Supplemental Information

Title: Proteomics Profiling Reveals Carbohydrate Metabolic Enzymes and 14-3-3 Proteins Play Important Roles for Starch Accumulation during Cassava Root Tuberization

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Supplementary Figures and Tables

Supplementary Fig. S1. Yields and 1-DE profiles of total proteins extracted from cassava main roots at different development stages.

Supplementary Fig. S2. Typical MS spectra and identification information of proteins from common 2-DE gels.

Supplementary Fig. S3. Typical MS spectra and identification of proteins from DIGE gels.

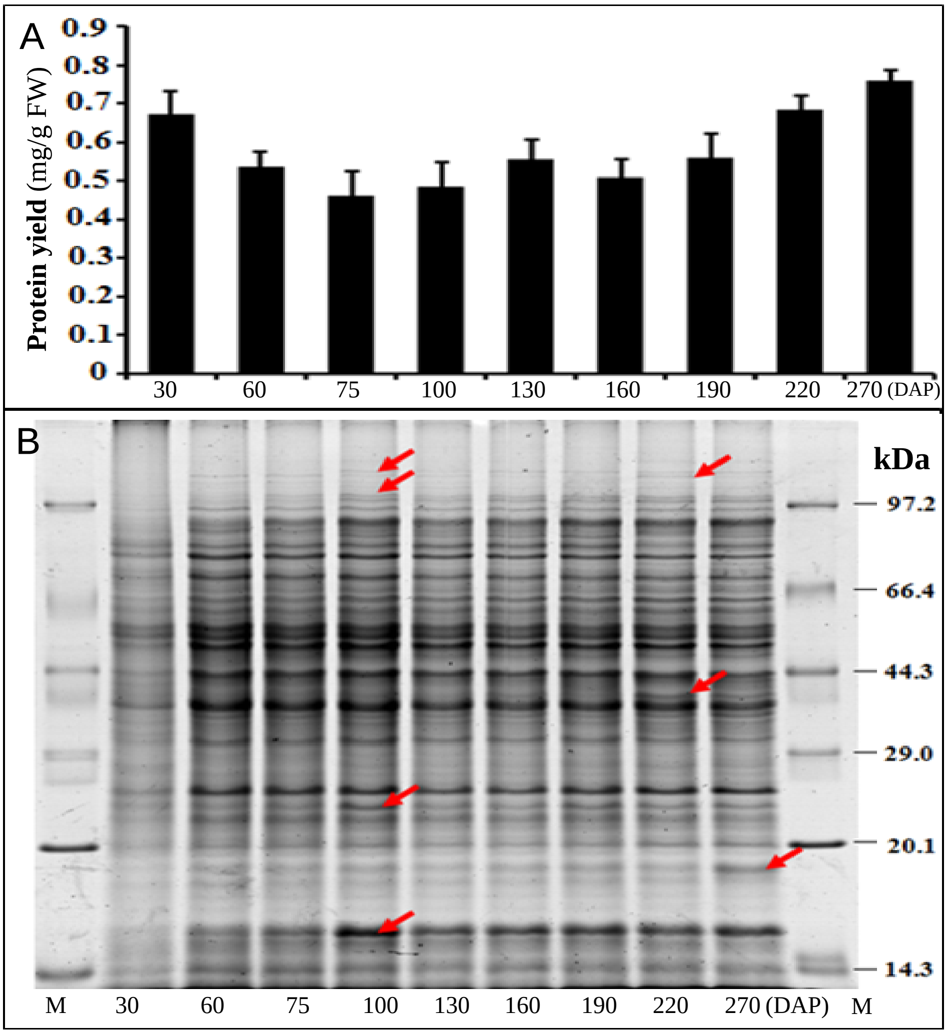
Supplementary Fig. S4. Main pathway ways overexpressed in all the differential proteins.

Supplementary Table S1. Information for differential protein spots on 2-DE gels and their corresponding MS identities.

Supplementary Table S2. Information for differential proteins on 2-D DIGE gels and the corresponding MS identities.

Supplementary Table S3. Primers used for RT and Q-PCR analysis.

Supplemental Figure S1: Yields (A) and 1-DE profiles (B) of total proteins extracted from cassava main roots at different development stages.



The cassava main roots were collected at 30, 60, 75, 100, 130, 160, 190, 220 and 270 (Stages S1-S9, respectively) days after planting. M, molecular weight markers. Arrows indicated the major differential protein bands on the 1-DE gels.

Supplemental Figure S2:

Supplemental spectra and MALDI TOF/TOF MS/MS identification information from common 2-DE gels

Annotated spectra for the 118 proteins identified by PMF and PFF.

CID: collision induced dissociation

MALDI TOF:

matrix assisted laser desorption/ionization time of flight

MS: mass spectrometry

PMF: peptide mass fingerprinting

PFF: peptide fragment fingerprinting

Spot No.: **1**

NCBI accession No.: **cassava4.1_006707m|PACid:17966570**

Protein name：**hypothetical protein**

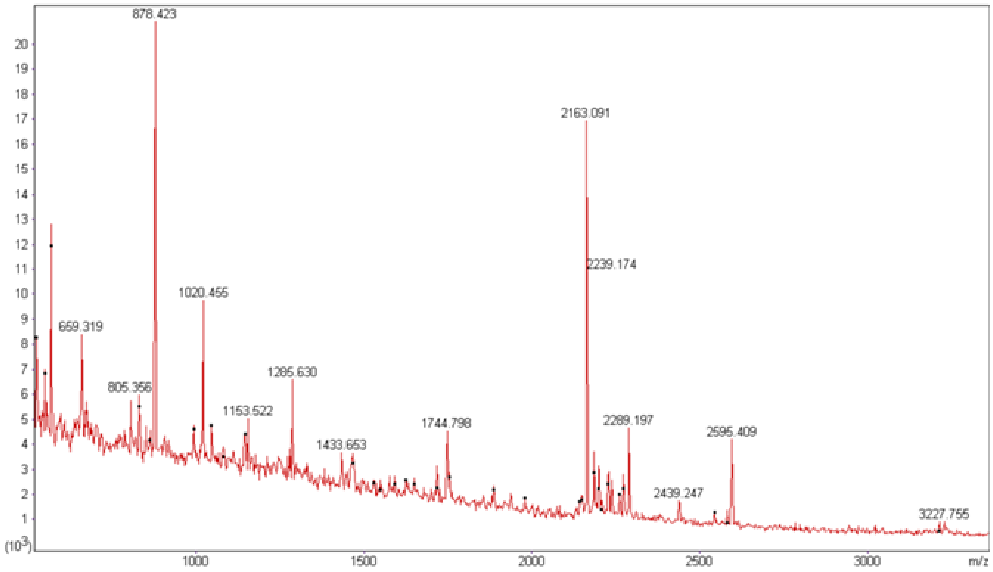
Plant species: ***Manihot esculenta*** Mascot score: **92**

Sequence coverage %: **27** p value: **0.0011**

Matched peptides No.: **13** Total peptides No.: **44**

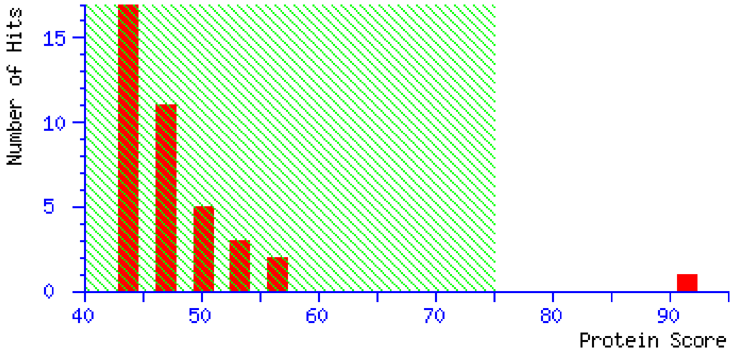
Calculated Mr: **55987** Calculated p*I*: **9.32**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **2**

NCBI accession No.: **cassava4.1_004263m|PACid:17968763**

Protein name：**Chaperonin 60 subunit alpha 1, chloroplastic**

Plant species: ***Manihot esculenta***

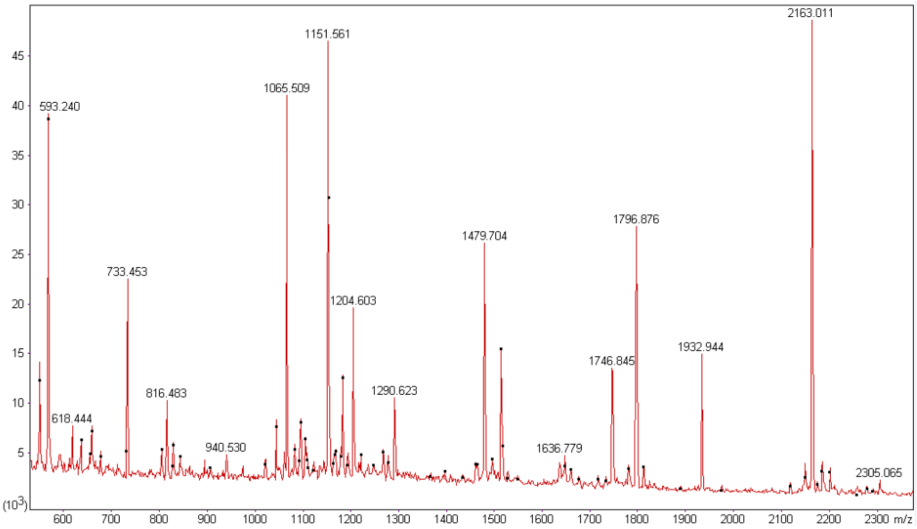
Mascot score: **215**

Sequence coverage %: **47**　　　　p value: **2.3e-017**

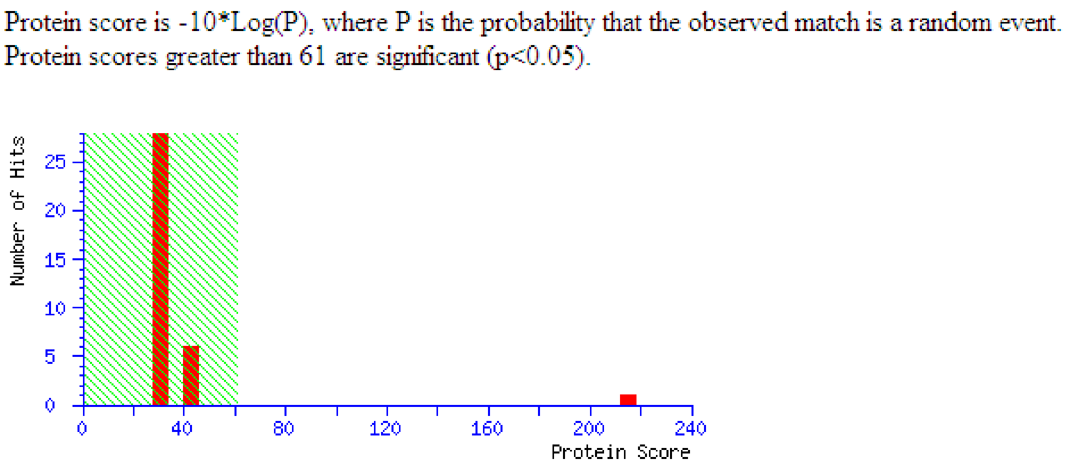
Matched peptides No.: **29**　　　　Total peptides No.: **64**

Calculated Mr: **62302**　　　　Calculated *p*I: **5.34**

Annotated PMF **spectra:**



Probability Based Mowse Score:


Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).

Spot No.: **3**

NCBI accession No.: **cassava4.1_006418m|PACid:17966937**

Protein name: **V-type proton ATPase subunit B1**

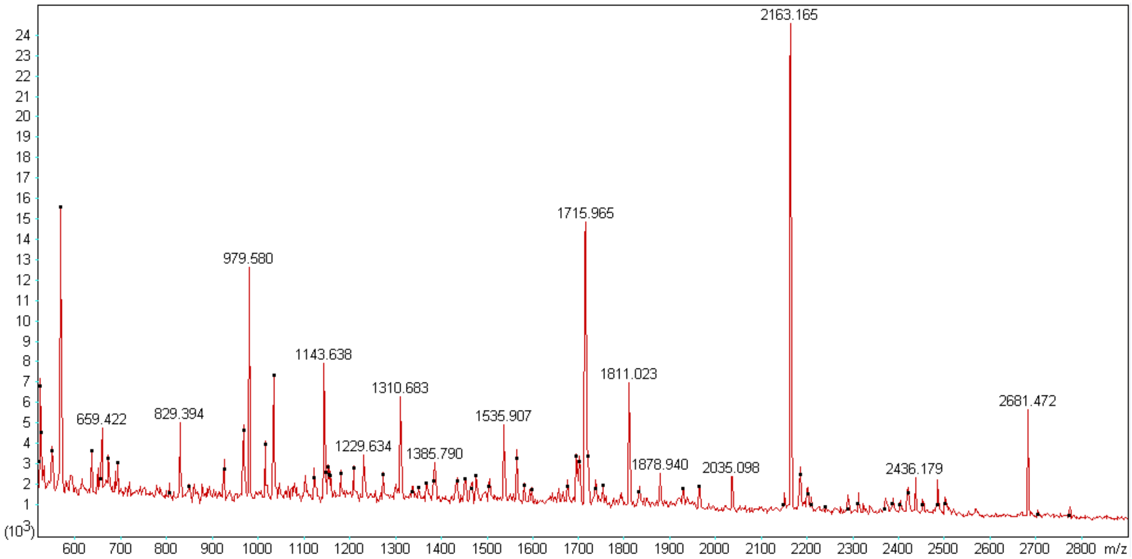
Plant species: ***Manihot esculenta*** Mascot score: **97**

Sequence coverage %: **46** p value: 1. 5e-005

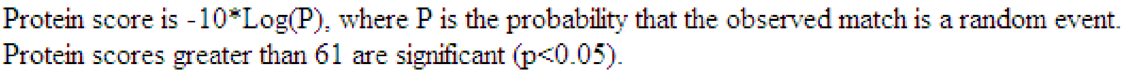
Matched peptides No.: **18** Total peptides No.: **75**

Calculated Mr: **54476** Calculated *p*I: **4.99**

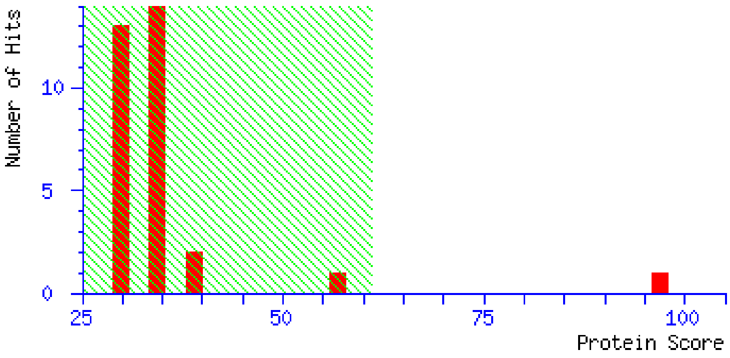
Annotated PMF **spectra:**



Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **4**

NCBI accession No.: **cassava4.1_006418m|PACid:17966937**

Protein name：**V-type proton ATPase subunit B2**

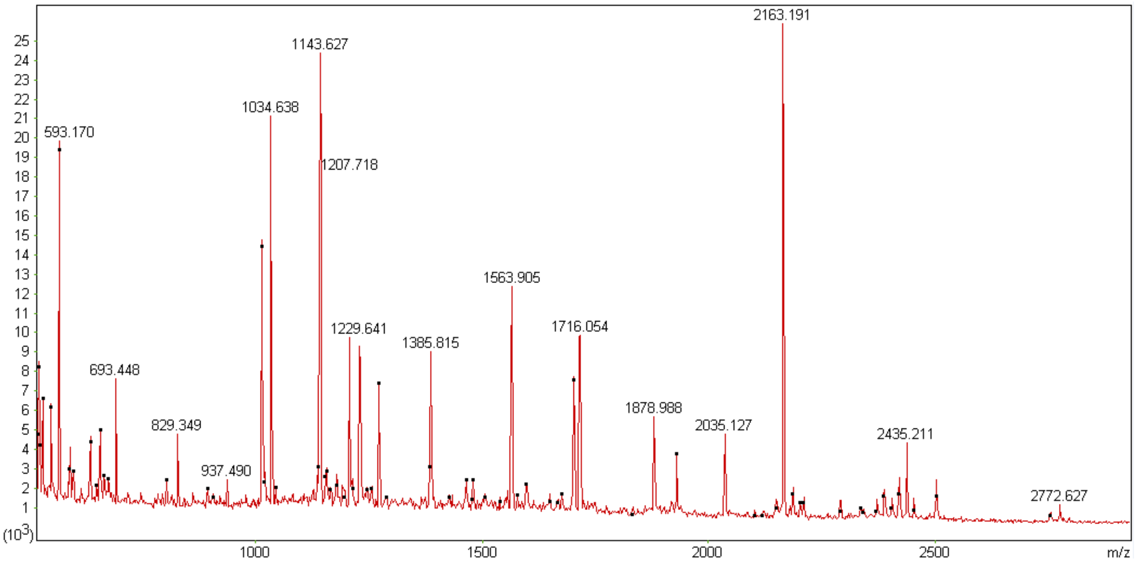
Plant species: ***Manihot esculenta*** Mascot score: **187**

Sequence coverage %: **48** p value: **1.5e-014**

Matched peptides No.: **27** Total peptides No.: **77**

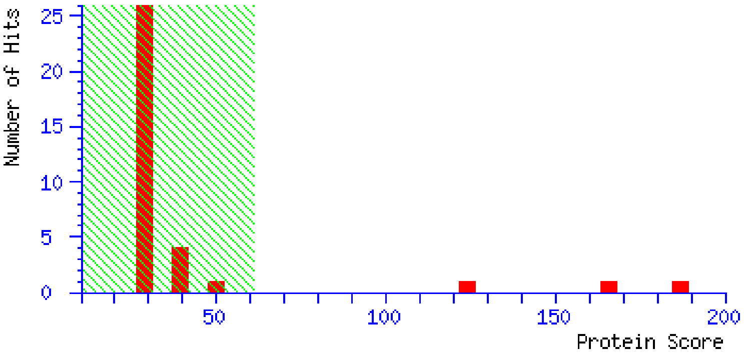
Calculated Mr: **54476** Calculated *p*I: **4.99**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **5**

