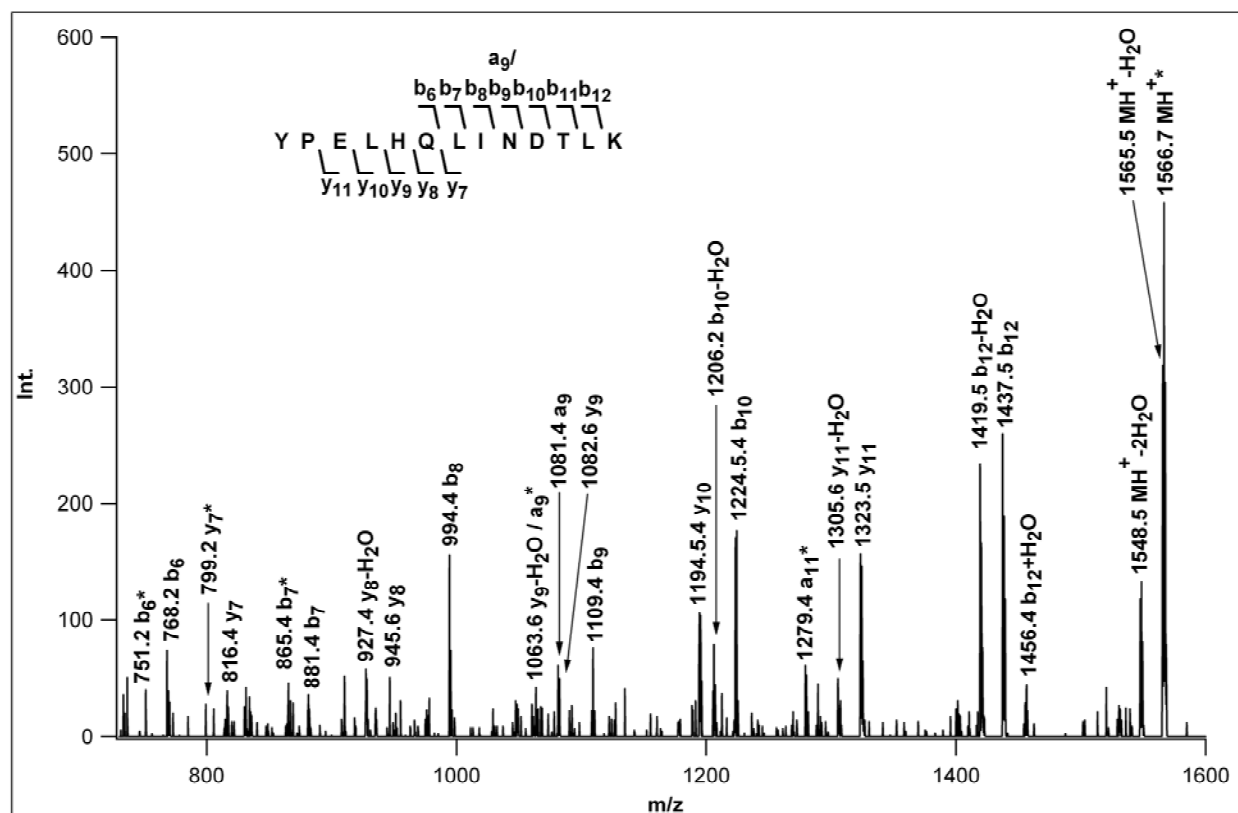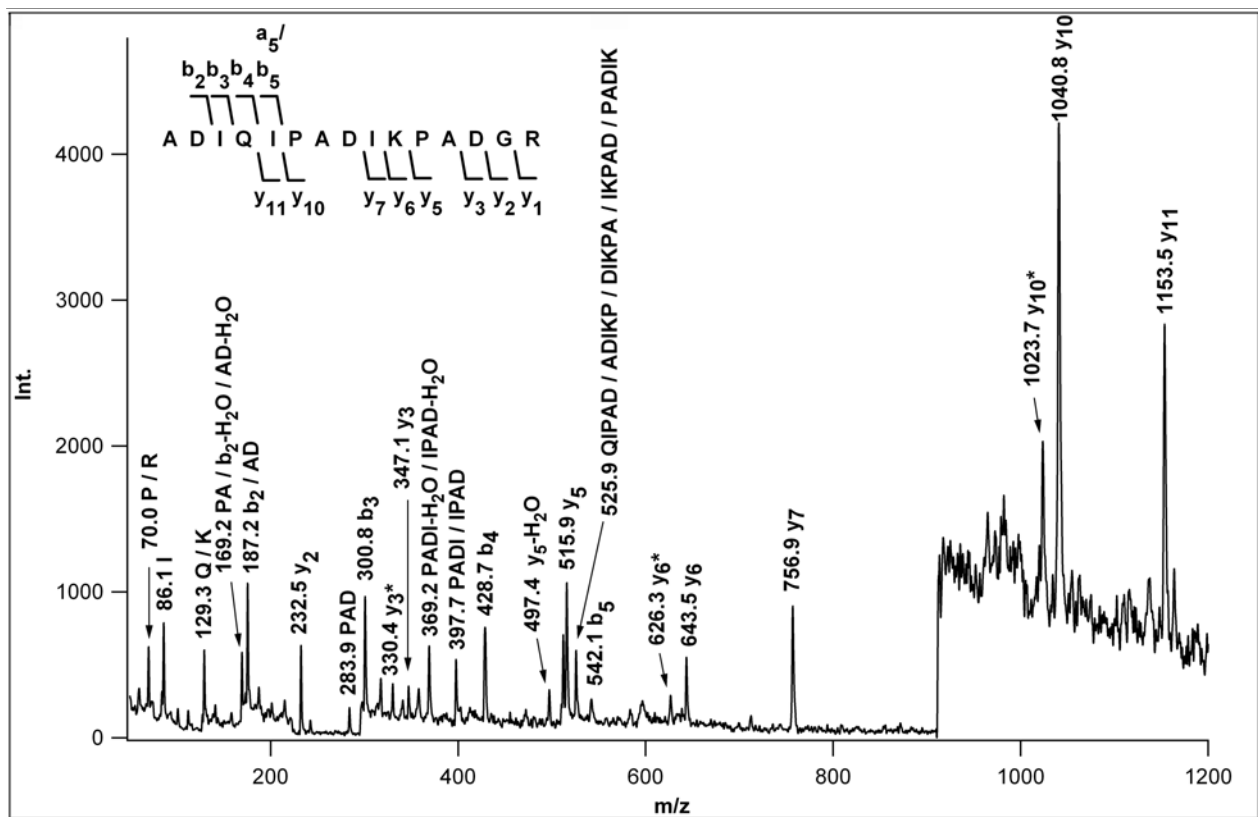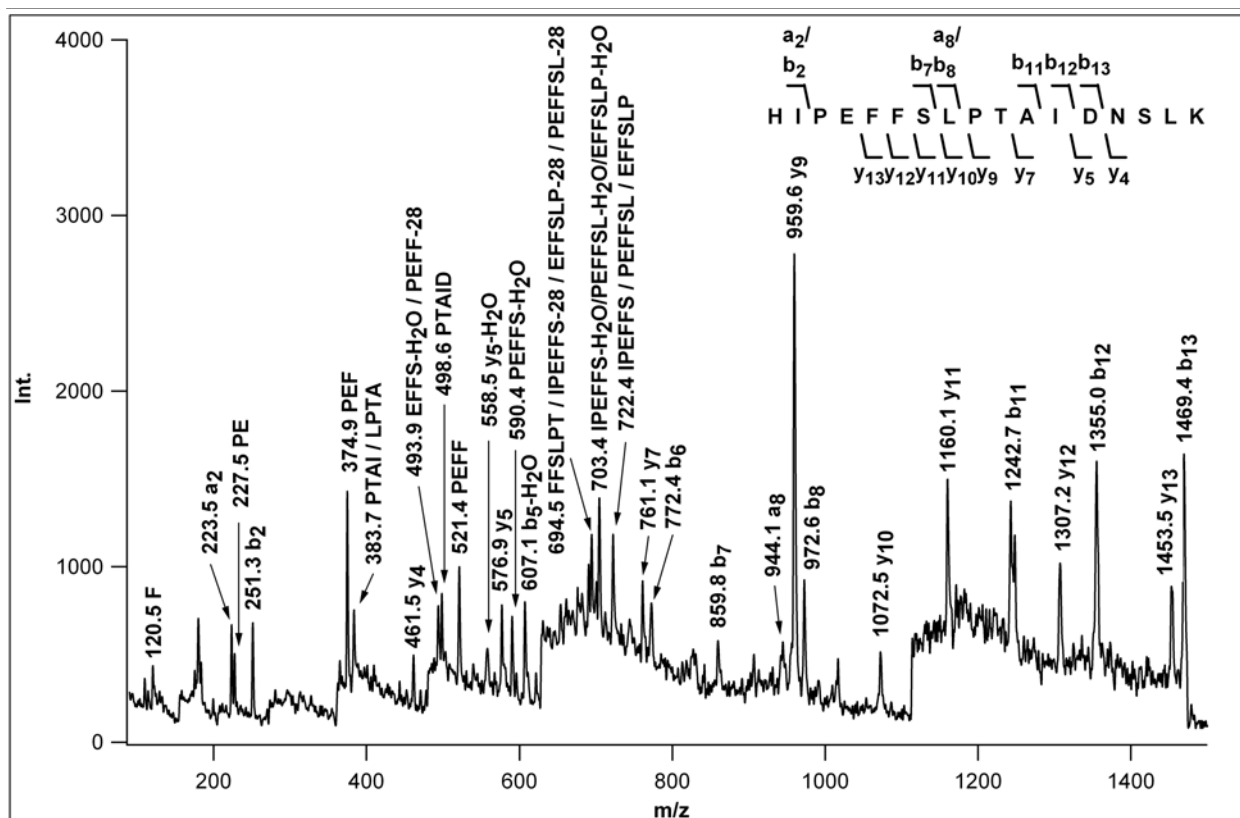
Figure S2 PSD-spectrum of MH$^+$ = 1583.84 peptide corresponding to the YPELHQLINDTLK [85-97] of putative superoxide dismutase (# 2).
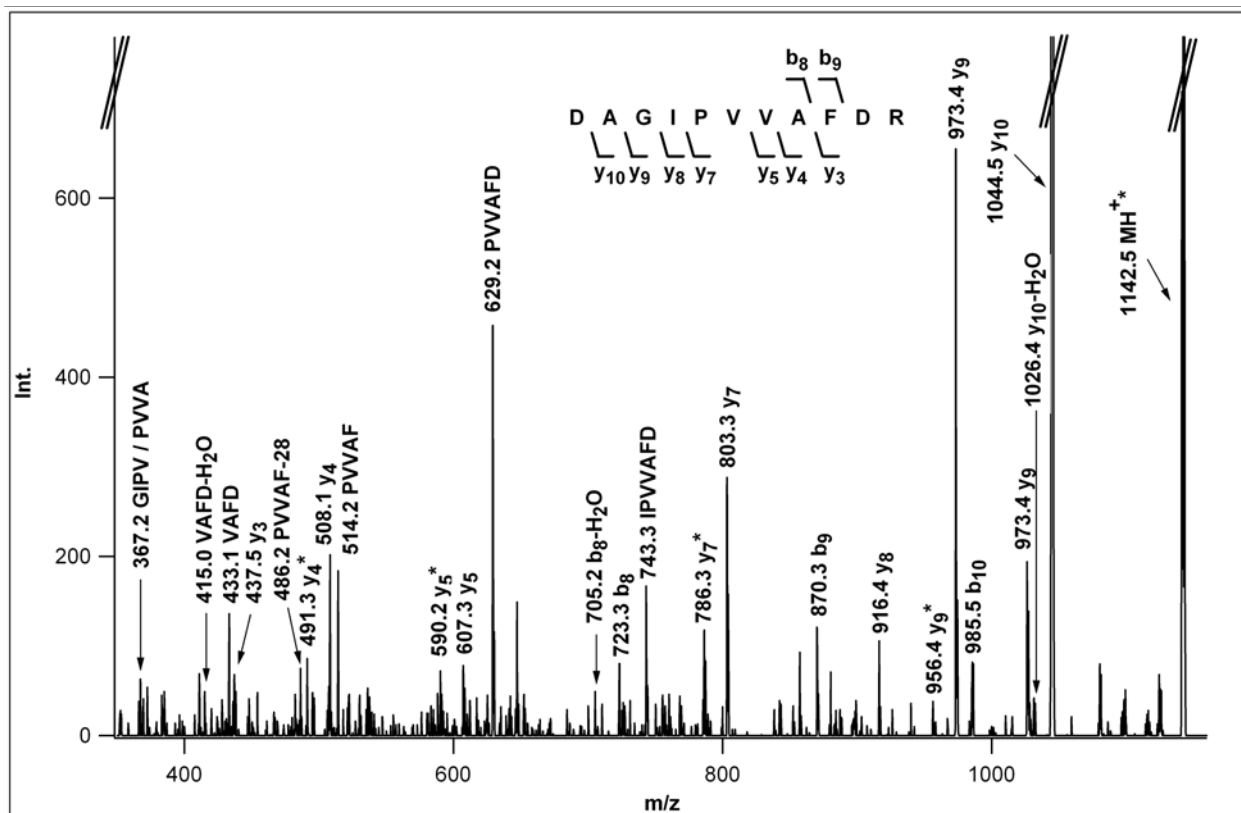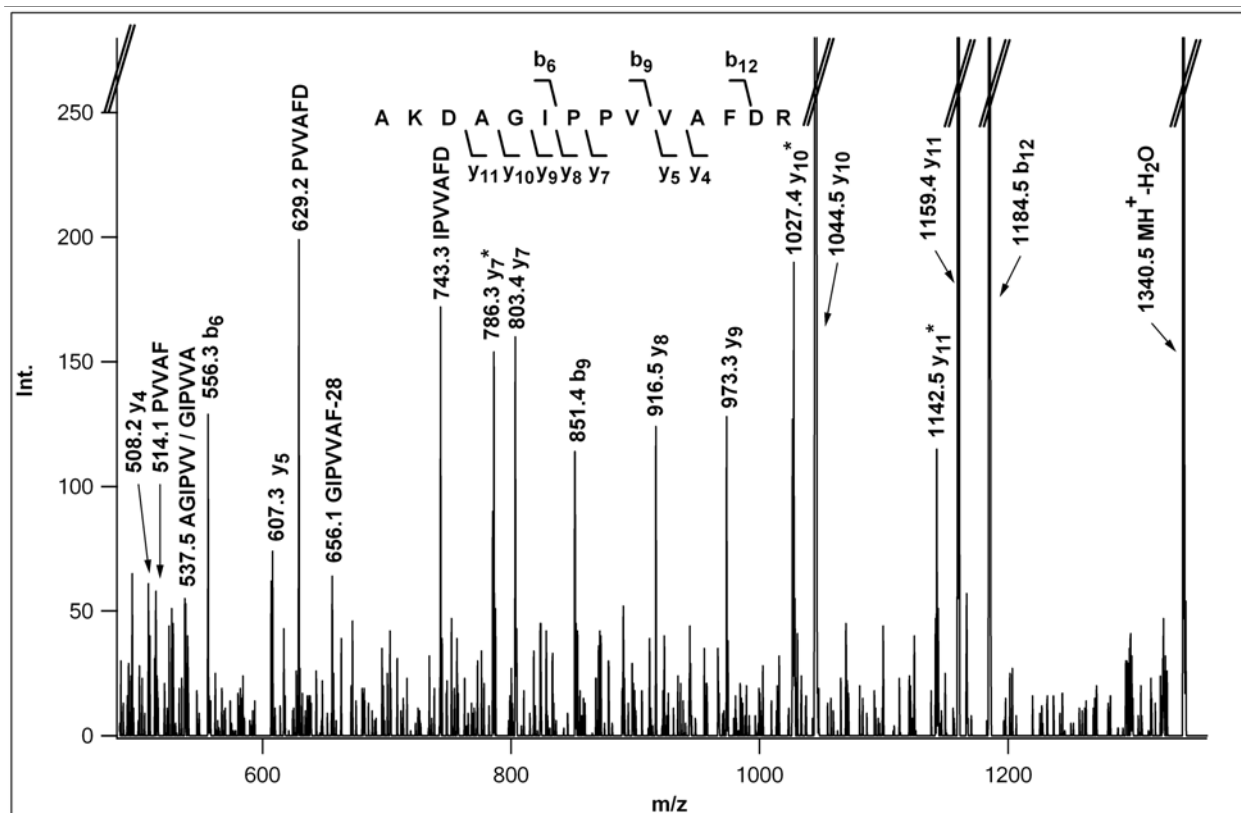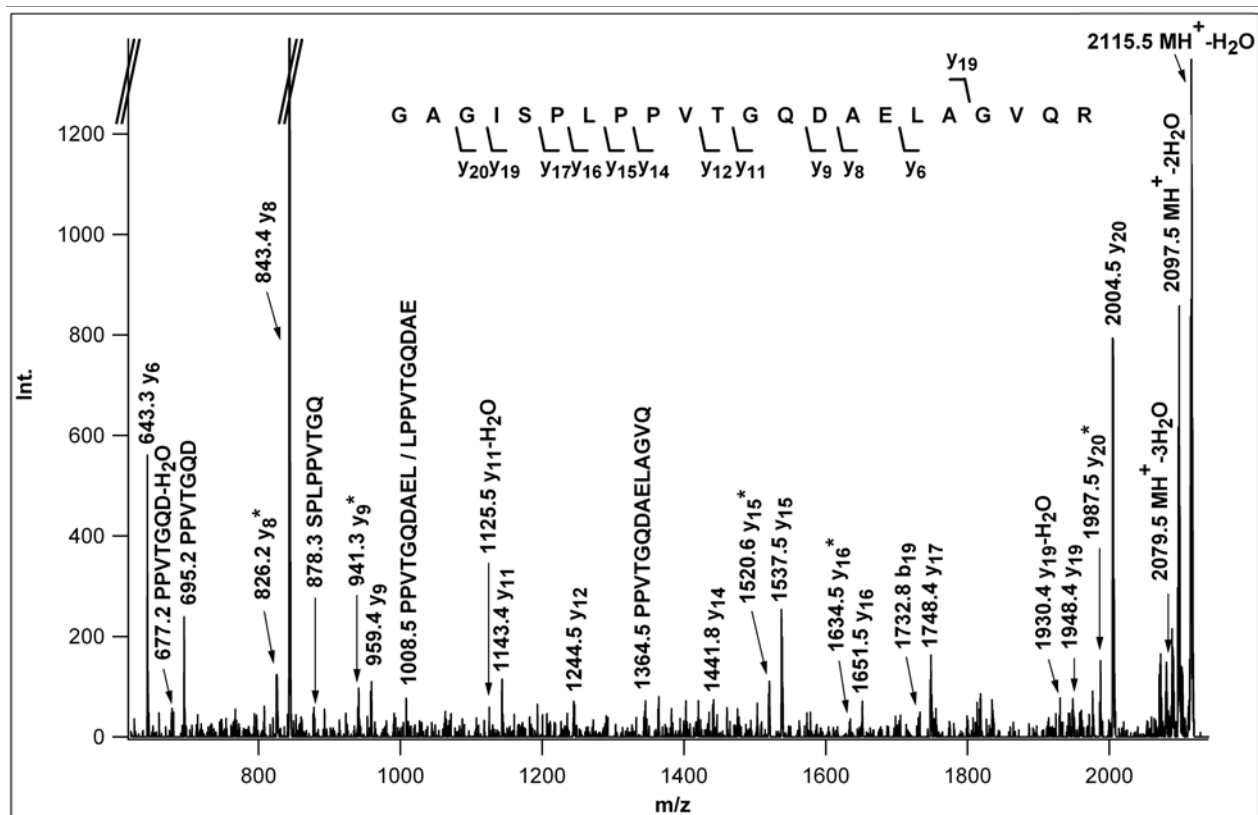
S3a