NCBI accession No.: **cassava4.1_007971m|PACid:17991617**

Protein name：**Tubulin alpha-6 chain**

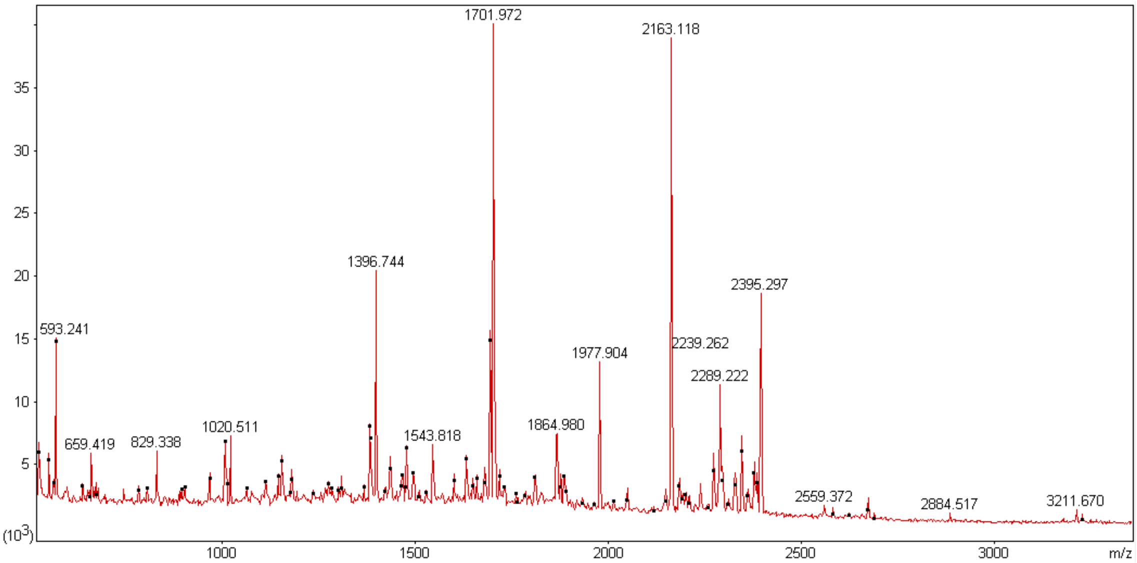
Plant species: ***Manihot esculenta*** Mascot score: **101**

Sequence coverage %: **51** p value: **5.8e-006**

Matched peptides No.: **15** Total peptides No.: **65**

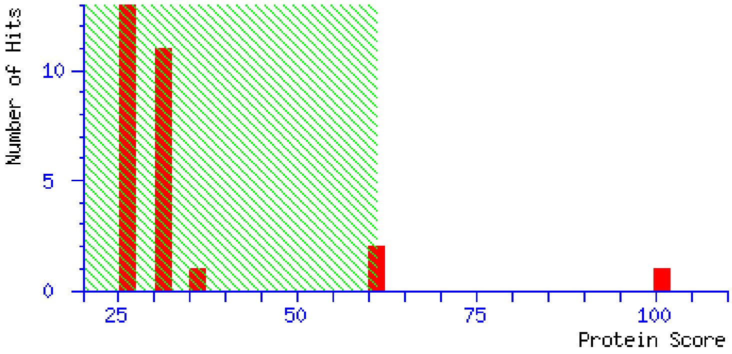
Calculated Mr: **48294** Calculated *p*I: **4.95**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **6**

NCBI accession No.: **cassava4.1_008310m|PACid:17966609**

Protein name： **26S protease regulatory subunit 6A homolog A**

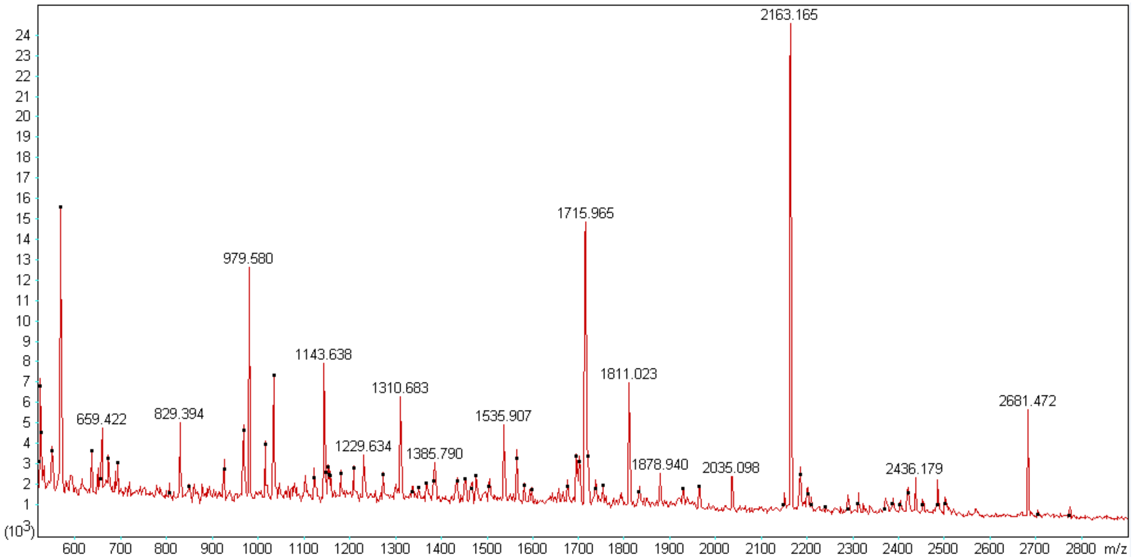
Plant species: ***Manihot esculenta*** Mascot score: **154**

Sequence coverage %: **59** p value: **2.9e-11**

Matched peptides No.: **29** Total peptides No.: **93**

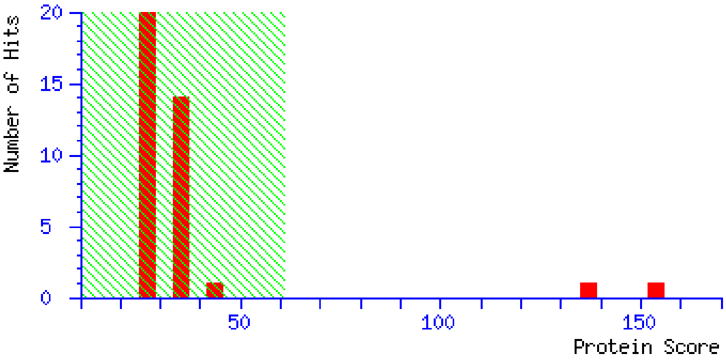
Calculated Mr: **47700** Calculated *p*I: **4.99**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **7**

NCBI accession No.: **cassava4.1_003343m|PACid:17989500**

Protein name： **Probable mediator of RNA polymerase II transcription subunit 37e** Plant species: ***Manihot esculenta***

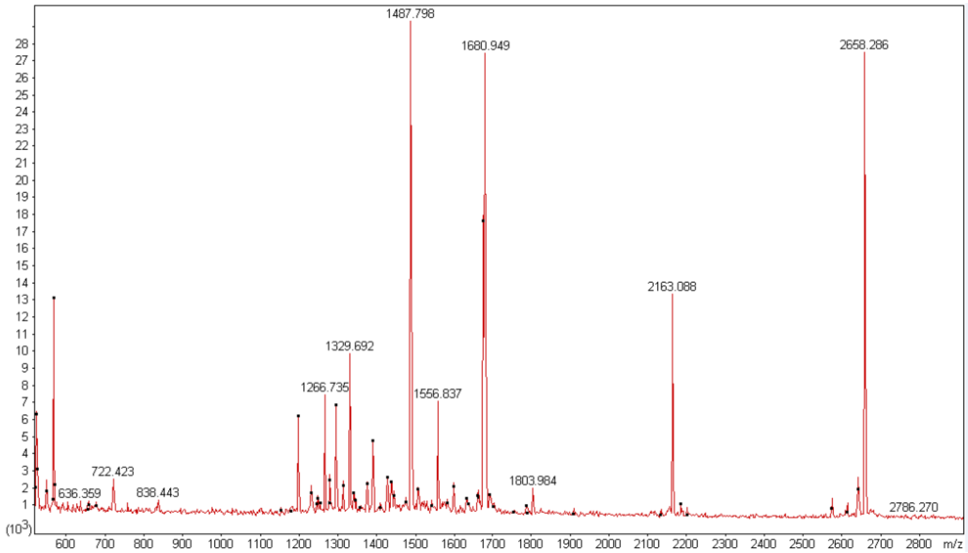
Mascot score: **115**

Sequence coverage %: **32** p value: 2. 3e-007

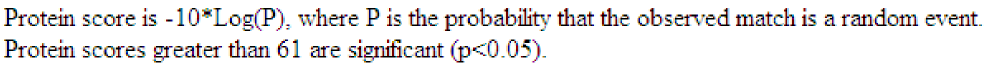
Matched peptides No.: **22** Total peptides No.: **60**

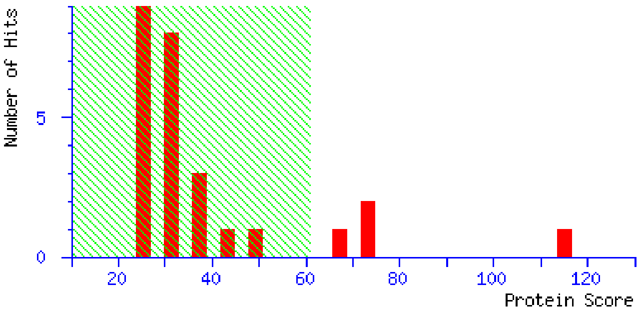
Calculated Mr: **71515** Calculated *p*I: **5.10**

Annotated PMF **spectra:**



Probability Based Mowse Score:


Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **8**

NCBI accession No.: **cassava4.1_003331m|PACid:17988720**

Protein name：**Probable mediator of RNA polymerase II transcription subunit 37e**

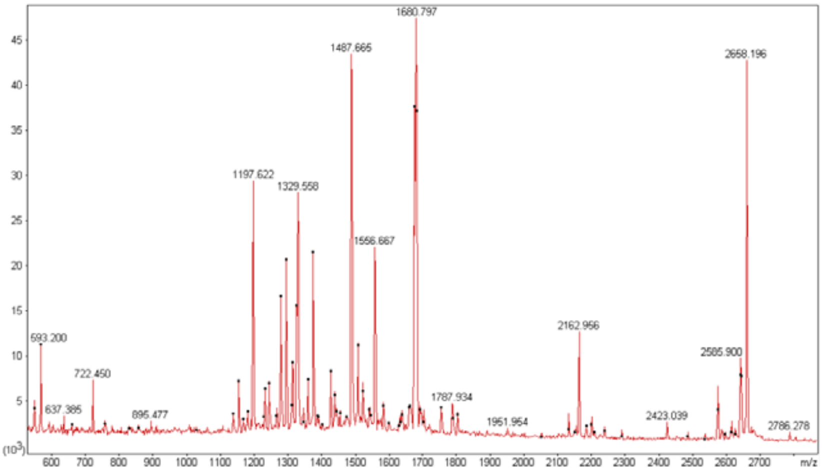
Plant species: ***Manihot esculenta*** Mascot score: **98**

Sequence coverage %: **40** p value: 1. 2e−005

Matched peptides No.: **23** Total peptides No.: **78**

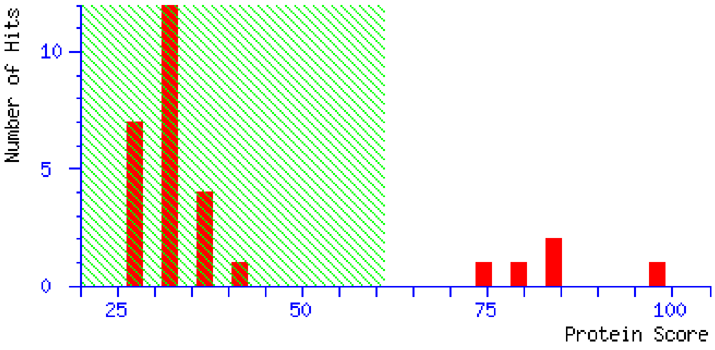
Calculated Mr: **71431** Calculated *p*I: **5.14**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **9**

NCBI accession No.: **cassava4.1_003340m|PACid:17988693**

Protein name：**Probable mediator of RNA polymerase II transcription subunit 37c**

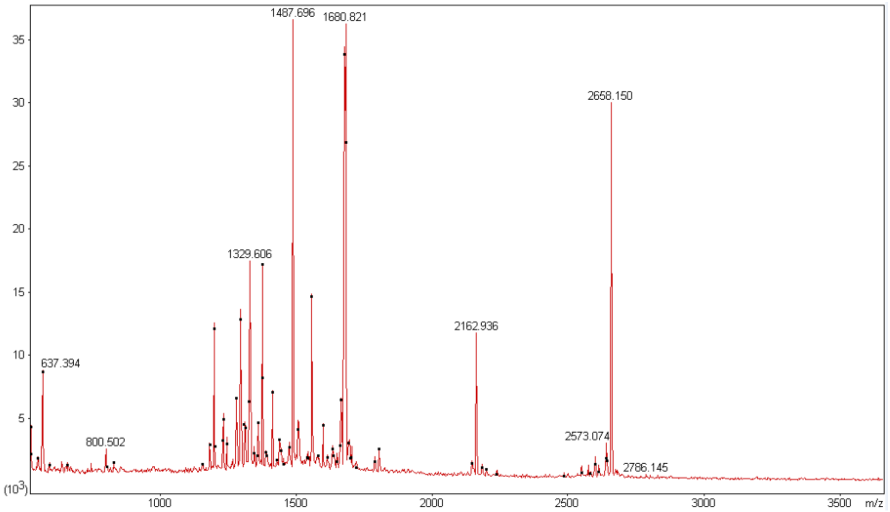
Plant species: ***Manihot esculenta***Mascot score: **128**

Sequence coverage %: **40** p value: 1. 2e−008

Matched peptides No.: **29** Total peptides No.: **74**

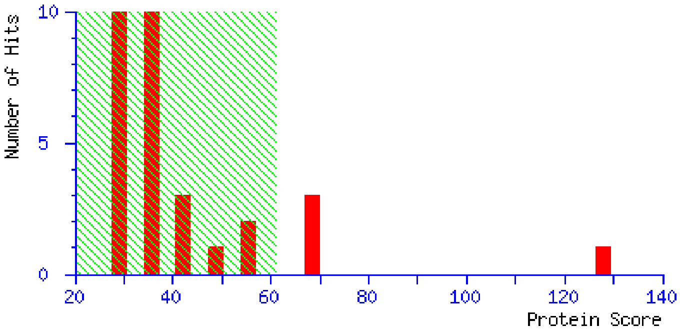
Calculated Mr: **71461** Calculated *p*I: **5.17**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **10**

NCBI accession No.: **cassava4.1_033108m|PACid:17973616**

Protein name： **Actin-7** Plant species: ***Manihot esculenta***

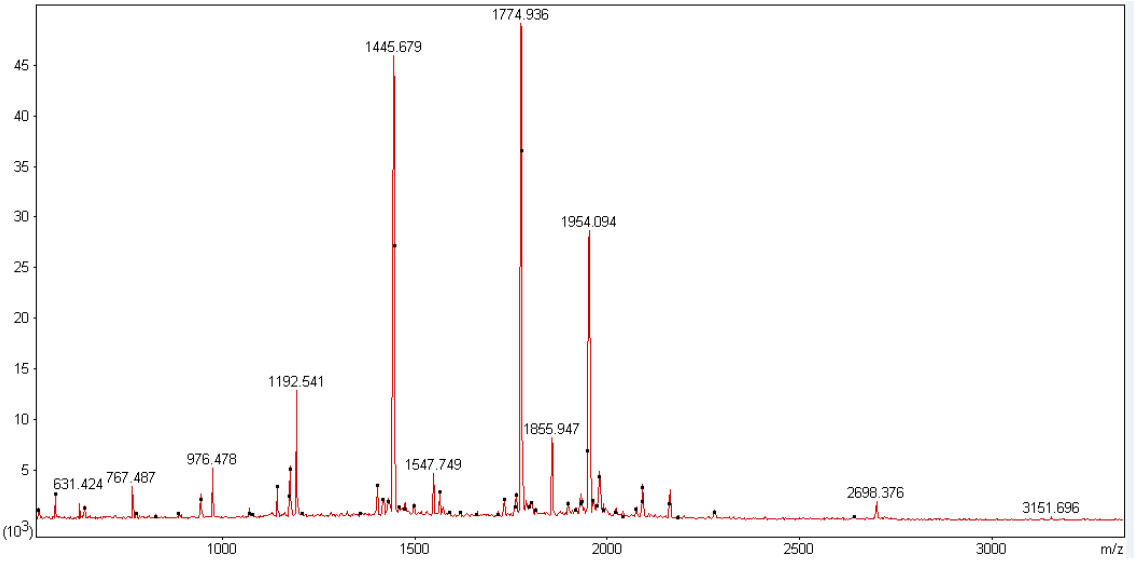
Mascot score: **127**

Sequence coverage %: **48** p value: 1. 5e−008

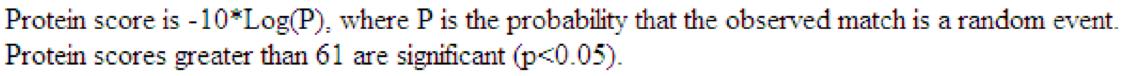
Matched peptides No.: **15** Total peptides No.: **62**