S3b

Figure S3 PSD-spectra of MH$^+$ = 1579.84 (S3a) and MH$^+$ = 1929.01 (S3b) peptides corresponding to ADIQIPADIKPADGR [2-16] and HIPEFFSLPTAIDNSLK [226-242] of putative aminotransferase (# 3 and 4).
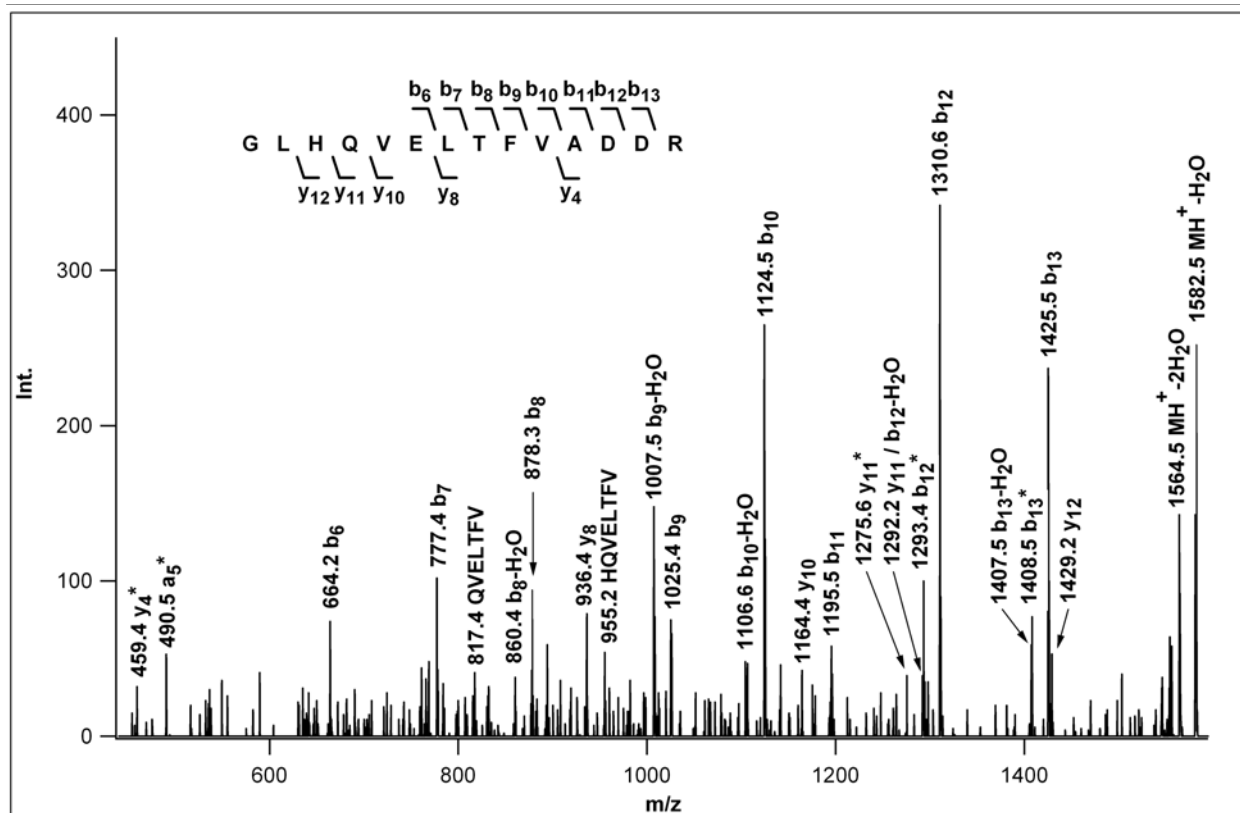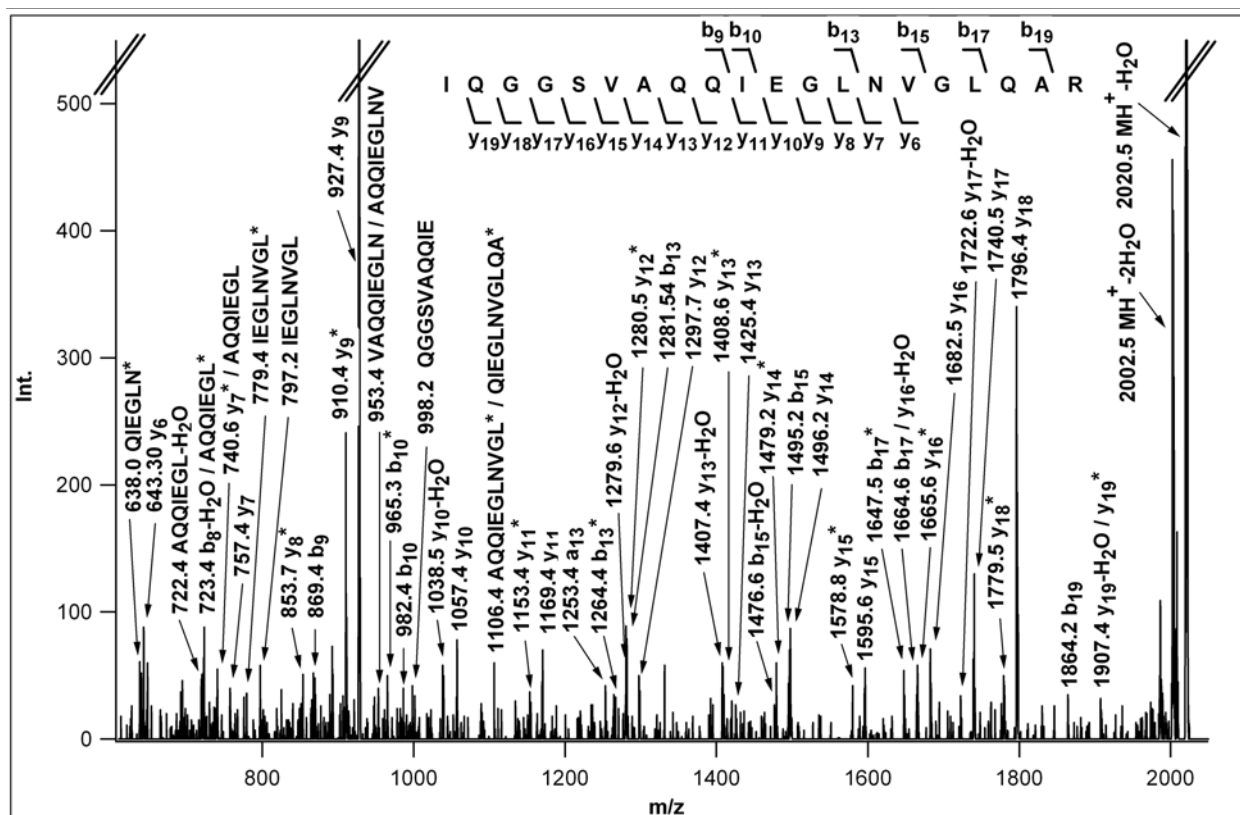
S4a

S4b

S4c

Figure S4 PSD-spectra of MH⁺ = 1159.61 (S4a), MH⁺ = 1358.74 (S4b) MH⁺ = 2133.13 (S4c) peptides corresponding to DAGIPVVAFDR [127-137], AKDAGIPVVAFDR [125-137] and GAGISPLPPVTGQDAELAGVQR [254-275] of putative ABC transporter solute-binding protein (# 5-8).
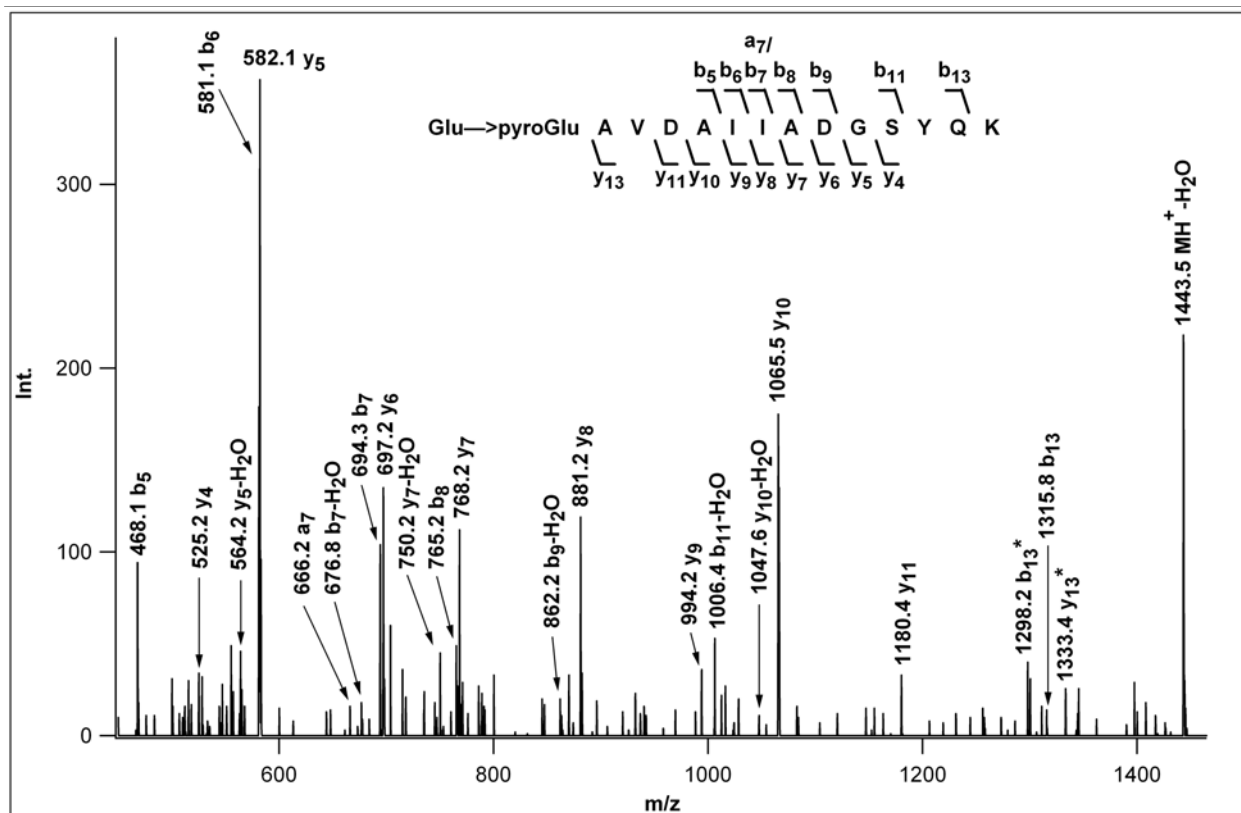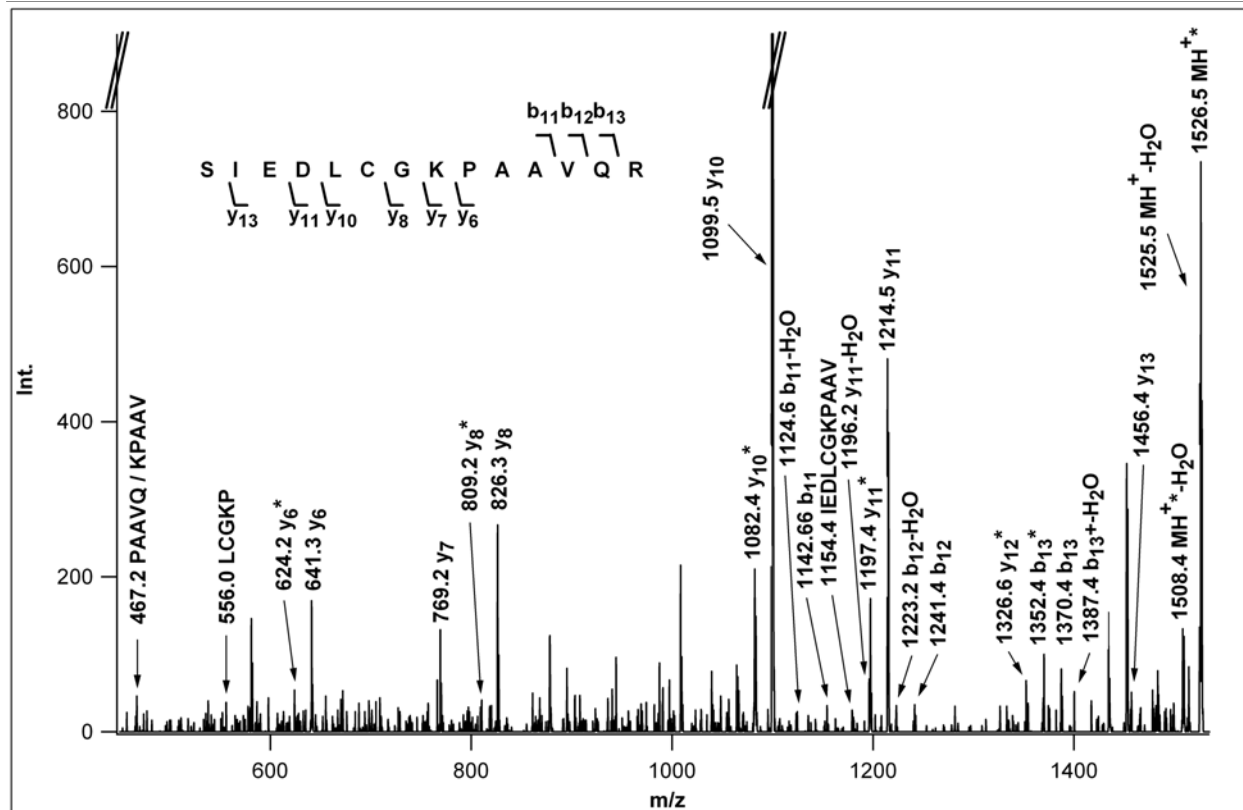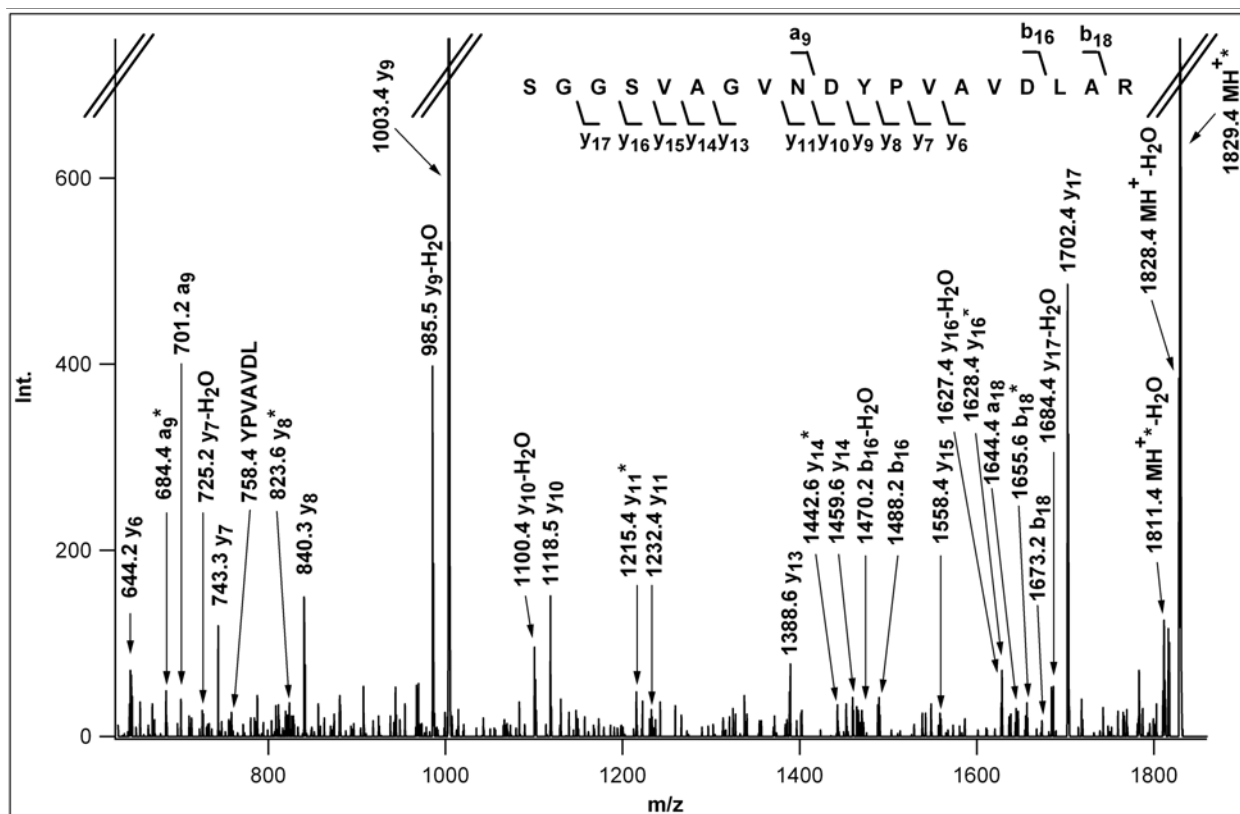
S5a