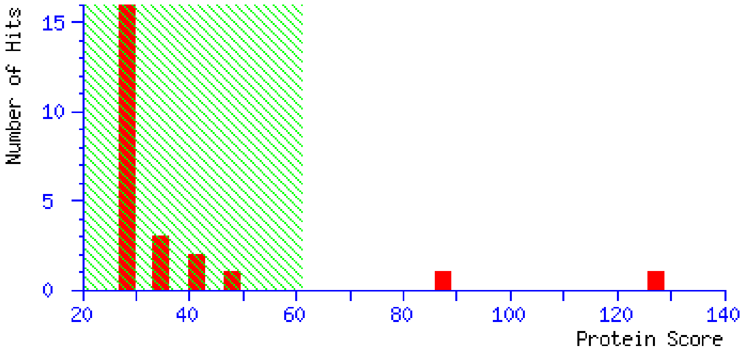
Calculated Mr: **41897** Calculated *p*I: **5.31**

Annotated PMF **spectra:**



Probability Based Mowse Score:


Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **11**

NCBI accession No.: **cassava4.1_003907m|PACid:17972056**

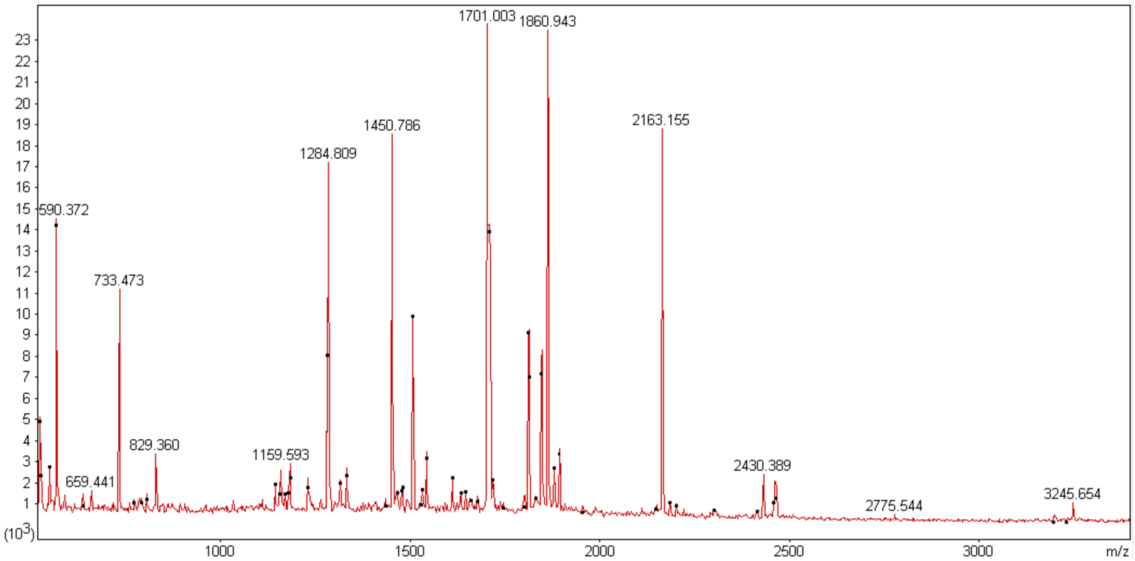
Protein name：**Chaperonin 60 subunit beta 2, chloroplastic** Plant species: ***Manihot esculenta***Mascot score: **147**

Sequence coverage %: **46** p value: 1. 5e−010

Matched peptides No.: **23** Total peptides No.: **63**

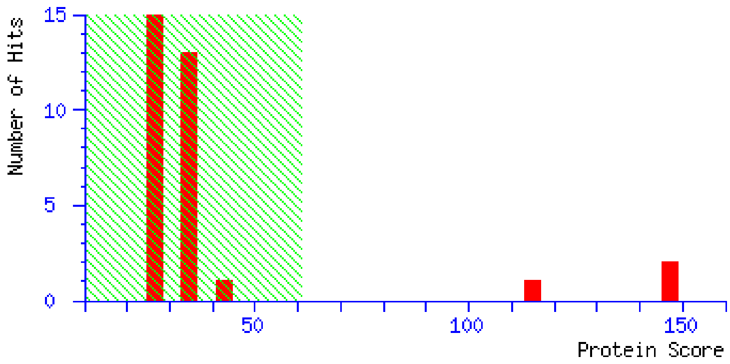
Calculated Mr: **64742** Calculated *p*I: **5.62**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **12**

NCBI accession No.: **cassava4.1_003883m|PACid:17972412**

Protein name：**Chaperonin 60 subunit beta 1, chloroplastic**

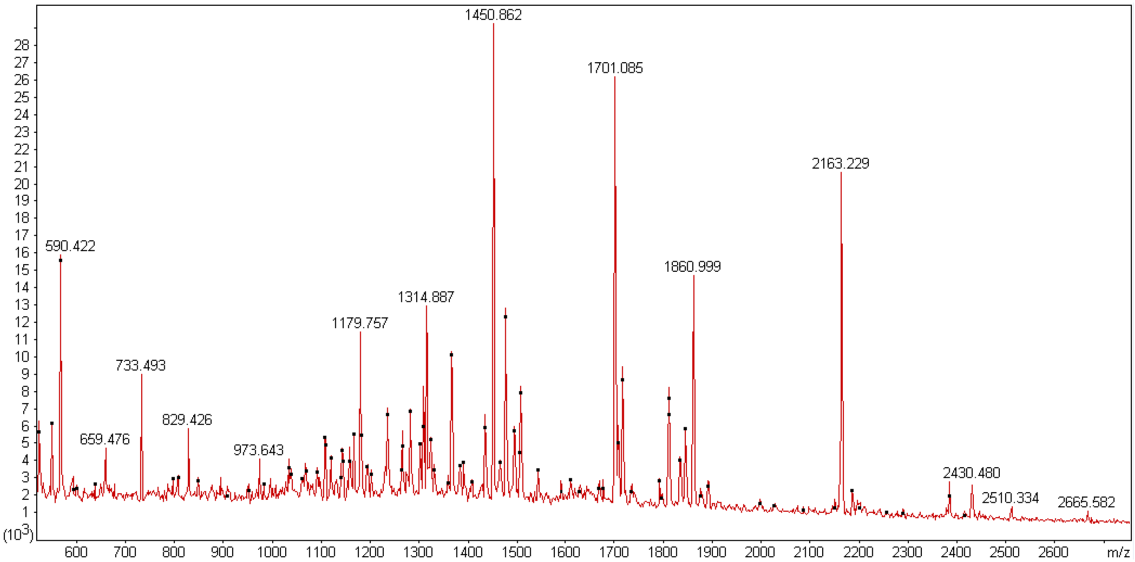
Plant species: ***Manihot esculenta*** Mascot score: **73**

Sequence coverage %: **31** p value: 0. 0035

Matched peptides No.: **15** Total peptides No.: **57**

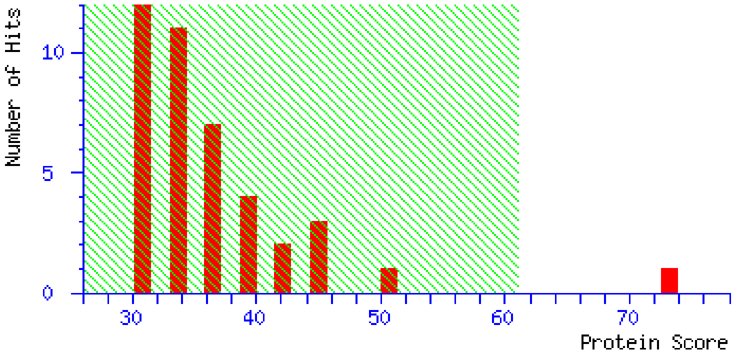
Calculated Mr: **64920** Calculated *p*I: **5.68**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant ($p<0.05$).



Spot No.: **13**

NCBI accession No.: **cassava4.1_004458m|PACid:17962184**

Protein name： **Chaperonin CPN60, mitochondrial**

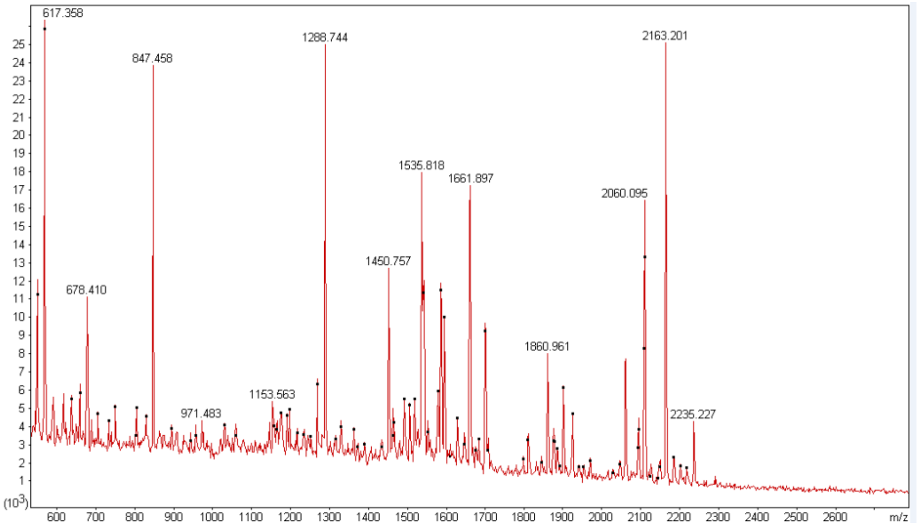
Plant species: ***Manihot esculenta*** Mascot score: **143**

Sequence coverage %: **49** p value: 3. 7e−010

Matched peptides No.: **28** Total peptides No.: **73**

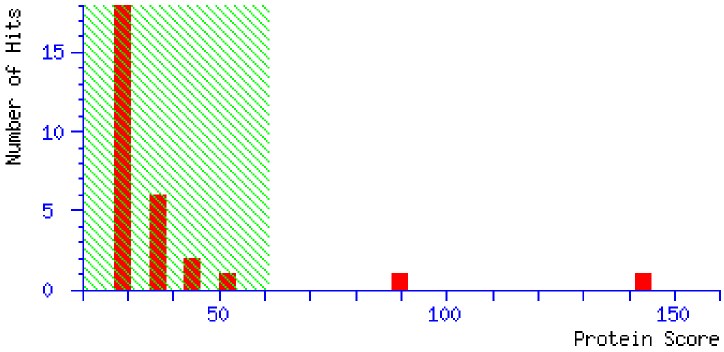
Calculated Mr: **61582** Calculated *p*I: **5.71**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **14**

NCBI accession No.: **cassava4.1_007513m|PACid:17961628**

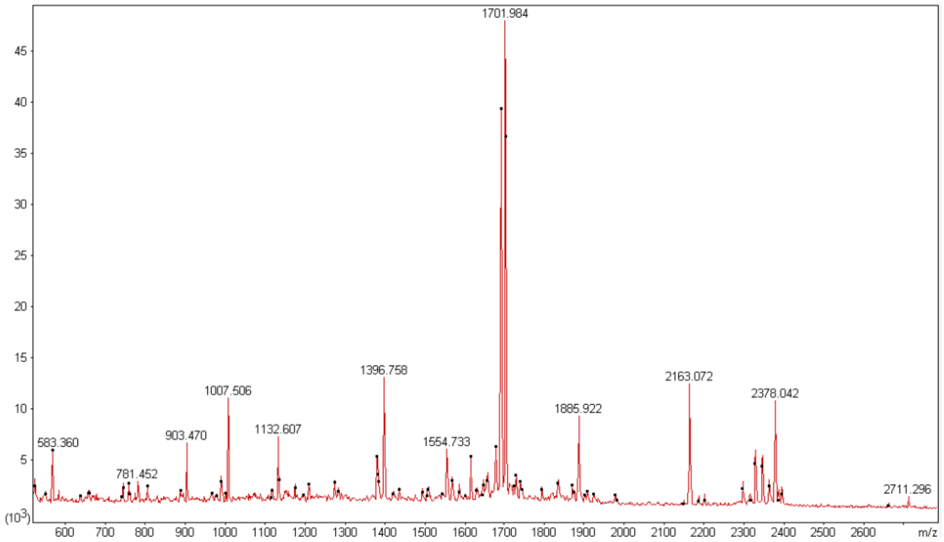
Protein name：**Tubulin alpha-6 chain** Plant species: ***Manihot esculenta*** Mascot score: **87**

Sequence coverage %: **40** p value: 0. 00014

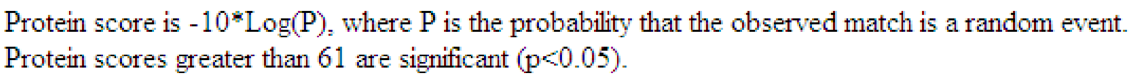
Matched peptides No.: **19** Total peptides No.: **80**

Calculated Mr: **50342** Calculated *p*I: **4.90**

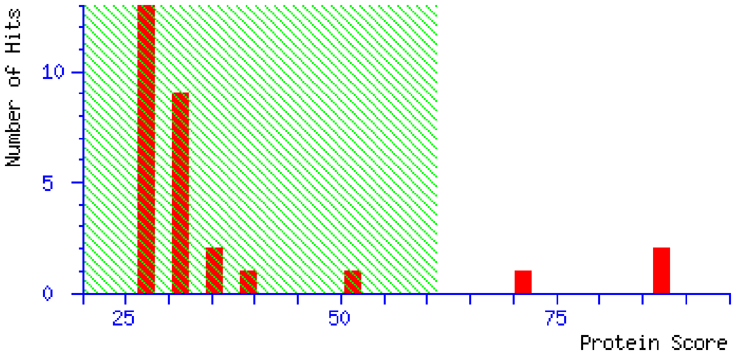
Annotated PMF **spectra:**



Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **15**

NCBI accession No.: **cassava4.1_007971m|PACid:17991617**

Protein name：**Tubulin alpha-6 chain**

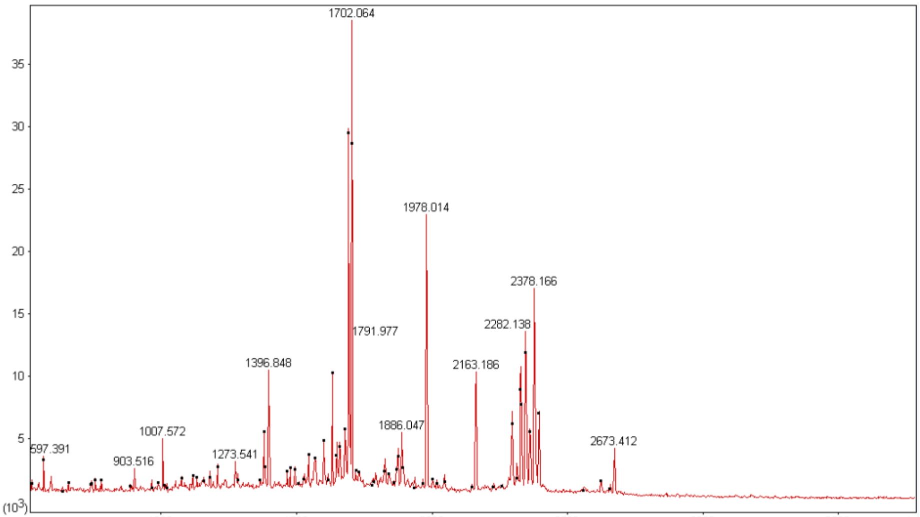
Plant species: ***Manihot esculenta*** Mascot score: **103**

Sequence coverage %: **48**   p value: 3.7e−006

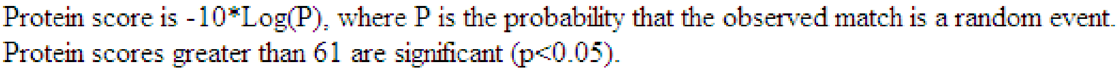
Matched peptides No.: **18**   Total peptides No.: **79**

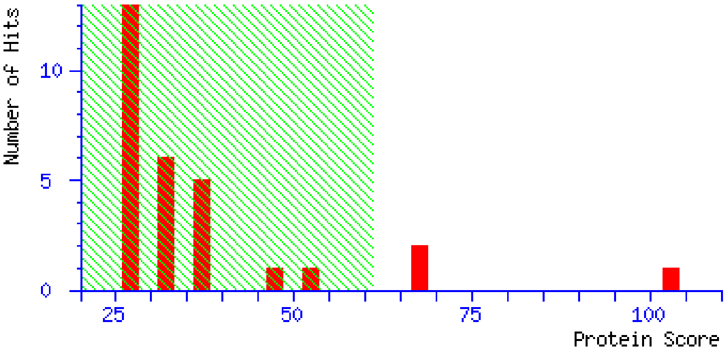
Calculated Mr: **48294**   Calculated *p*I: **4.95**

Annotated PMF **spectra:**



Probability Based Mowse Score:


Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **16**

NCBI accession No.: **cassava4.1_007560m|PACid:17972004**

Protein name：**Tubulin alpha-6 chain**

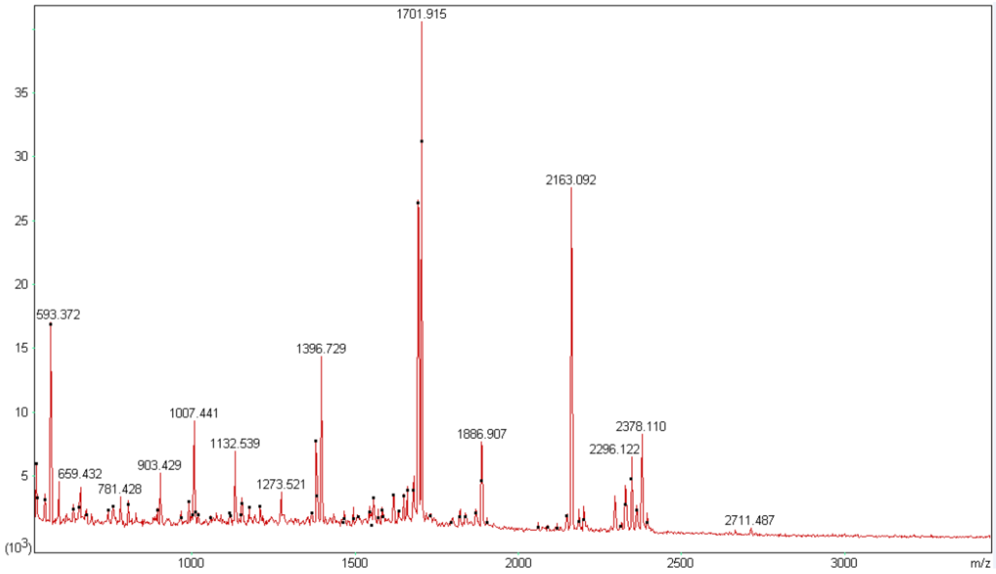
Plant species: ***Manihot esculenta*** Mascot score: **89**

Sequence coverage %: **41** p value: 9e−005

Matched peptides No.: **17** Total peptides No.: **75**

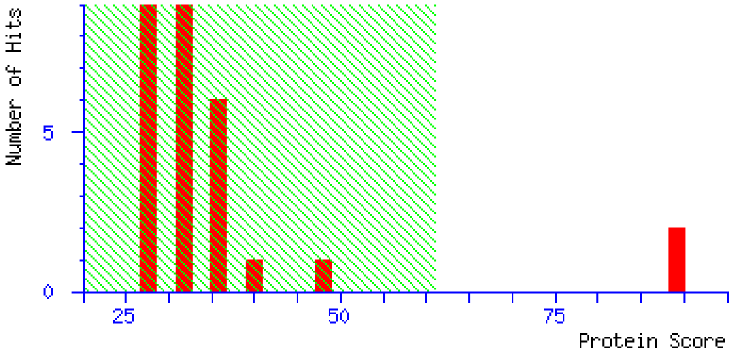
Calculated Mr: **50295** Calculated *p*I: **5.00**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **17**

NCBI accession No.: **cassava4.1_033108m|PACid:17973616**

Plant species: ***Manihot esculenta***

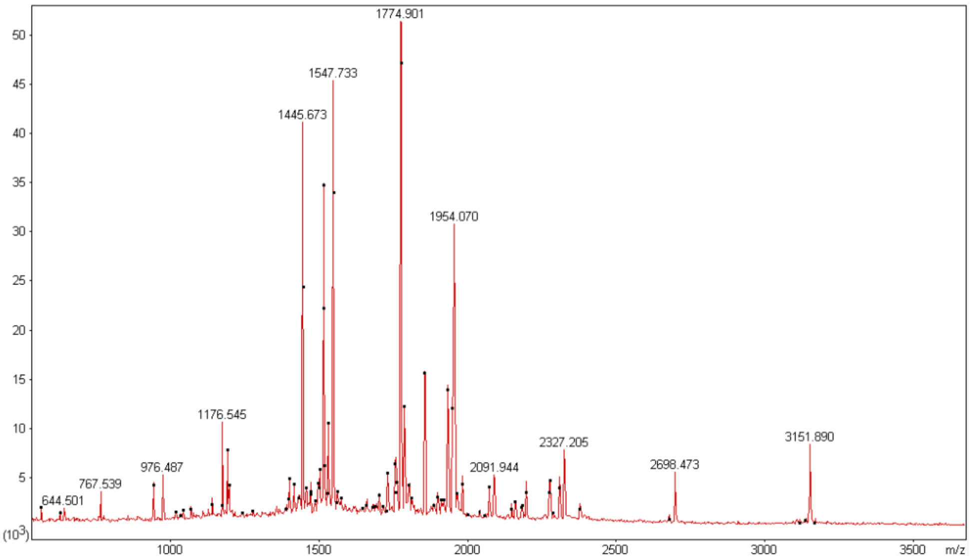
Protein name： **Actin-7**　　Mascot score: **173**

Sequence coverage %: **70**　　p value: **`3.7e-013`**

Matched peptides No.: **24**　　Total peptides No.: **90**

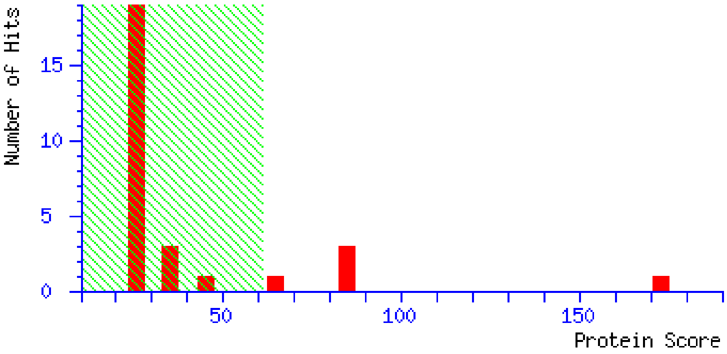
Calculated Mr: **41897**　　Calculated *p*I: **5.31**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **18**

NCBI accession No.: **cassava4.1_004726m|PACid:17976529**

Protein name：**ATP synthase beta subunit 1** Plant species:

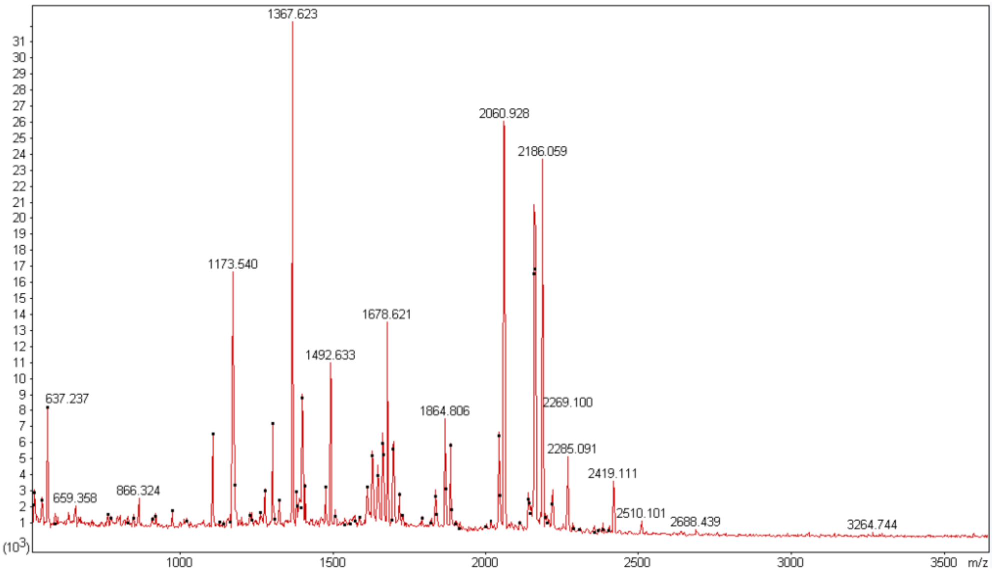
Manihot esculenta Mascot score: **190**

Sequence coverage %: **62** p value: 7. 3e−015

Matched peptides No.: **29** Total peptides No.: **89**

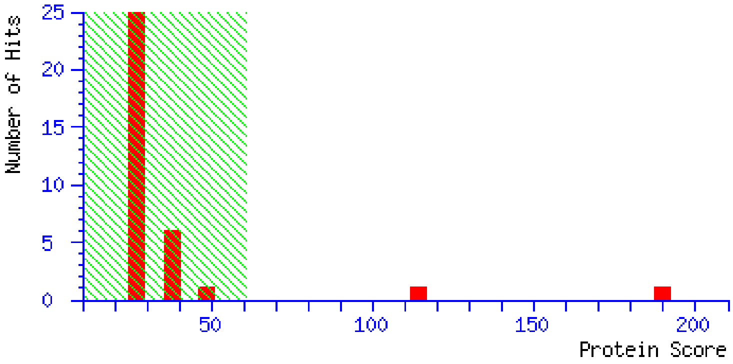
Calculated Mr: **60085** Calculated *p*I: **6.13**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **19**

NCBI accession No.: **cassava4.1_004630m|PACid:17991144**

Plant species: ***Manihot esculenta***

Protein name： **ATP synthase subunit beta-3, mitochondrial**

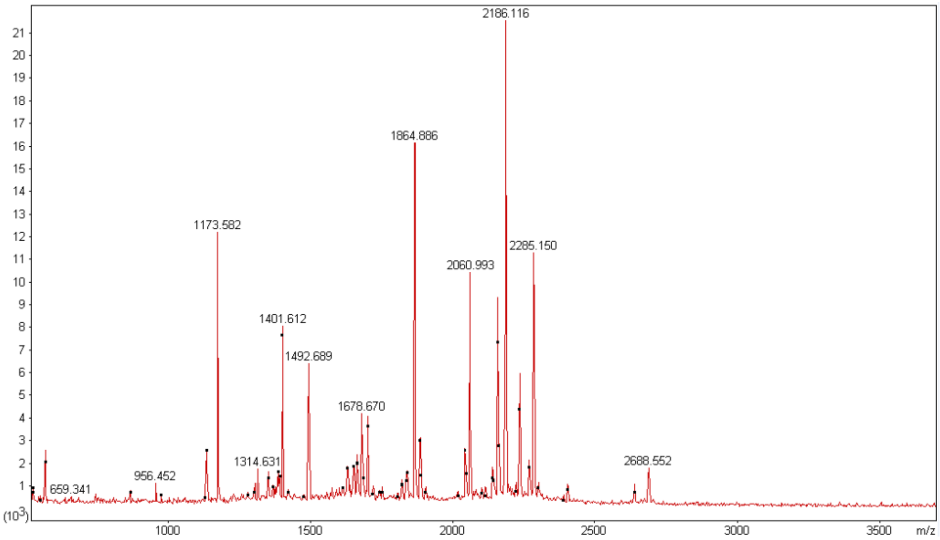
Mascot score: **175**

Sequence coverage %: **61**　　　p value: **`2.3e-013`**

Matched peptides No.: **29**　　　Total peptides No.: **63**

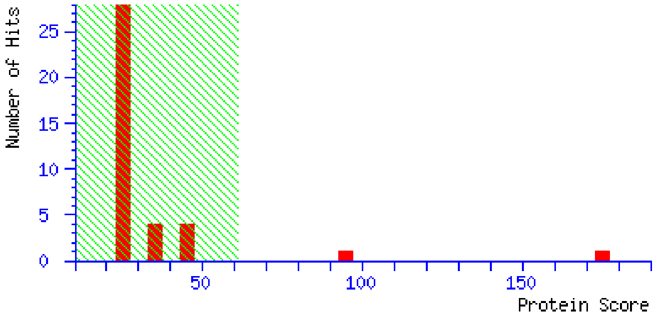
Calculated Mr: **60594**　　　Calculated *p*I: **6.26**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **20**

NCBI accession No.: **cassava4.1_005518m|PACid:17993865**

Plant species: ***Manihot esculenta***

Protein name： **Glucose-1-phosphate adenylyltransferase**

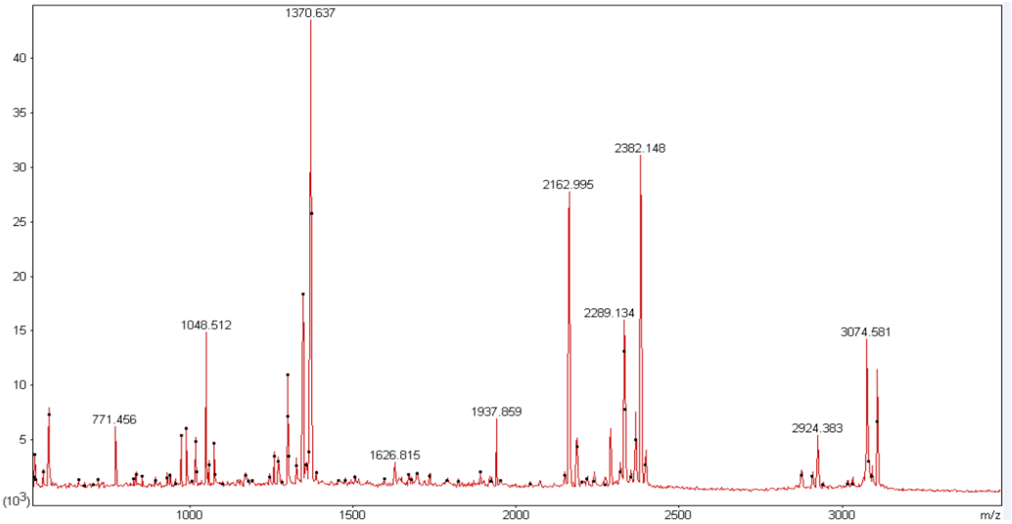
Mascot score: **182**

Sequence coverage %: **58** p value: **4.6e-014**

Matched peptides No.: **30** Total peptides No.: **84**

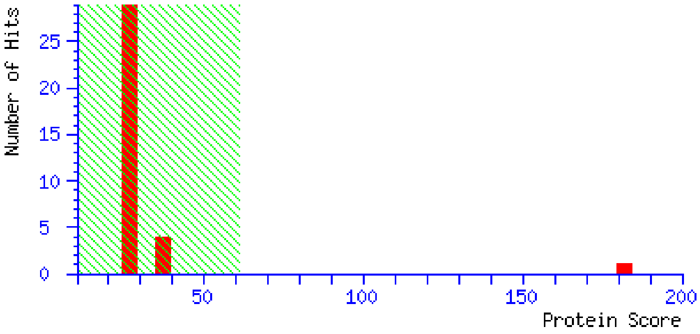
Calculated Mr: **57581** Calculated *p*I: **6.69**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **21**

NCBI accession No.: **cassava4.1_008086m|PACid:17989319**

Plant species: ***Manihot esculenta***

Protein name: **Glutamine synthetase cytosolic isozyme 1-1**

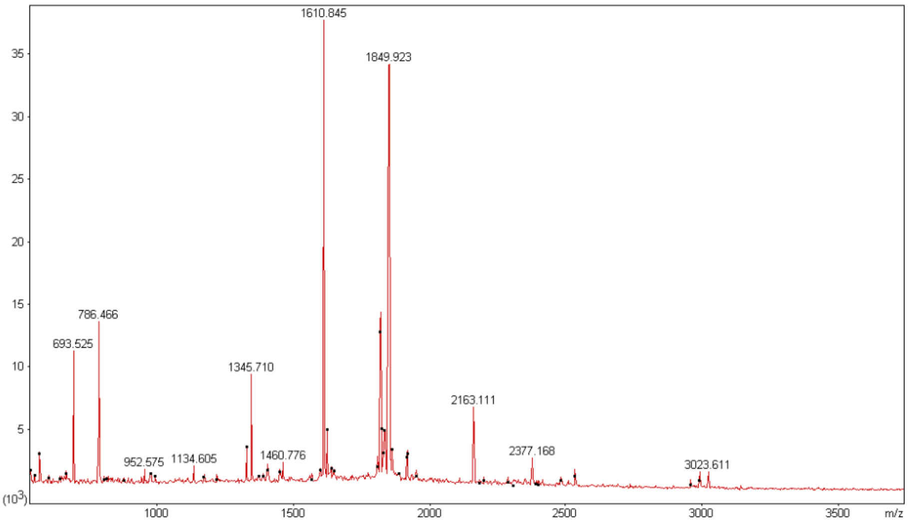
Mascot score: **101**

Sequence coverage %: **33** p value: **5.8e-006**

Matched peptides No.: **14** Total peptides No.: **54**

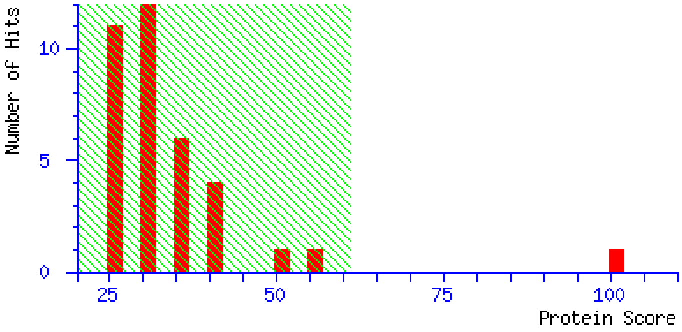
Calculated Mr: **47502** Calculated *p*I: **6.27**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **22**

NCBI accession No.: **cassava4.1_033108m|PACid:17973616**

Plant species: ***Manihot esculenta***

Protein name: **Actin-7**

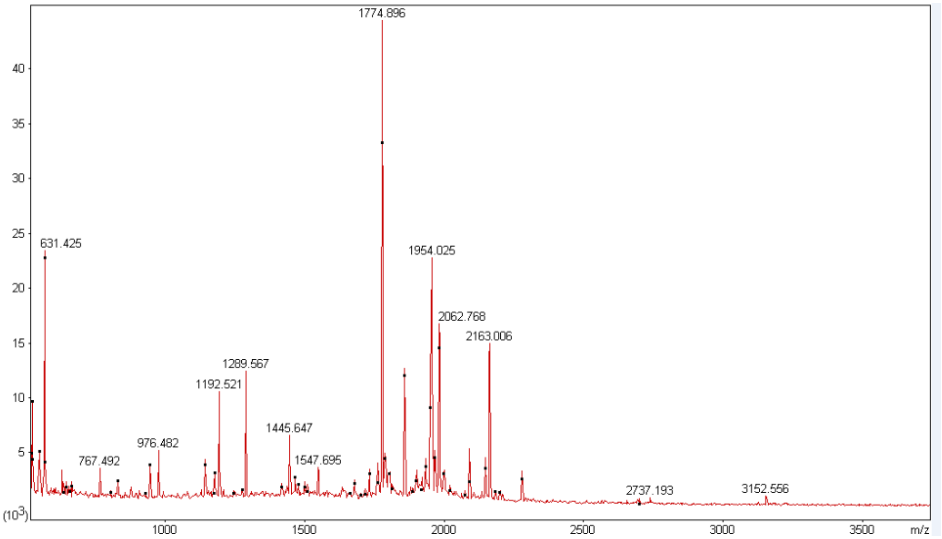
Mascot score: **96**

Sequence coverage %: **44** p value: **2e-005**

Matched peptides No.: **15** Total peptides No.: **64**

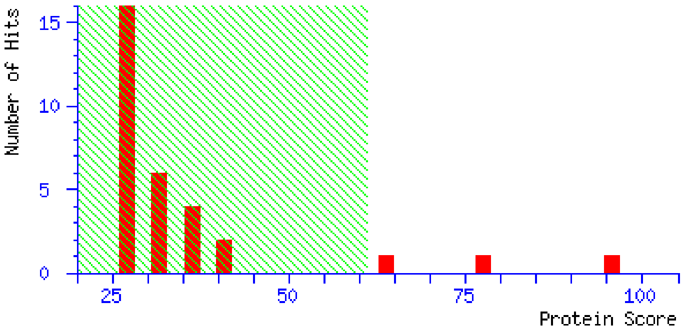
Calculated Mr: **41897** Calculated *p*I: **5.31**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **23**