S5b

Figure S5 CID-spectra of $MH^+ = 1599.81$ (S5a) and $MH^+ = 2038.10$ (S5b) peptides corresponding to GLHQVELTFVADDR [192-205] and IQGGSVAQQIEGLNVGLQAR [38-57] of hypothet. pro. sporulation-control protein (# 9).
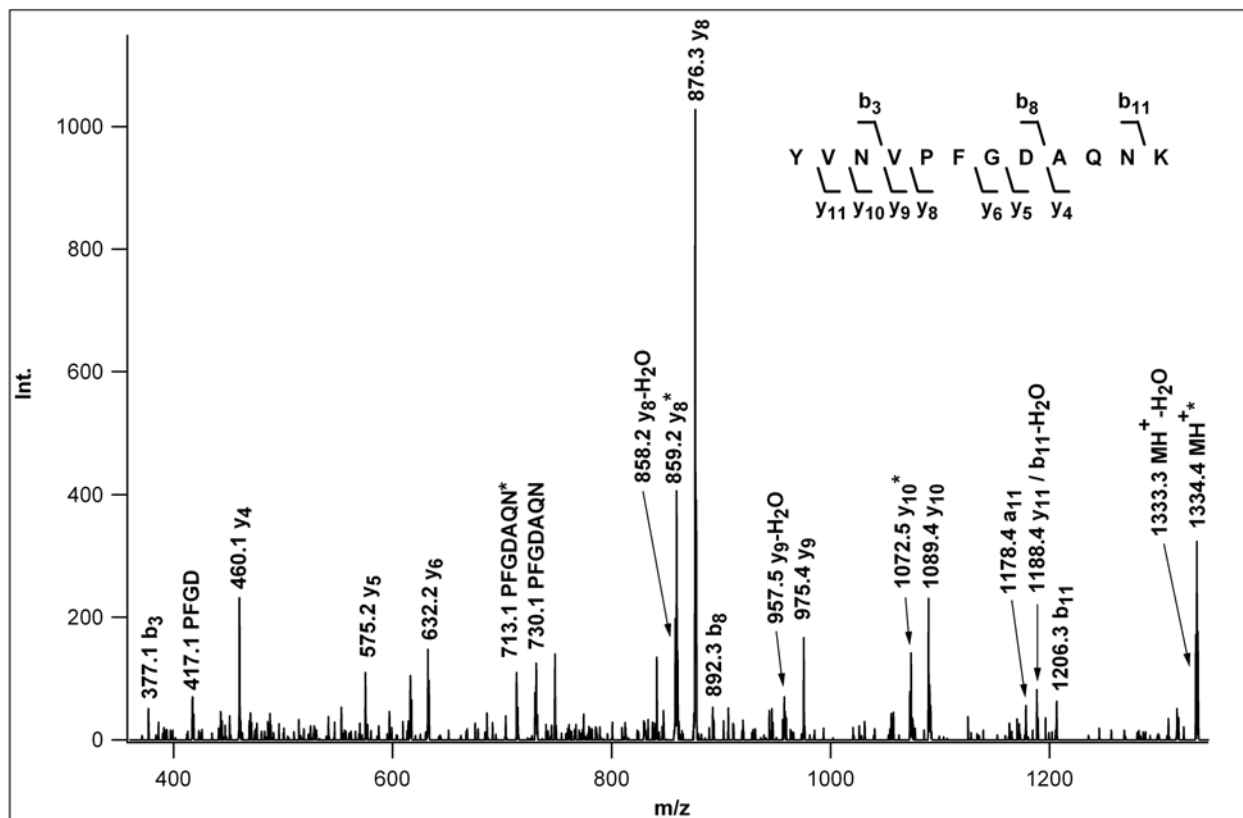
S6a

S6b

S6c

Figure S6 PSD-spectra of MH$^+$ = 1461.72 (S6a), MH$^+$ = 1543.79 (S6b) MH+ = 1846.93 (S6c) peptides corresponding to the Glu→pyroGluAVDAIIADGSYQK [286-299], SIEDLCGKPAAVQR [178-191] and SGGSVAGVNDYPVAVDLAR [231-249] of putative arginine/ornithine binding protein (# 10).

S7a
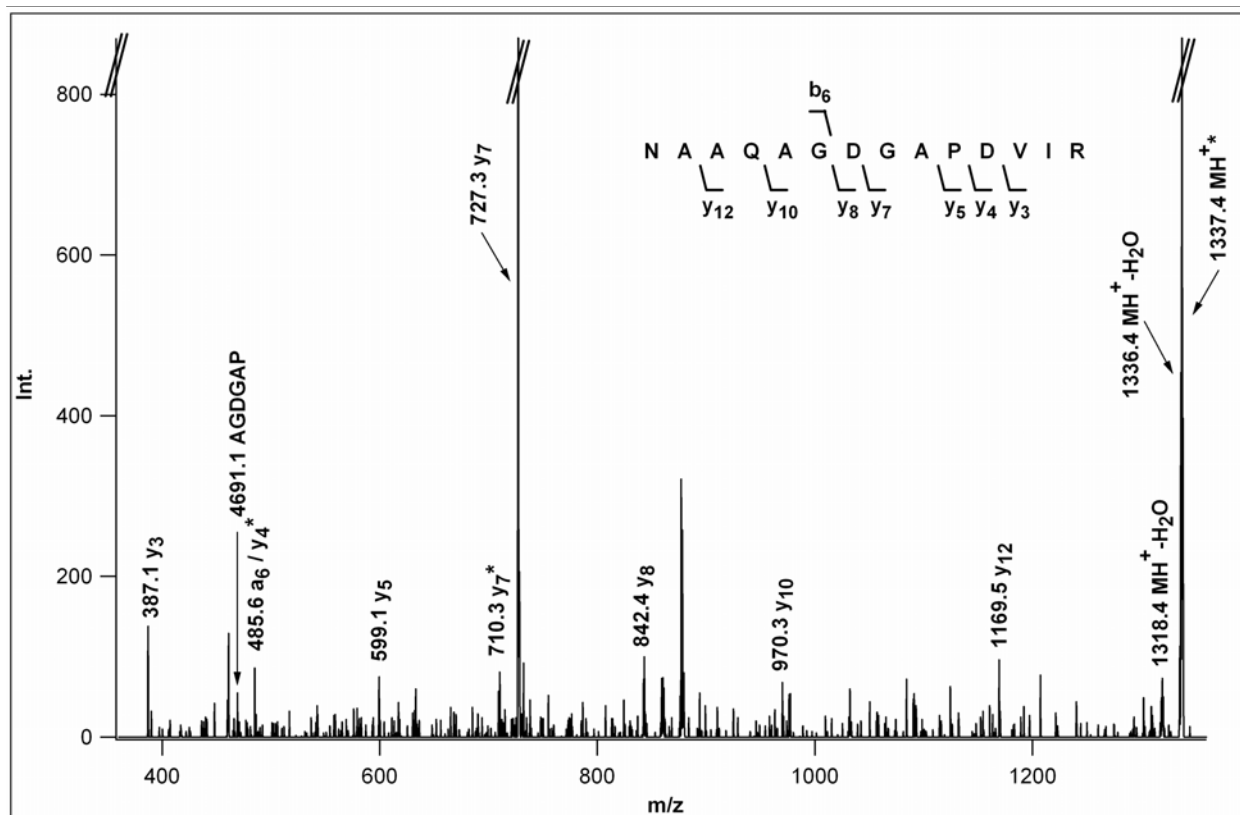
S7b

Figure S7 CID-spectra of MH^+ = 1351.66. (S7a) and MH^+ = 1354.67 (S7b) peptides corresponding to YVNVPFGDAQNK [73-84] and NAAQAGDGAPDVIR [87-100] of putative ABC transporter maltose-binding protein (# 11).