NCBI accession No.: **cassava4.1_033108m|PACid:17973616**

Plant species: ***Manihot esculenta***

Protein name： **Actin-7**

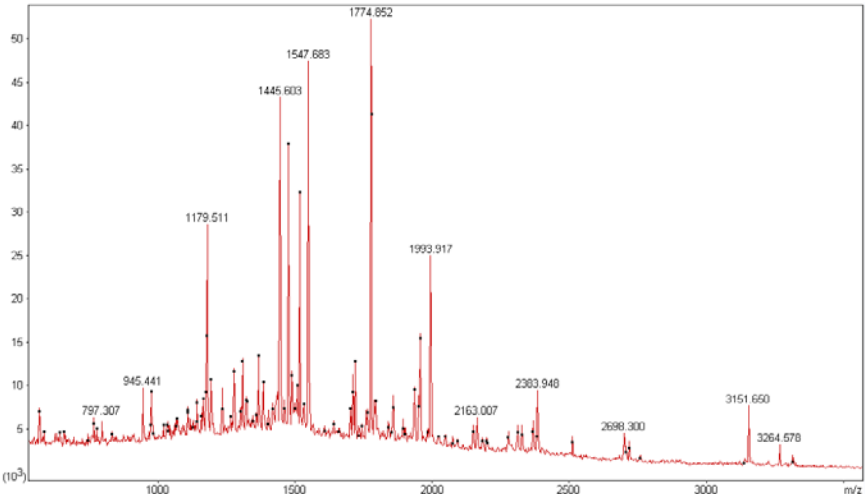
Mascot score: **93**

Sequence coverage %: **52**　　　p value: **`3.4e-005`**

Matched peptides No.: **18**　　　Total peptides No.: **87**

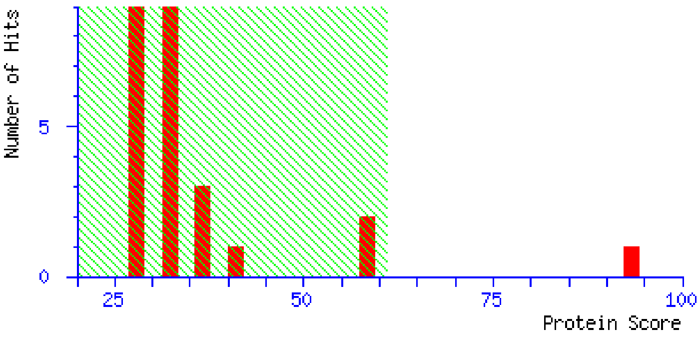
Calculated Mr: **41897**　　　Calculated *p*I: **5.31**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: 24

NCBI accession No.: **cassava4.1_033108m|PACid:17973616**

Plant species: ***Manihot esculenta***

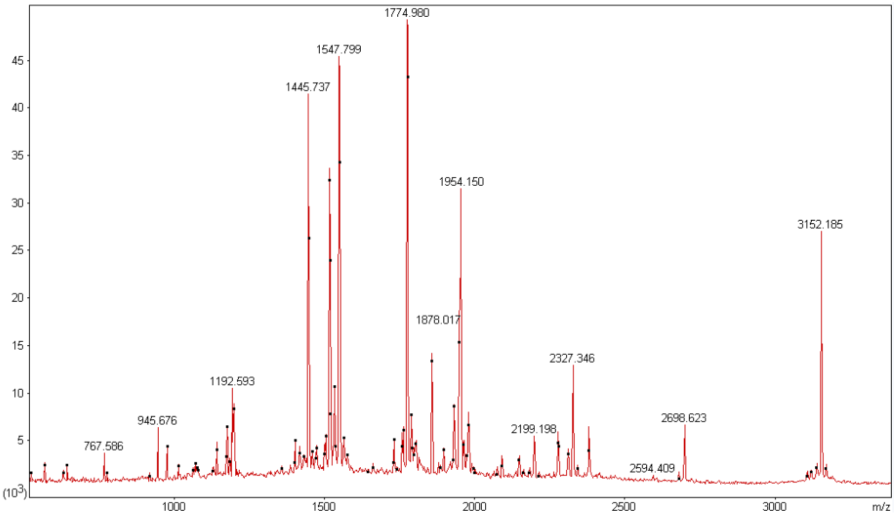
Protein name：**Actin-7** Mascot score: **195**

Sequence coverage %: **63** p value: **2.3e-015**

Matched peptides No.: **24** Total peptides No.: **85**

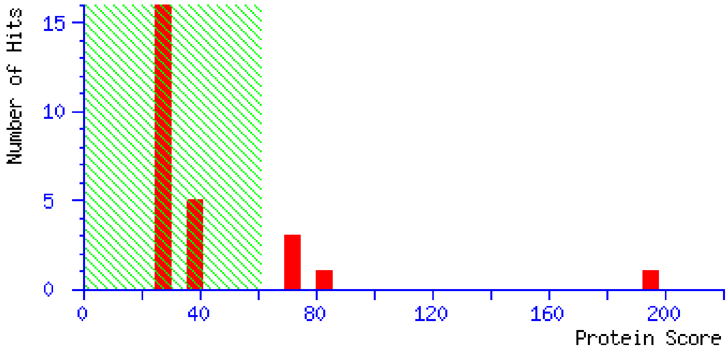
Calculated Mr: **41897** Calculated *p*I: **5.31**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **25**

NCBI accession No.: **cassava4.1_008387m|PACid:17968420**

Plant species: ***Manihot esculenta***

Protein name: **Succinyl-CoA ligase [ADP-forming] subunit beta, mitochondrial**

Mascot score: **128**

Sequence coverage %: **47**

p value: **1.2e-008**

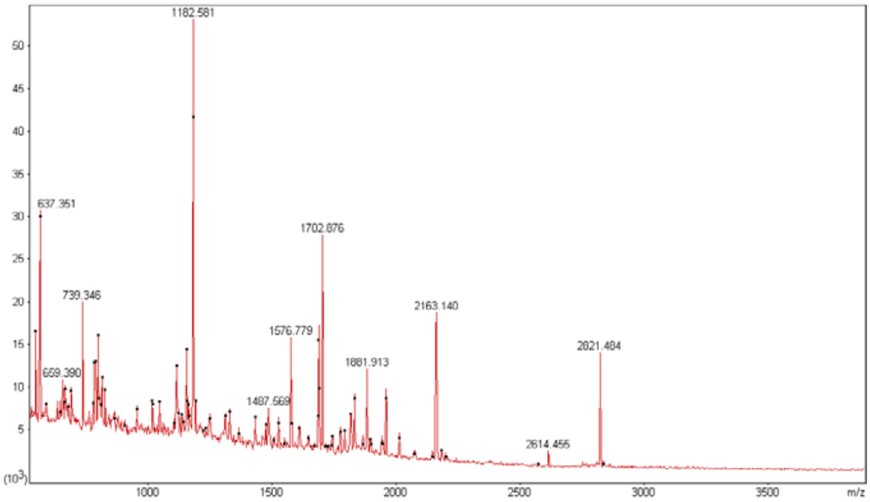
Matched peptides No.: **22**

Total peptides No.: **78**

Calculated Mr: **45532**

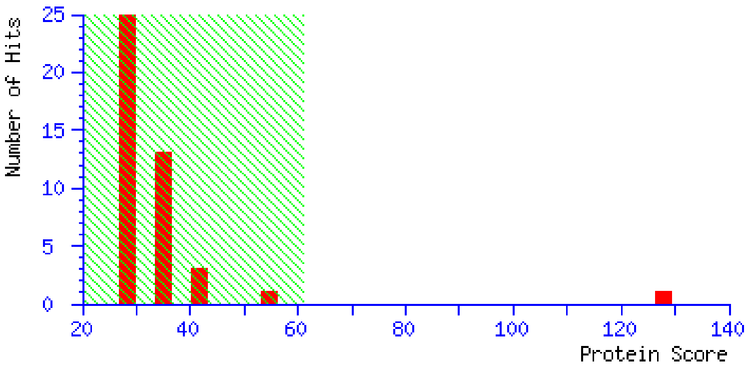
Calculated *p*I: **5.88**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **26**

NCBI accession No.: **cassava4.1_010597m|PACid:17964465**

Plant species: **Manihot esculenta**

Protein name： **Glutamine synthetase cytosolic isozyme 1-1**

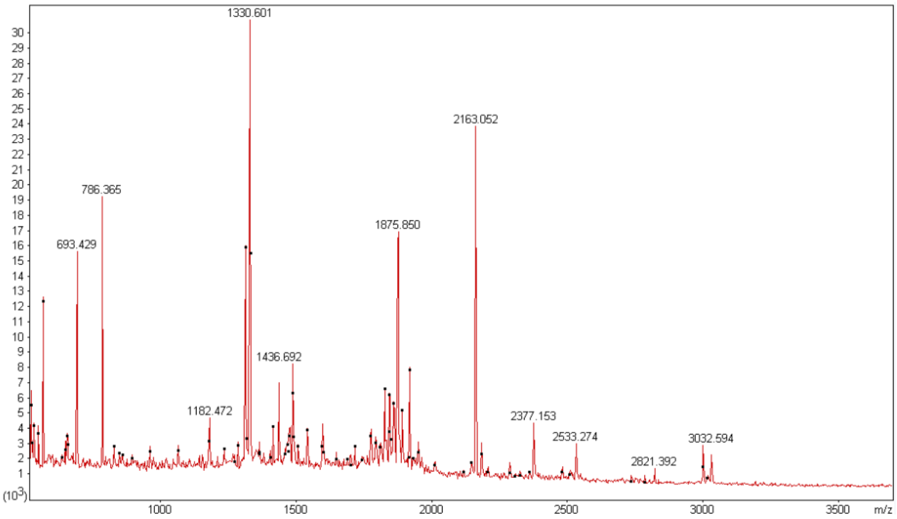
Mascot score: **107**

Sequence coverage %: **51**   p value: **1.5e-006**

Matched peptides No.: **15**   Total peptides No.: **80**

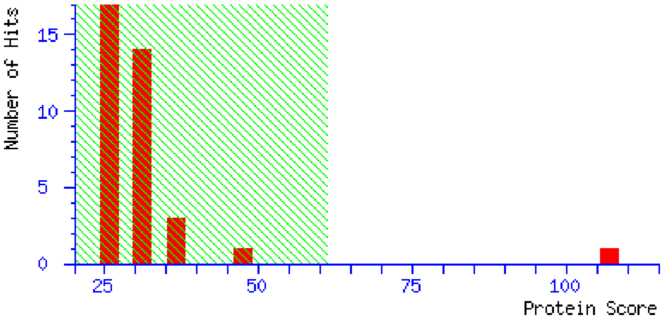
Calculated Mr: **39359**   Calculated *p*I: **5.37**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **27**

NCBI accession No.: **cassava4.1_011177m|PACid:17972447**

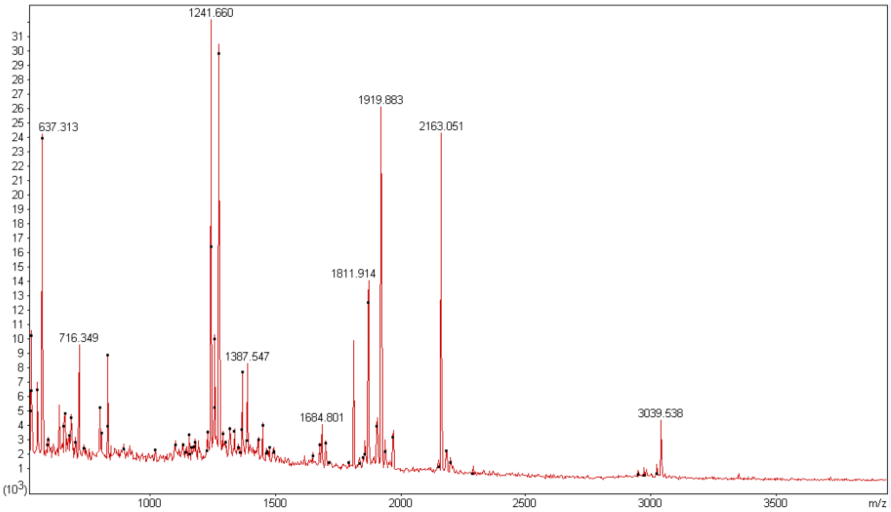
Protein name： **Adenosine kinase 1** Plant species: ***Manihot esculenta***

PFF Mascot score: [113] **Sequence coverage %:** [7]

Matched peptides No.: [**2**] p value: 3.1e-006

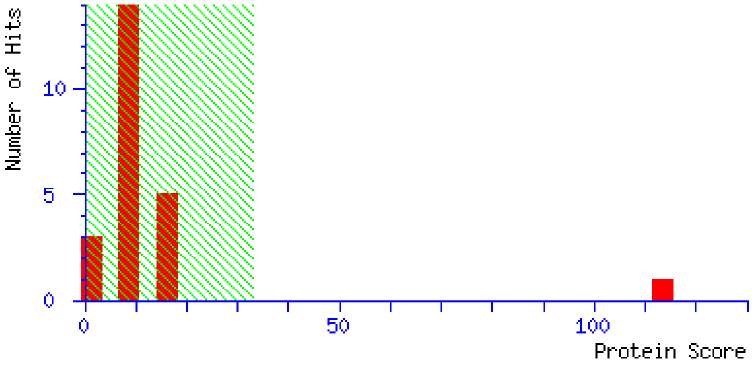
Calculated Mr: **38107** Calculated *p*I: **5.38**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **28**

NCBI accession No.: **cassava4.1_002747m|PACid:17960141**

Plant species: ***Manihot esculenta***

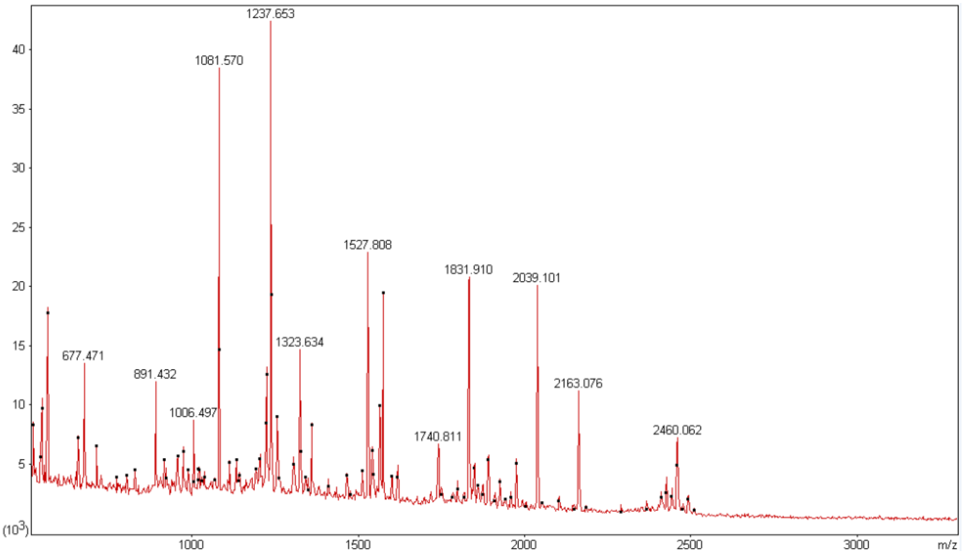
Protein name：**Heat shock protein 90-3** Mascot score: **127**

Sequence coverage %: **37** p value: **1.5e-008**

Matched peptides No.: **33** Total peptides No.: **77**

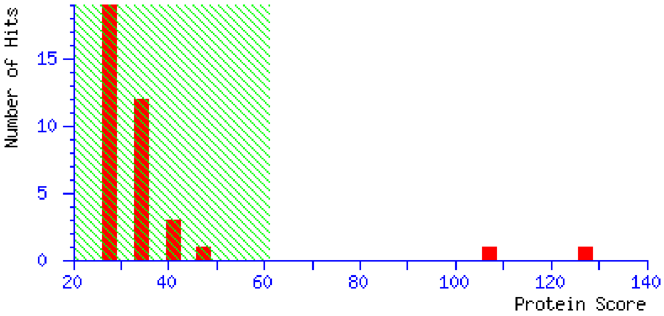
Calculated Mr: **80250** Calculated *p*I: **4.99**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **29**

NCBI accession No.: **cassava4.1_002466m|PACid:17978799**

Plant species: ***Manihot esculenta***

Protein name： **Alpha-glucan phosphorylase 1**

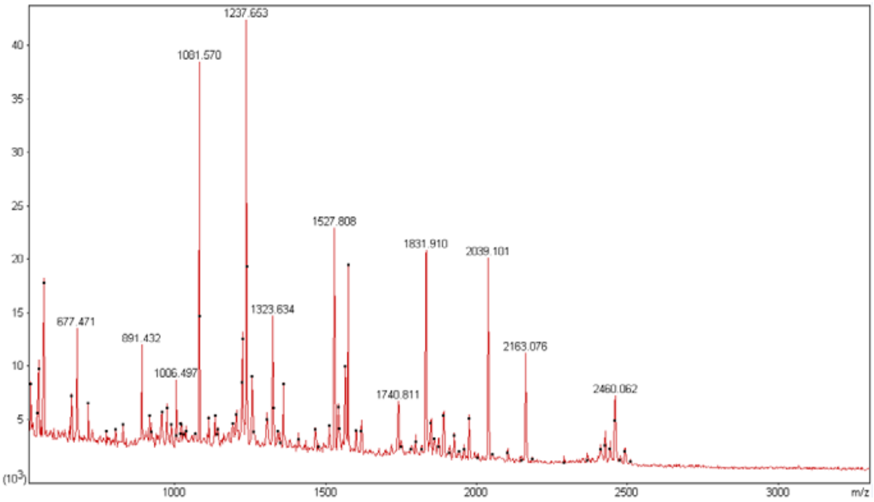
Mascot score: **81**

Sequence coverage %: **24** p value: **0.00058**

Matched peptides No.: **24** Total peptides No.: **95**

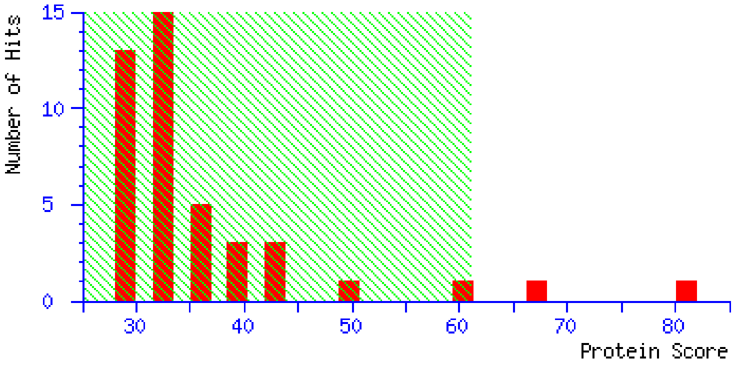
Calculated Mr: **81918** Calculated *p*I: **8.50**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **30**

NCBI accession No.: **cassava4.1_002466m|PACid:17978799**

Plant species: **Manihot esculenta**

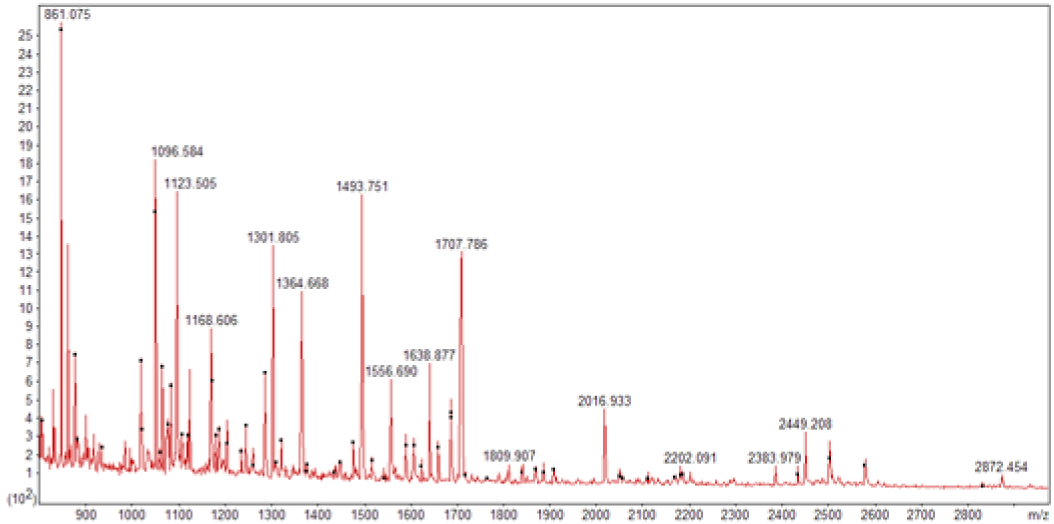
Protein name：**Alpha-glucan phosphorylase 1**

PFF **Mascot** score: **[387]** Sequence coverage %: **[12]**

Matched peptides No.: **[7]** p value: 3.5e-008

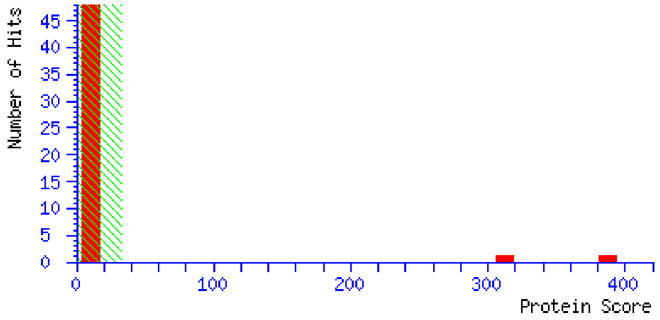
Calculated Mr: 81918 Calculated *p*I: **8.50**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **31**

NCBI accession No.: **cassava4.1_002614m|PACid:17978880**

Plant species: ***Manihot esculenta***

Protein name：**Alpha-glucan phosphorylase 1**

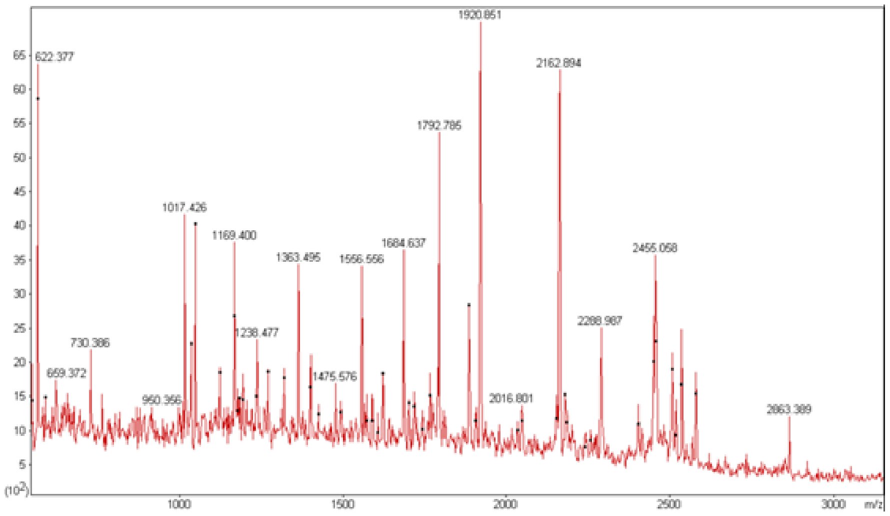
Mascot score: **76** p value: **0.019**

Sequence coverage %: **32**

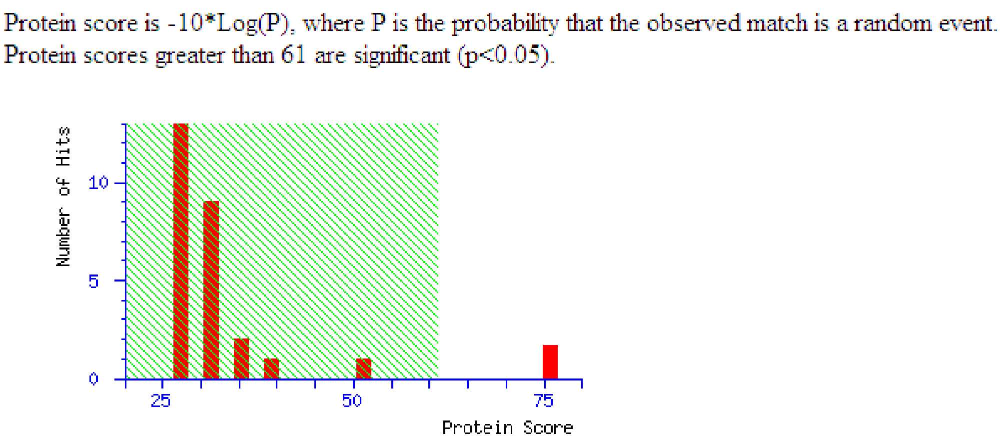
Matched peptides No.: **16** Total peptides No.: **58**

Calculated Mr: **80611** Calculated *p*I: **6.71**

Annotated PMF **spectra:**



Probability Based Mowse Score:


Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).

Spot No.: **32**

NCBI accession No.: **cassava4.1_002466m|PACid:17978799**

Plant species: ***Manihot esculenta***

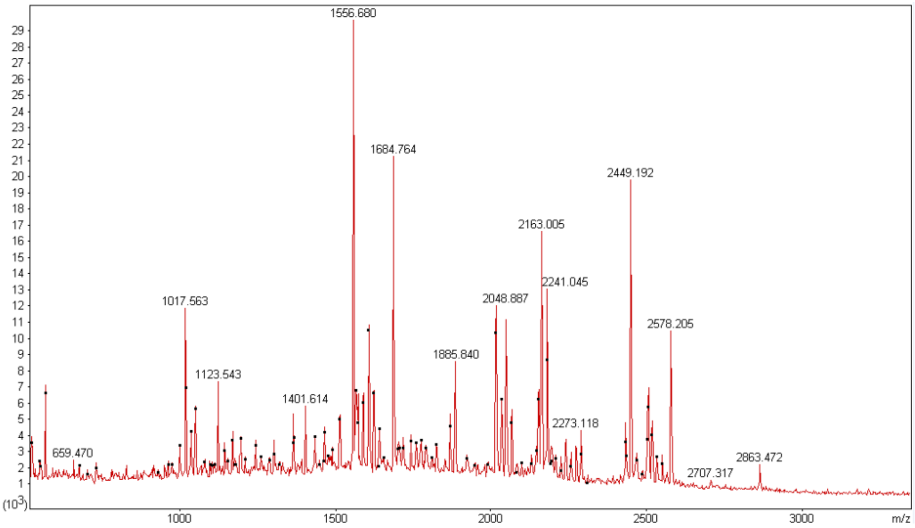
Protein name：**Alpha-glucan phosphorylase 1**

Sequence coverage %: **[2]** Matched peptides No.: **[5]**

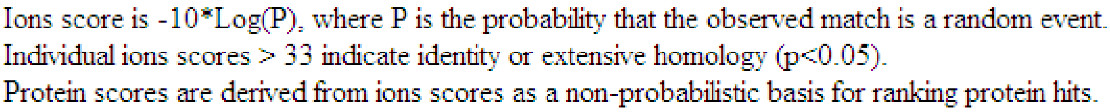
PFF **Mascot** score: **[110]** p value: **6.8e-005**

Calculated Mr: **81918** Calculated *p*I: **8.50**

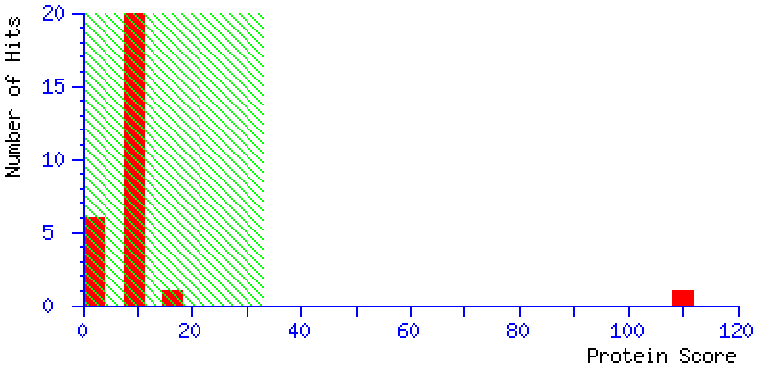
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **33**

NCBI accession No.: cassava4.1_002466m|PACid:17978799

Plant species: ***Manihot esculenta***

Protein name： **Alpha-glucan phosphorylase 1**

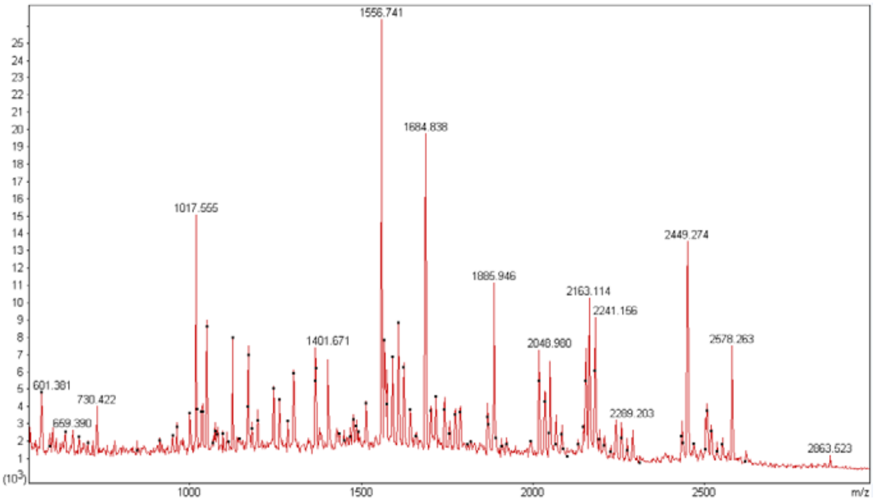
Mascot score: **101**

Sequence coverage %: **40**　　p value: 5.8e-006

Matched peptides No.: **24**　　Total peptides No.: **98**

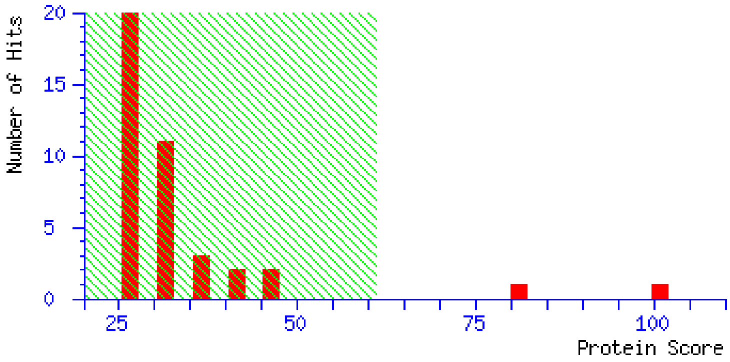
Calculated Mr: **81918**　　Calculated *p*I: **8.50**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **34**

NCBI accession No.: **cassava4.1_014251m|PACid:17989805**

Plant species: ***Manihot esculenta***

Protein name： **14-3-3-like protein GF14 omega**

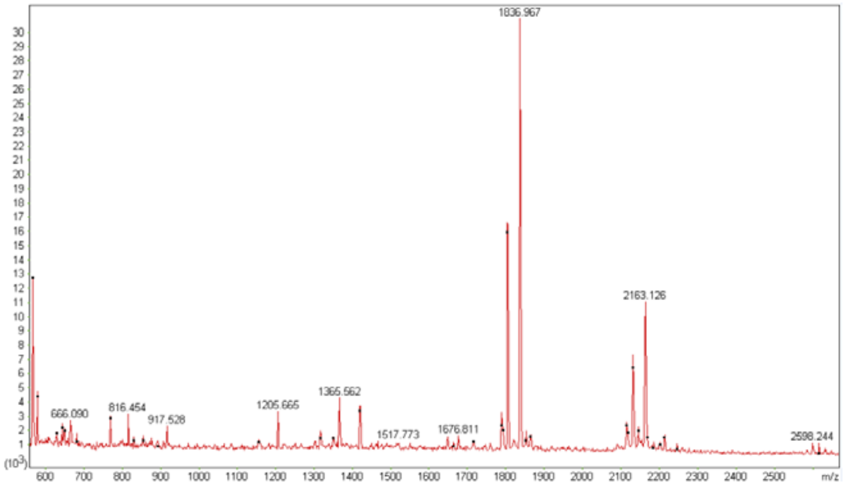
Mascot score: **115**

Sequence coverage %: **44**   p value: **`2.3e-007`**

Matched peptides No.: **16**   Total peptides No.: **46**

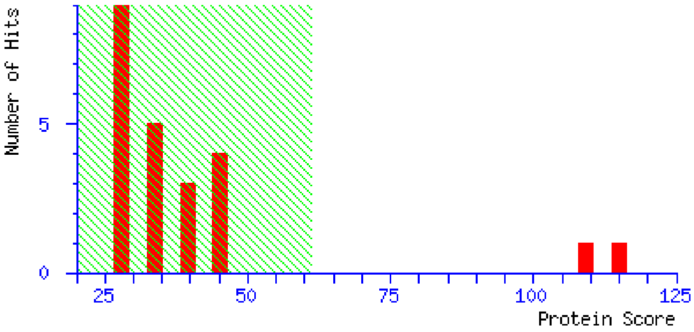
Calculated Mr: **29447**   Calculated *p*I: **4.77**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **35**

NCBI accession No.: **cassava4.1_014208m|PACid:17964823**

Plant species: **Manihot esculenta**

Protein name：**14-3-3-like protein GF14 omega**

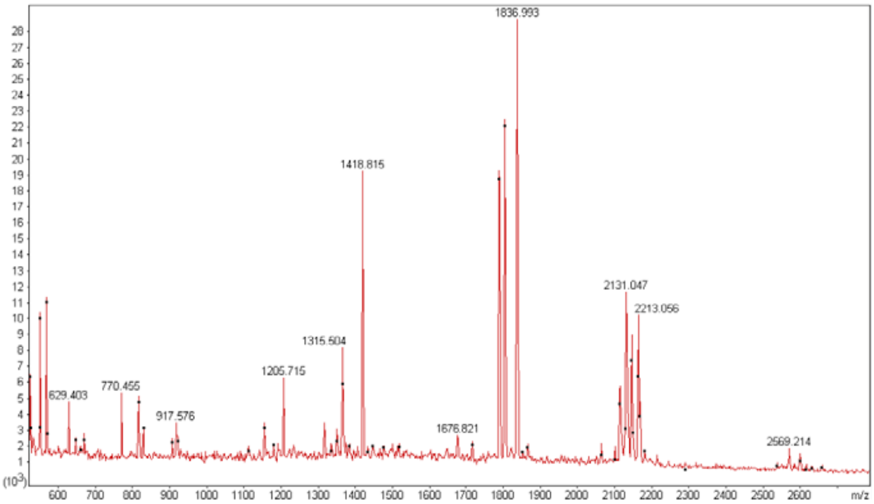
Mascot score: **159** p value: **9.2e-012**