S8a

16
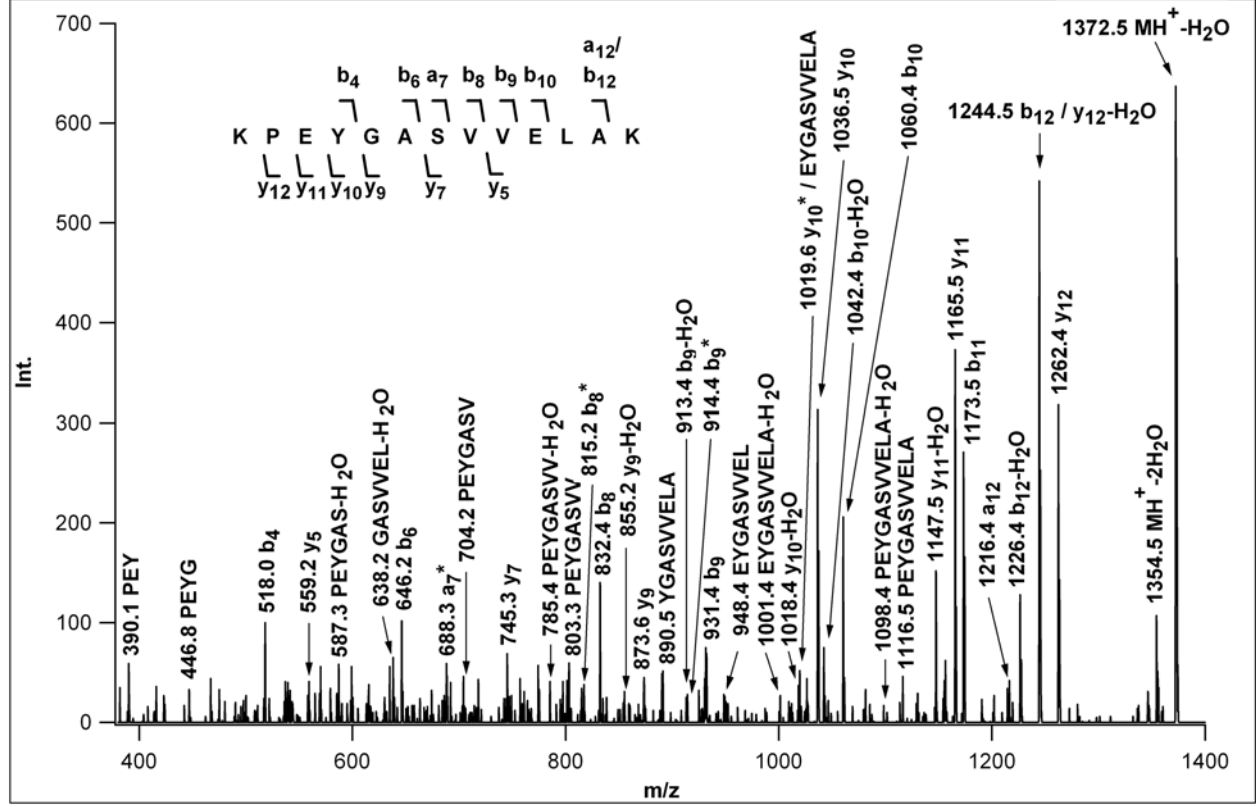
S8b
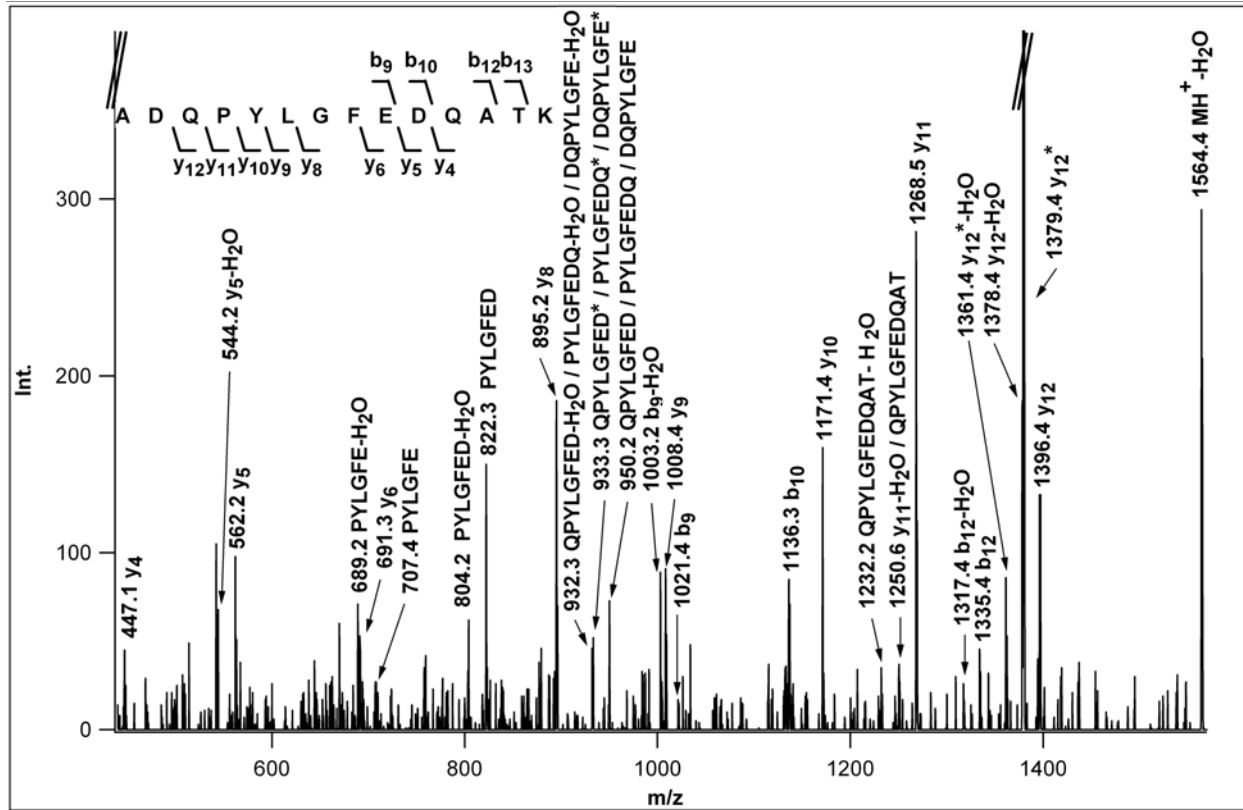
S8c
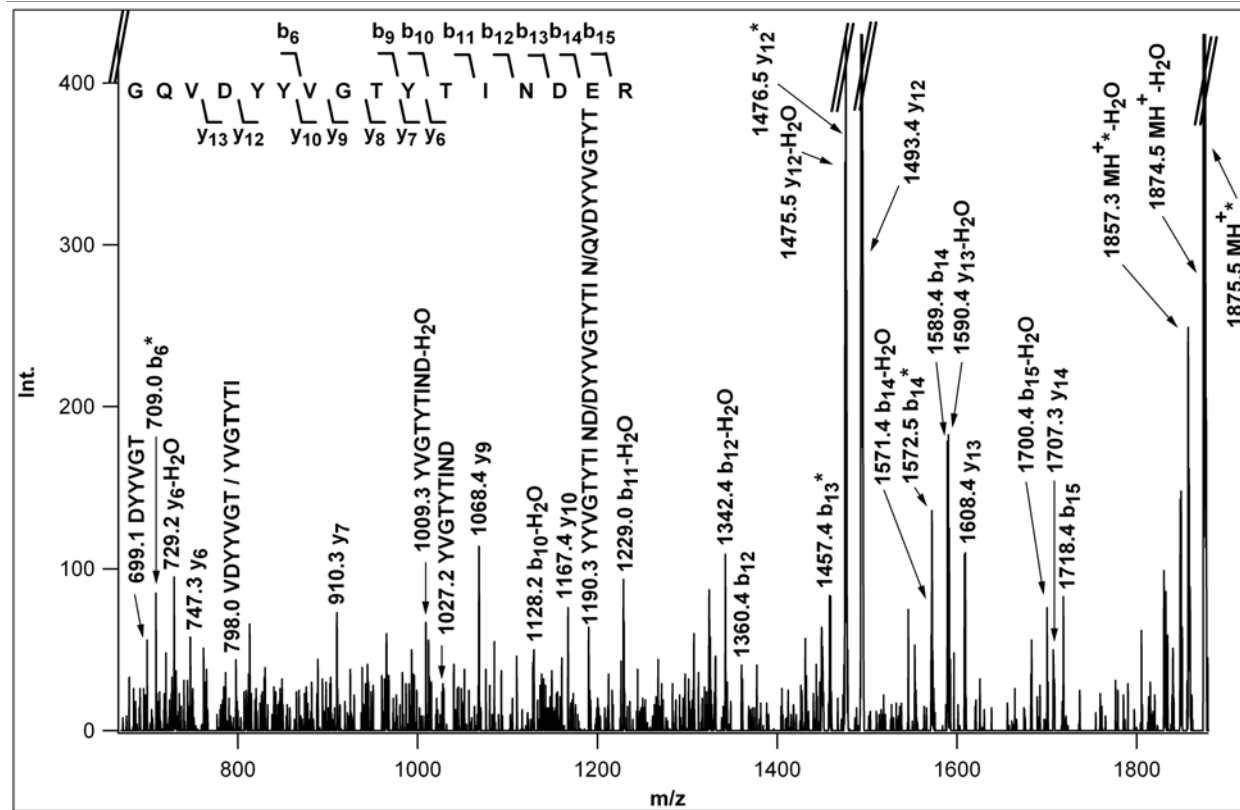
S8d