Sequence coverage %: **54**

Matched peptides No.: **21** Total peptides No.: **56**

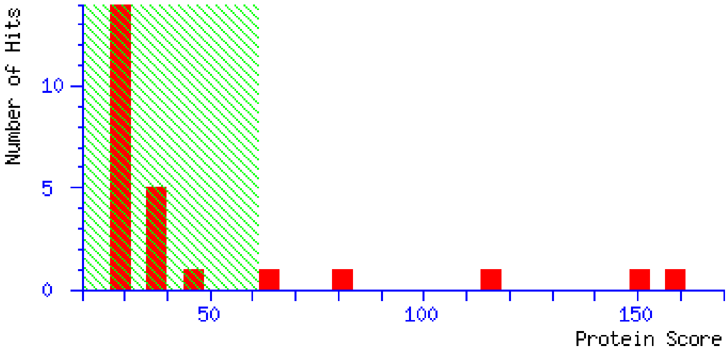
Calculated Mr: **29548** Calculated *p*I: **4.76**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **36**

NCBI accession No.: **cassava4.1_014065m|PACid:17989625**

Plant species: ***Manihot esculenta***

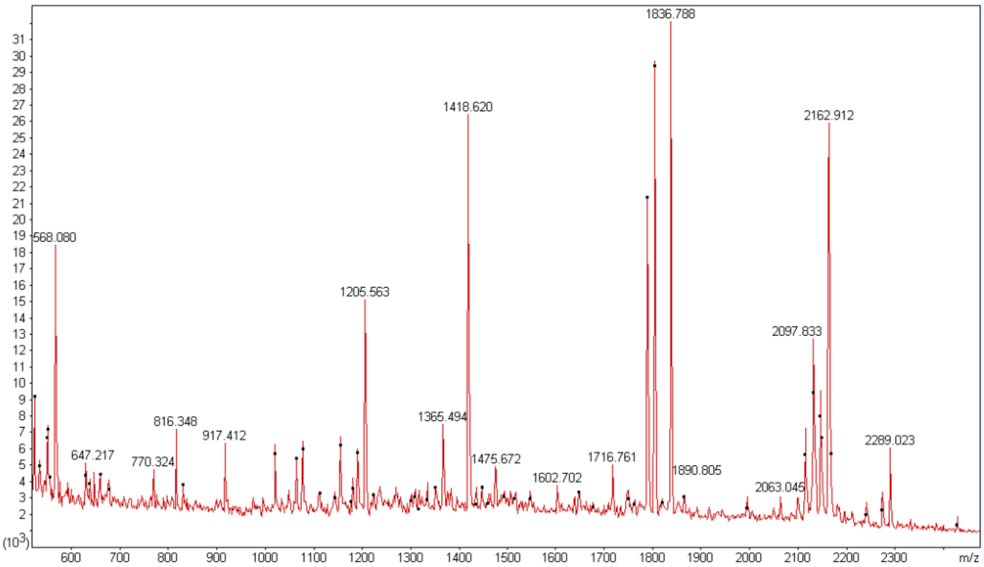
Protein name：**14-3-3-like protein GF14 psi** Mascot score: **111**

Sequence coverage %: **60** p value: **5.8e-07**

Matched peptides No.: **16** Total peptides No.: **67**

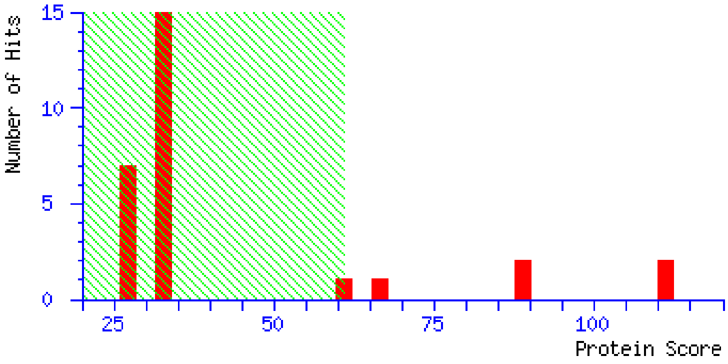
Calculated Mr: **29927** Calculated *p*I: **4.75**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **37**

NCBI accession No.: **cassava4.1_011584m|PACid:17982732**

Protein name：**Probable fructokinase-1**

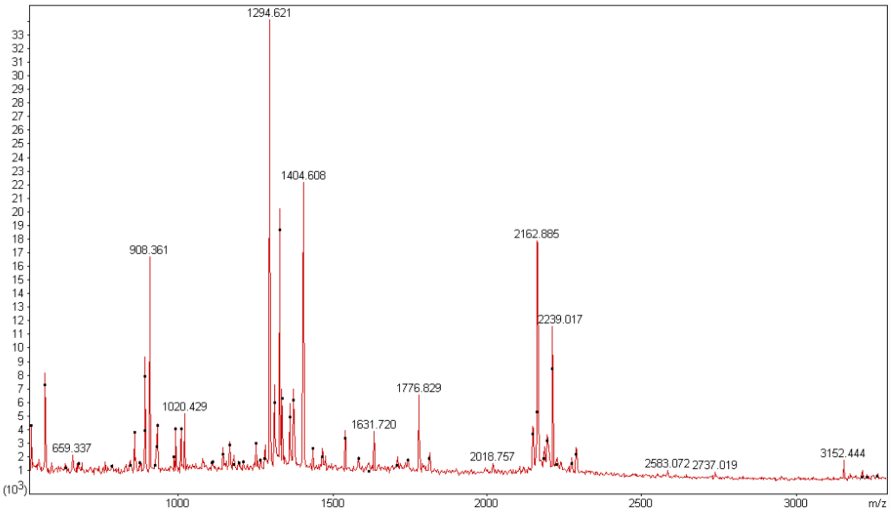
Plant species: ***Manihot esculenta***

PFF Mascot score: [154] **Sequence coverage %:** [7]

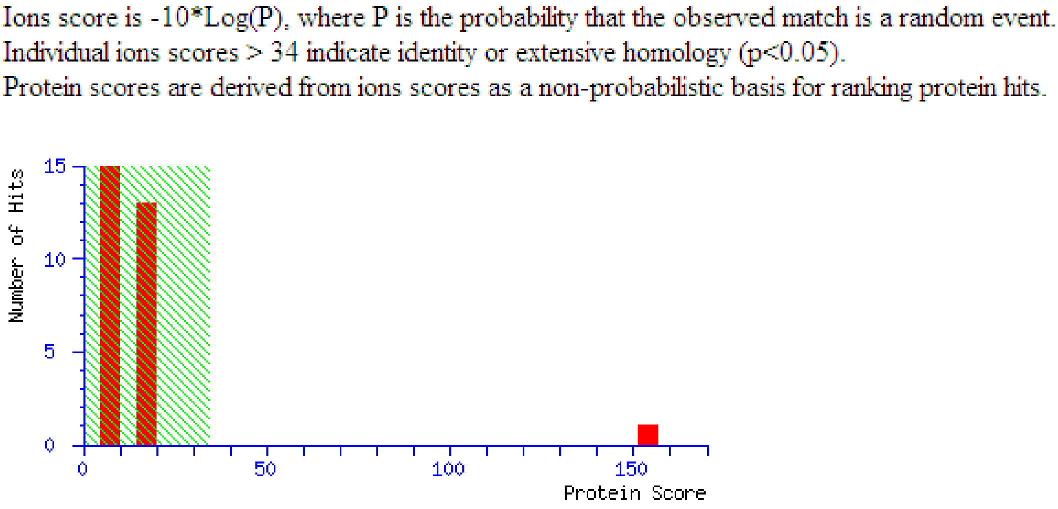
Matched peptides No.: [**2**] p value: **6.9e-007**

Calculated Mr: **35621** Calculated *p*I: **5.12**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Spot No.: **38**

NCBI accession No.: **cassava4.1_011584m|PACid:17982732**

Plant species: ***Manihot esculenta***

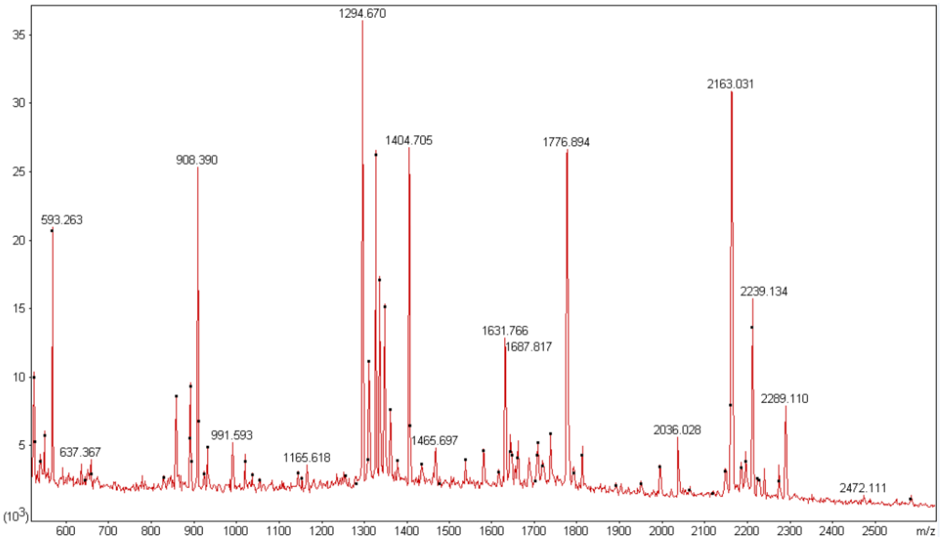
Protein name： **Probable fructokinase-1**

PFF Mascot score: [147] **Sequence coverage %: [**11**]**

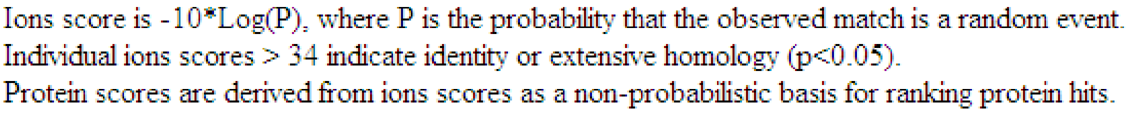
Matched peptides No.: **[3]** p value: **9.6e-006**

Calculated Mr: **35621** Calculated *p*I: **5.12**

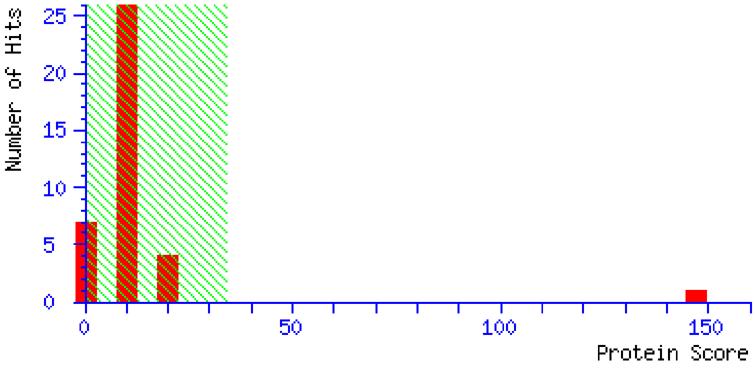
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **39**

NCBI accession No.: **cassava4.1_013158m|PACid:17968853** p value: **0.0017**

Plant species: ***Manihot esculenta***

Protein name：**Probable lactoylglutathione lyase, chloroplast**

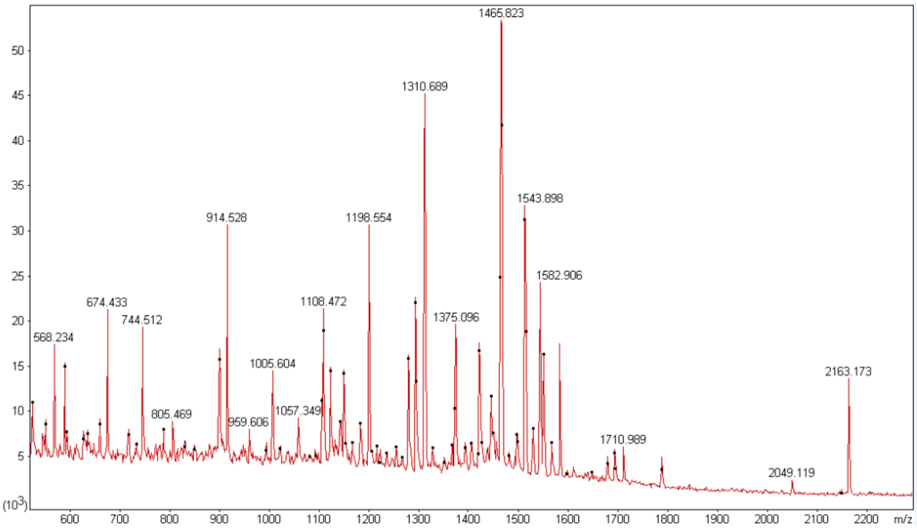
Mascot score: **151**

Sequence coverage %: **55** p value: **5.8e-011**

Matched peptides No.: **19** Total peptides No.: **77**

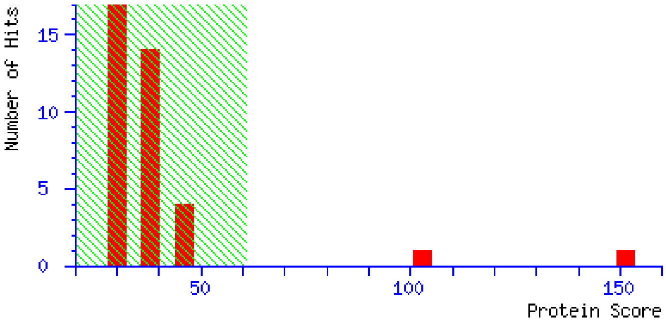
Calculated Mr: **32759** Calculated *p*I: **5.17**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **40**

NCBI accession No.: **cassava4.1_013158m|PACid:17968853**

Plant species: ***Manihot esculenta***

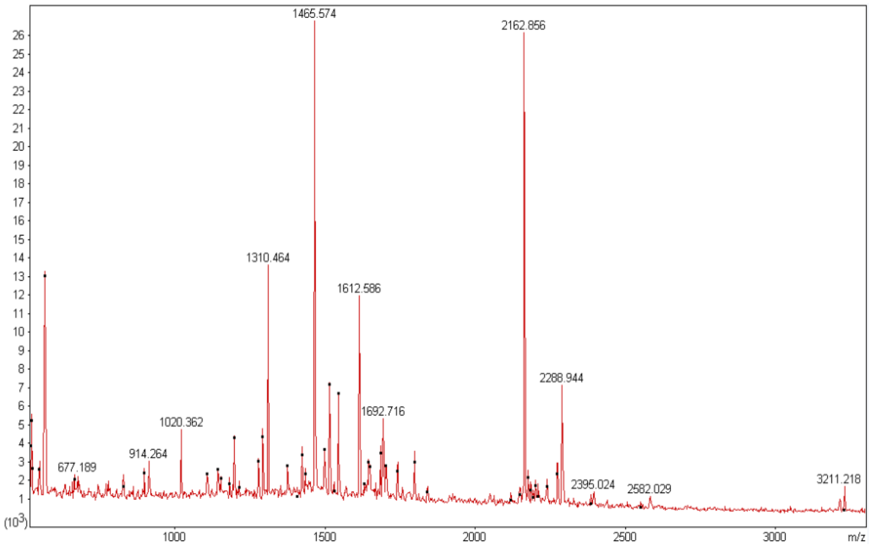
Protein name：**Probable lactoylglutathione lyase, chloroplast**

PFF Mascot score: **[73]** Sequence coverage %: **[8]**

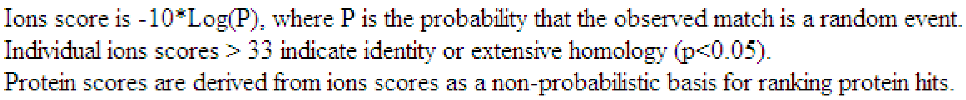
Matched peptides No.: **[2]** p value: 6.1e-006

Calculated Mr: **32759** Calculated *p*I: **5.17**

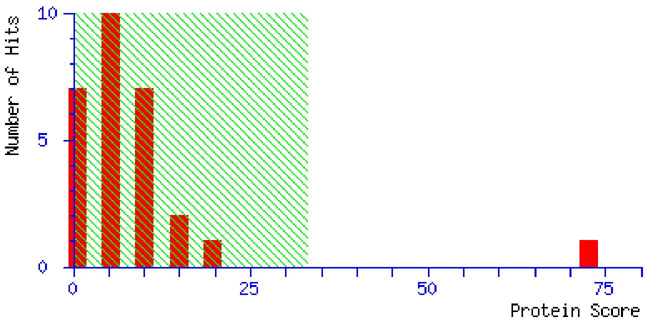
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **41**

NCBI accession No.: **cassava4.1_012601m|PACid:17970211**

Plant species: ***Manihot esculenta***

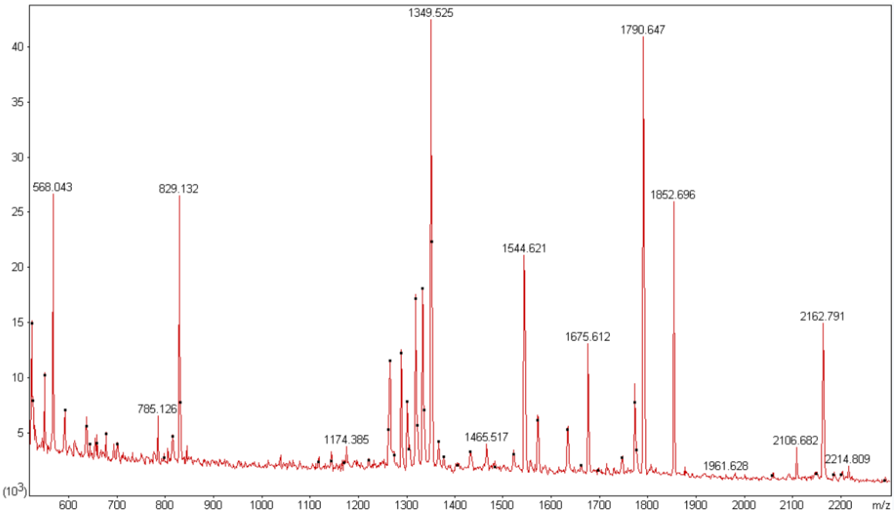
Protein name：**Putative carboxyphosphonoenolpyruvate mutase**