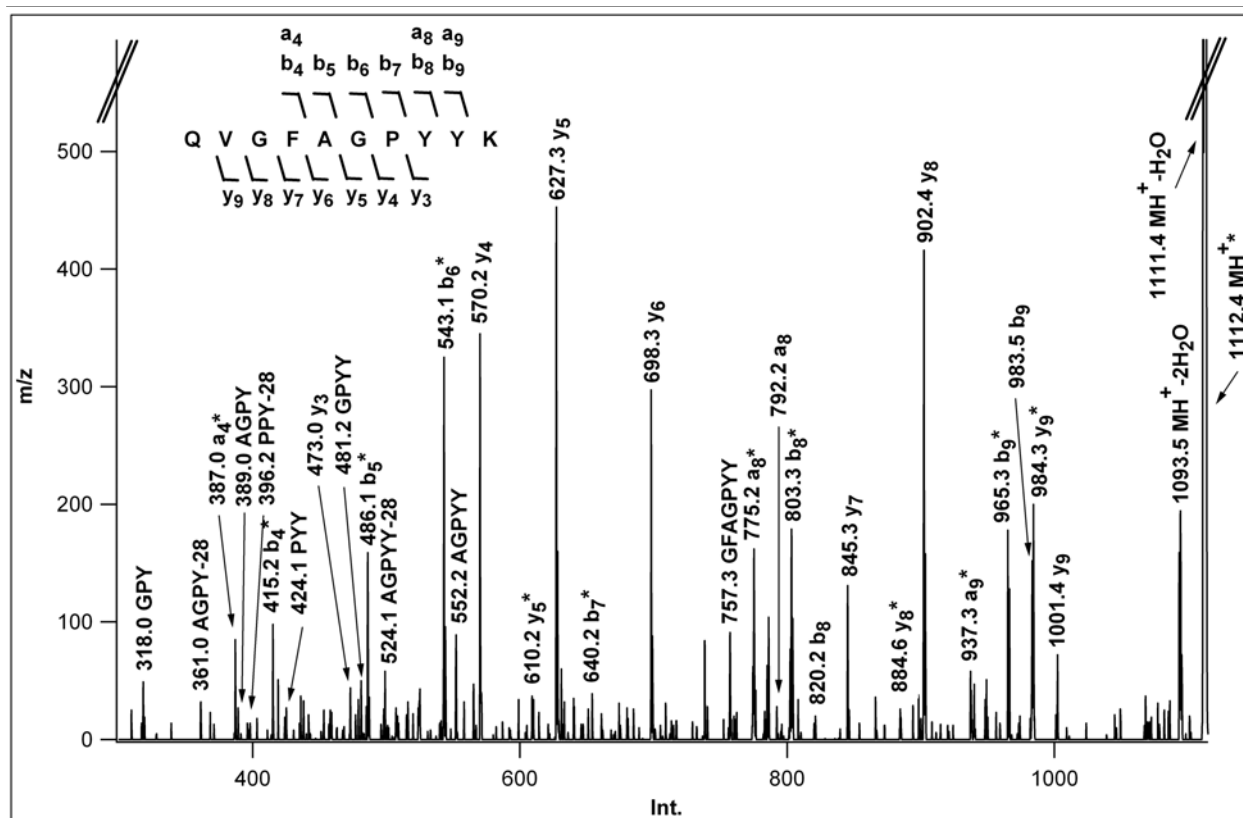**Figure S8** PSD-spectra of MH$^+$ = 1129.57 (S8a), MH$^+$ = 1390.76 (S8b), MH+ = 1582.74 (S8c) and MH+ = 1892.87 (S8d) peptides corresponding to QVGFAGPYYK [149-158], KPEYGASVVELAK [197-209], ADQPYLGFEDQATK [77-90] and GQVDYYVGTYTINDER [131-146] of putative glutamate ABC transporter substrate-binding protein (# 12 and 13).

19
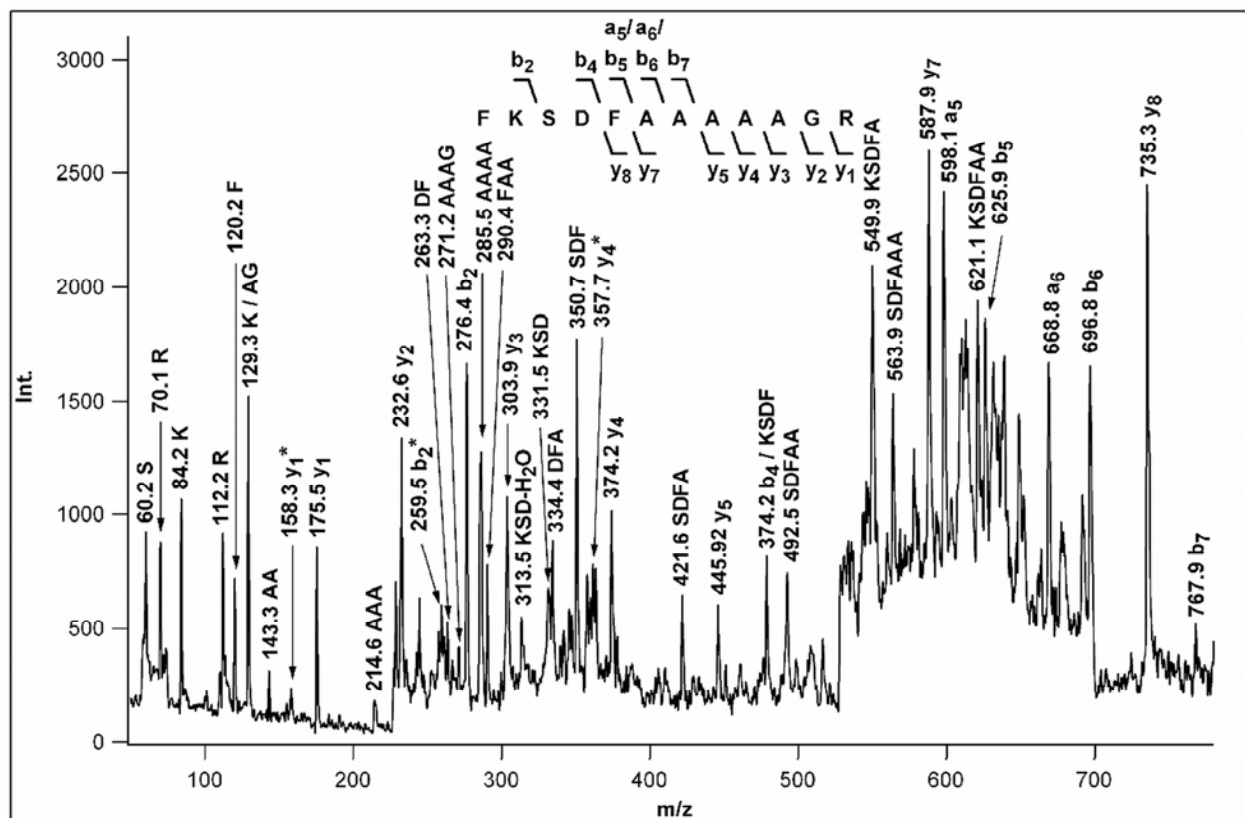
S9

Figure S9 PSD spectrum of MH$^+$ = 1211.61 peptide, corresponding to the FKSDFAAAAAGR [115-126] sequence of manganese (Mn) superoxide dismutase SodA (# 14).

S10a

S10b

22
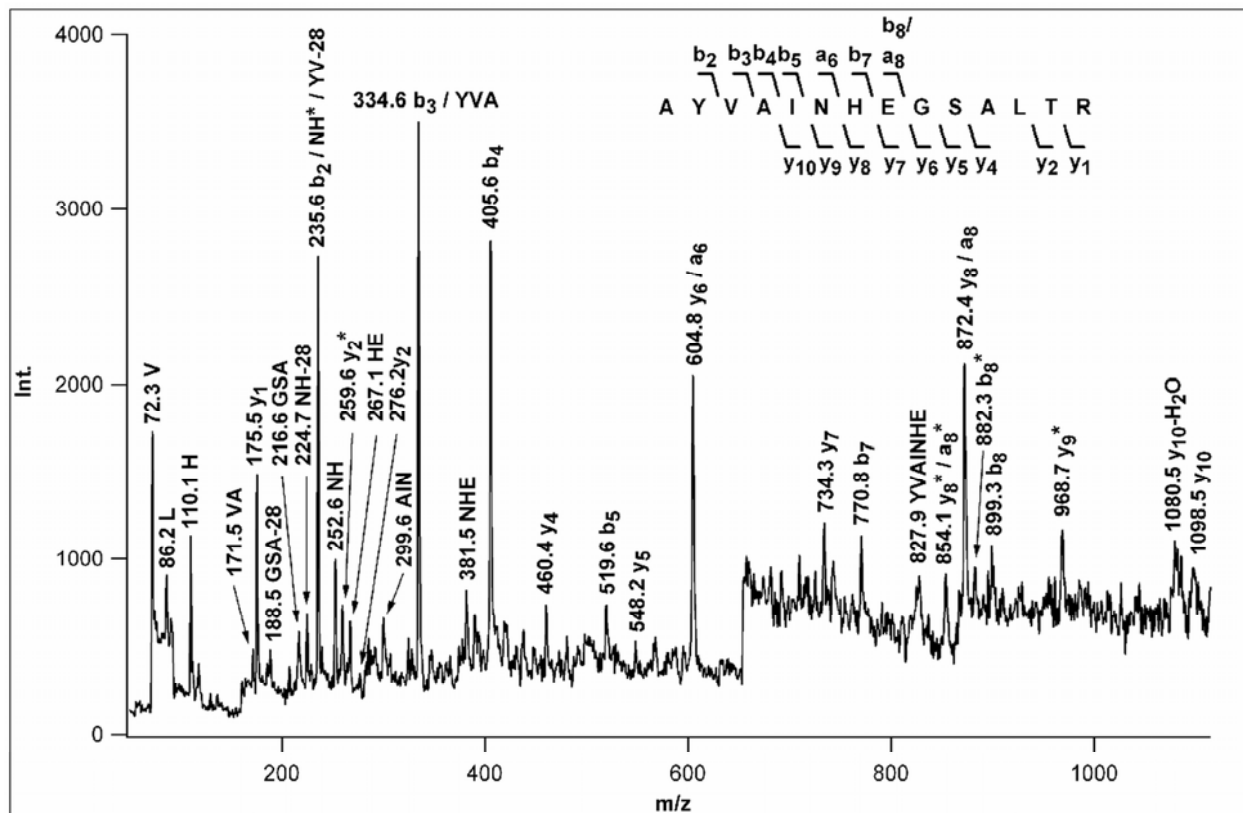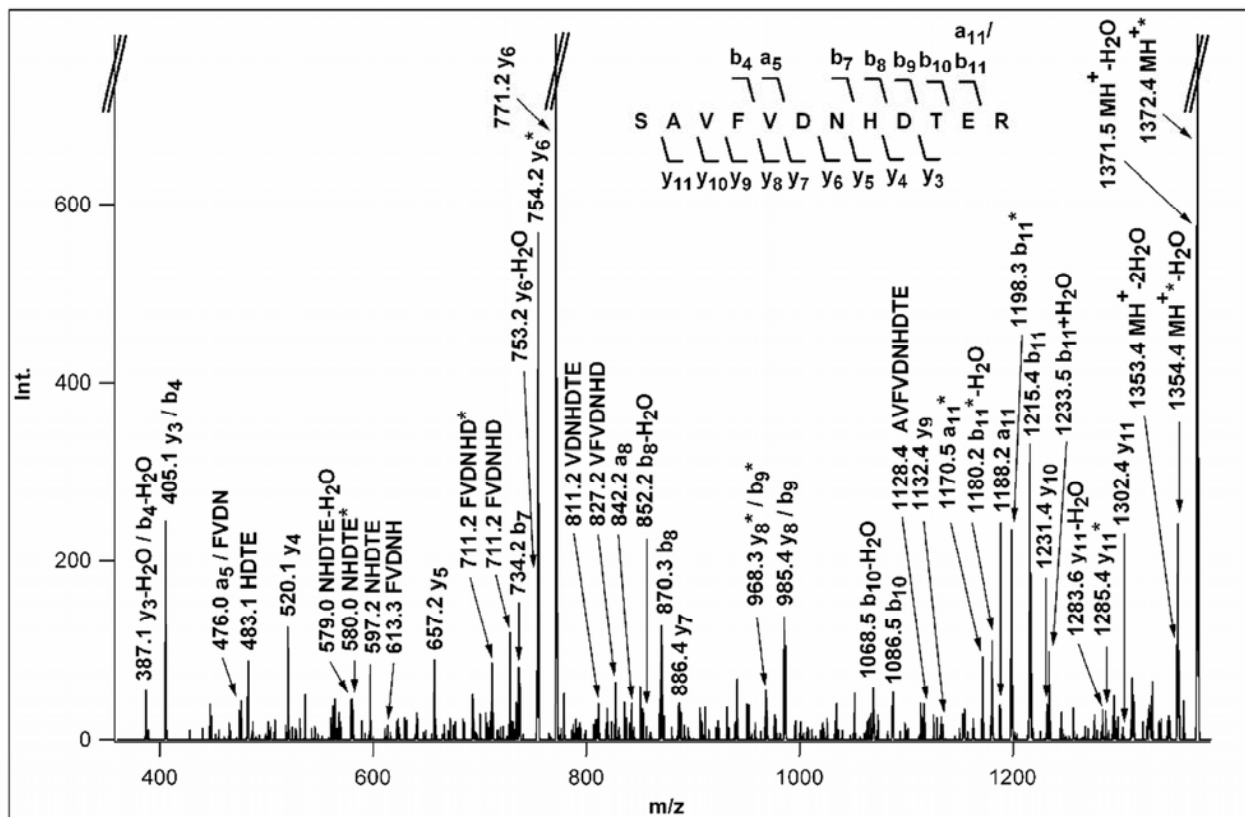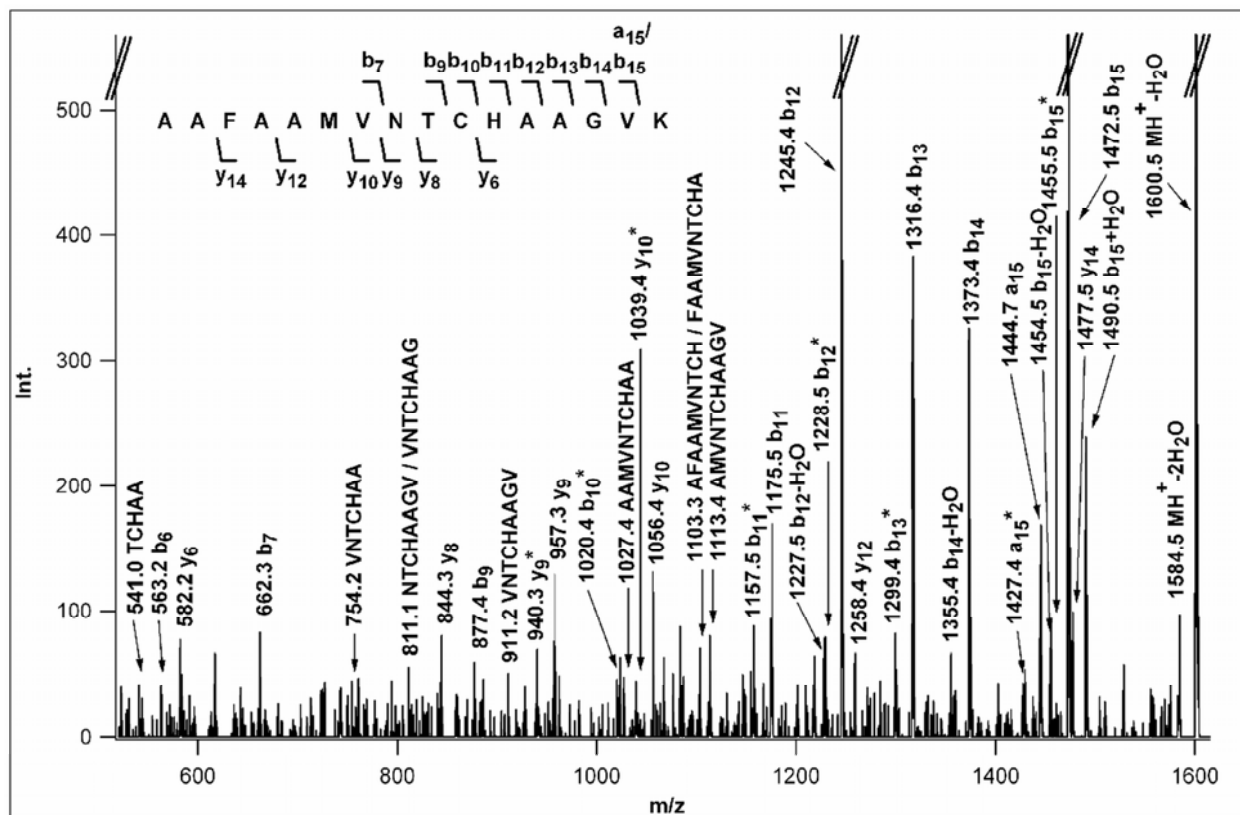
S10c

Figure S10 PSD spectrum of MH$^+$ = 1501.78 (S10a) and CID spectra of MH$^+$ = 1389.64 (S10b) and MH$^+$ = 2133.13 (S10c) peptides, corresponding to the AYVAINHEGSALTR [406-419], SAVFVDNHDTER [295-306] and AAFAAMVNTCHAAGVK [103-118] sequences of putative putative alpha-amylase (# 15 and 16).

23

Table S1

Oligonucleotides used for semi-quantitative RT PCR analysis. Oligonucleotides ending with 'f' were used as forward primers in the amplification step, those ending with 'r' for cDNA synthesis with reversed transcriptase and as reverse primers during amplification. **#**, position is indicated relative to the start of the target gene; **c**, complementary to coding strand.

Oligonucleotide	Target	Position 5' end [#]	Sequence (5' → 3')
RT_1460+169f	SGR1460	+169	CACTCCAGCTGCTTCTCGAT
RT_1460+419r	SGR1460	+419c	AGCGAGGCCGTCAGGGTGATC
RT_1498+105f	SGR1498	+105	AGGAGGTTCGGAGAAGAAGG
RT_1498+313r	SGR1498	+313c	CCTTGTTGGTGATCATGGTG
RT_1737+286f	SGR1737	+286	GACATCGAGATCGCCAAGAT
RT_1737+558r	SGR1737	+558c	GATCGAGCAGACCTTCTTGC
RT_2237+514f	SGR2237	+514	AACCCGCAGAACATCAAGTC
RT_2237+729r	SGR2237	+729c	GACCGGGTAGTCGTTGACAC
RT_2245+118f	SGR2245	+118	GAGAAGTACCAGGCCAACGA
RT_2245+396r	SGR2245	+396c	TCAGGCCTTCTTGGTCTCC
RT_3109+429f	SRG3109	+429	CTTCACCCACAACGAGACCT
RT_3109+695r	SRG3109	+695c	GAGAAGAACTCCGGGATGTG
RT_5275+215f	SGR5275	+215	AGTACGTCAACGTGCCCTTC

RT_5275+496r	SGR5275	+496c	CCTCCTTGAGCAGCTTCTTG
RT_5280+478f	SGR5280	+478	TCCCAGATCGGGAACAACTA
RT_5280+719r	SGR5280	+719c	GCCTCGTGCTTCCAGTAGAC
RT_5704+530f	SGR5704	+530	CGTTCTACCAGGAGATCGAGTT
RT_5704+749r	SGR5704	+749c	AGCCACTGGTTGAGGTATGC