PFF Mascot score: [187] **Sequence coverage %: [10]**

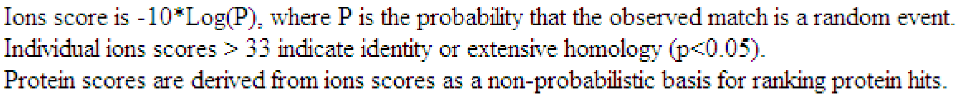
Matched peptides No.: **[2]** p value: **1.2e-009**

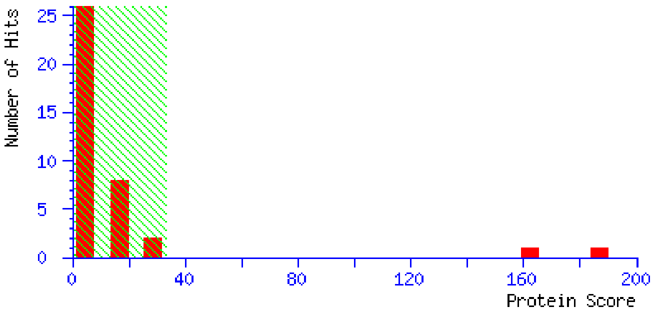
Calculated Mr: **32938** Calculated *p*I: **5.32**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **42**

NCBI accession No.: **cassava4.1_011578m|PACid:17975802**

Plant species: ***Manihot esculenta***

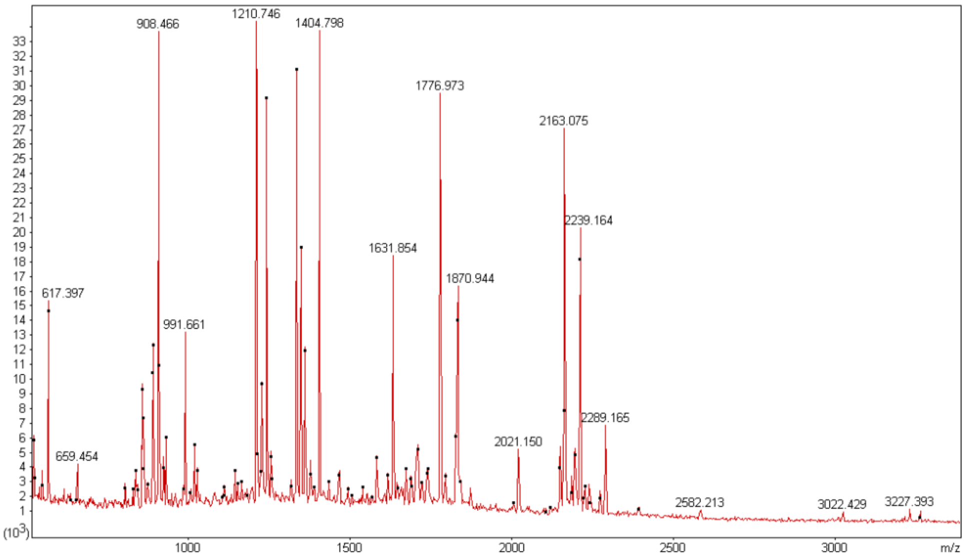
Protein name：**Probable fructokinase-1**

PFF Mascot score: **[146]** Sequence coverage %: **[11]**

Matched peptides No.: **[3]** p value: **0.00019**

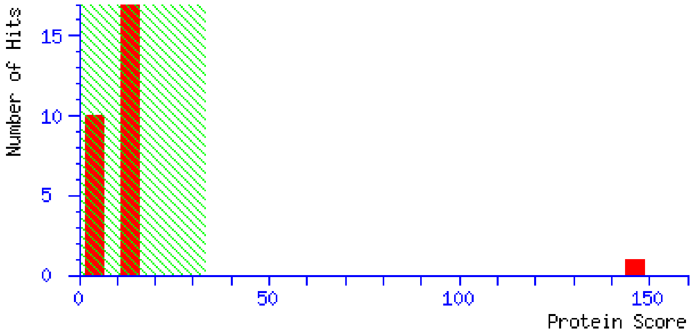
Calculated Mr: **35491** Calculated *p*I: **5.29**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **43**

NCBI accession No.: **cassava4.1_010863m|PACid:17977552**

Plant species: **Manihot esculenta**

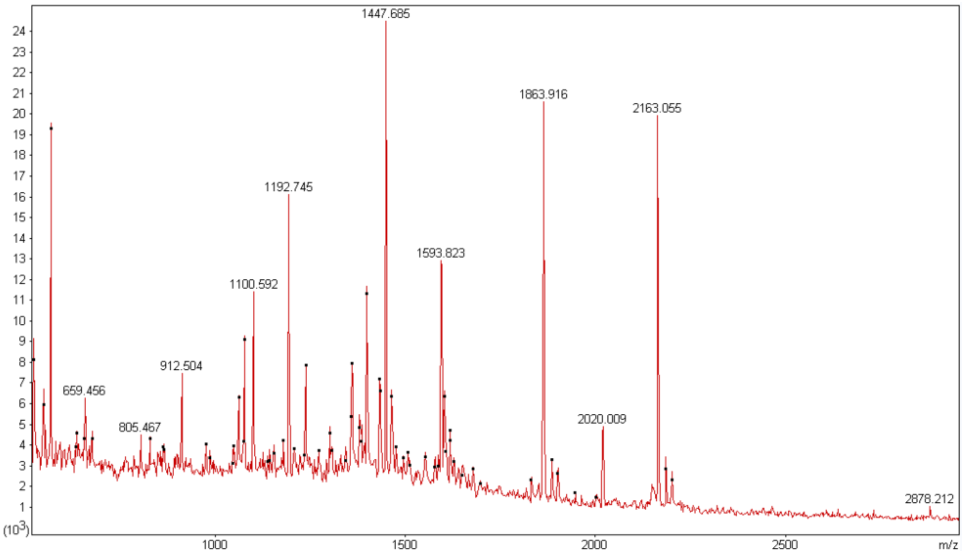
Protein name: NADP-dependent alkenal double bond reductase P1

PFF Mascot score: **[81]** Sequence coverage %: **[7]**

Matched peptides No.: **[2]** p value: **3.6e-006**

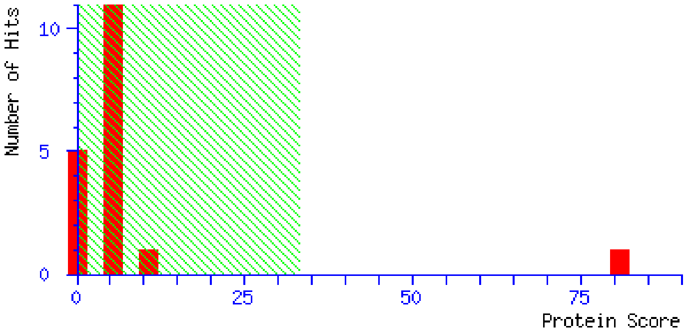
Calculated Mr: **38818** Calculated *p*I: **5.41**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **44**

NCBI accession No.: **cassava4.1_010863m|PACid:17977552**

Plant species: ***Manihot esculenta***

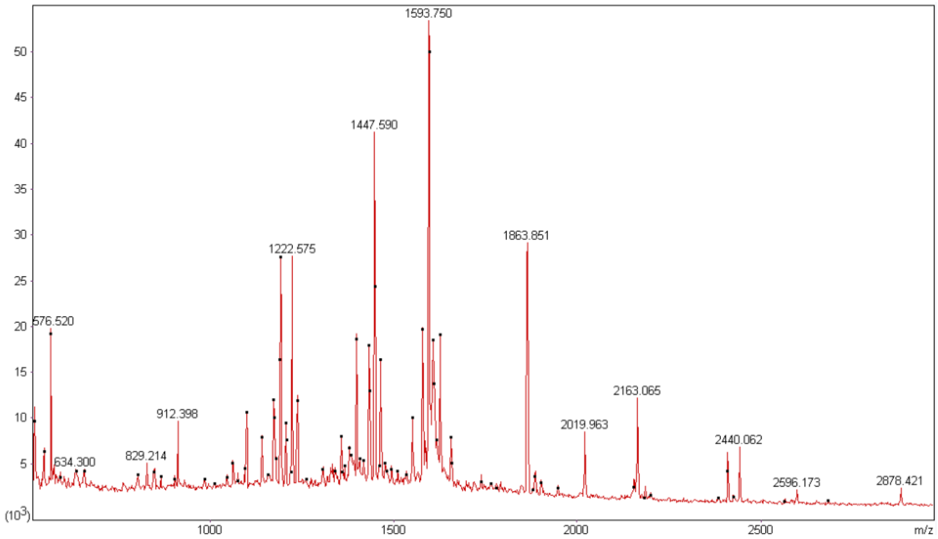
Protein name：**NADP-dependent alkenal double bond reductase**

PFF Mascot score: **[99]** Sequence coverage %: **[7]**

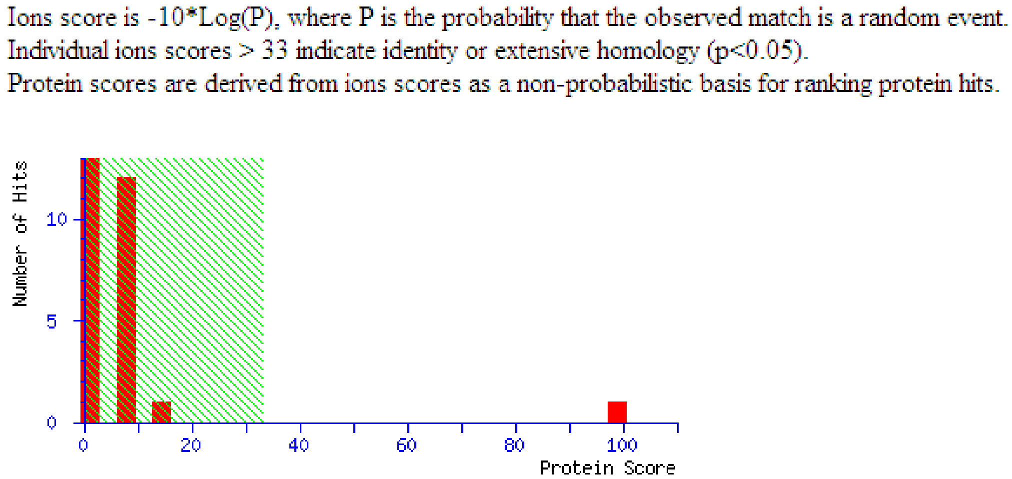
Matched peptides No.: **[2]** p value: **7.3e-008**

Calculated Mr: **38818** Calculated *p*I: **5.41**

Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Spot No.: **45**

NCBI accession No.: **cassava4.1_011869m|PACid:17965954**

Plant species: ***Manihot esculenta***

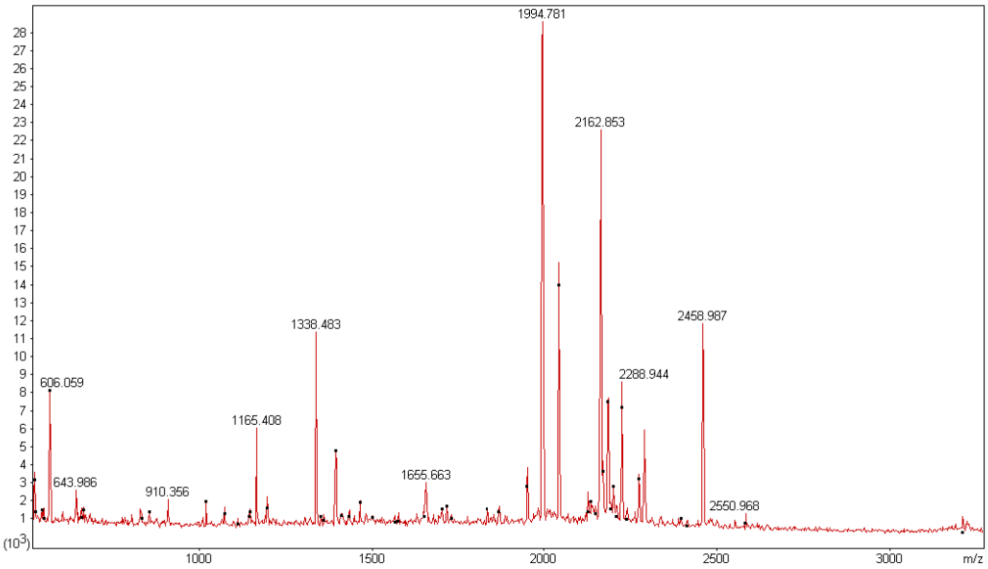
Protein name：**DNA-damage-repair/toleration protein DRT102**

PFF Mascot score: **[151]** Sequence coverage %: **[8]**

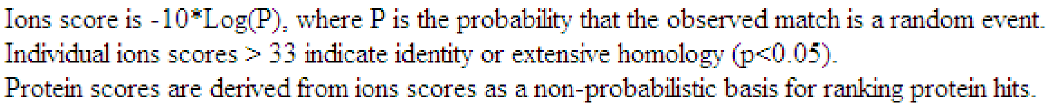
Matched peptides No.: **[2]** p value: **1.6e-008**

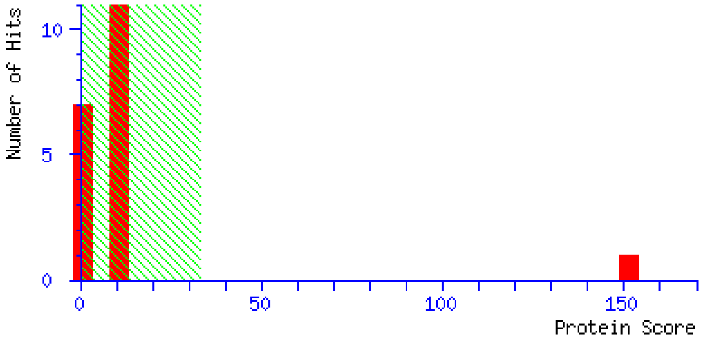
Calculated Mr: 35467 Calculated *p*I: **5.12**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **46**

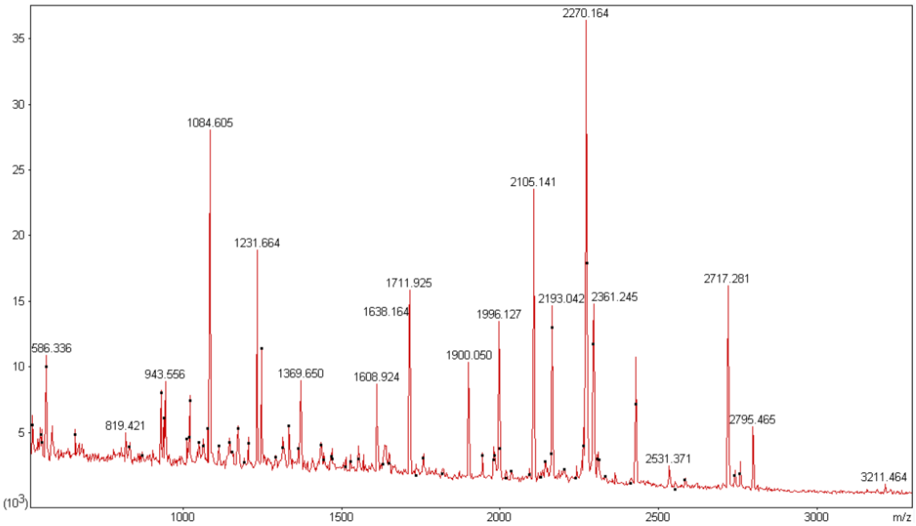
NCBI accession No.: **cassava4.1_012448m|PACid:17968446** Plant species: ***Manihot esculenta*** Protein name：**Putative NAD(P)H oxidoreductase, isoflavone reductase**

PFF Mascot score: **[254]** Sequence coverage %: **[15]**

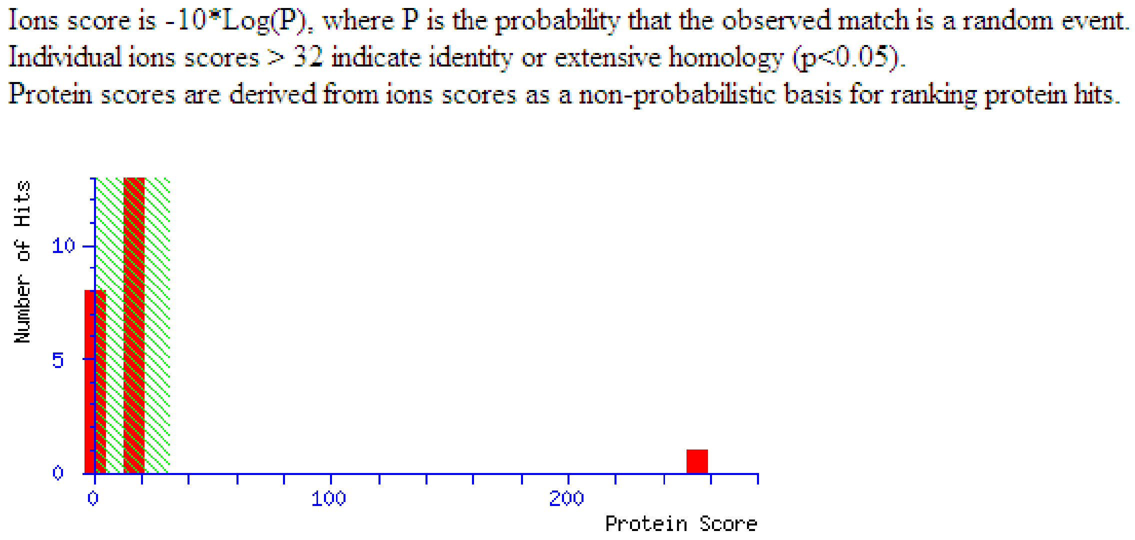
Matched peptides No.: **[3]** p value: **4.7e-012**

Calculated Mr: 33873 Calculated *p*I: **5.47**

Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 32 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Spot No.: **47**

NCBI accession No.: **cassava4.1_010620m|PACid:17987783**

Plant species: ***Manihot esculenta***

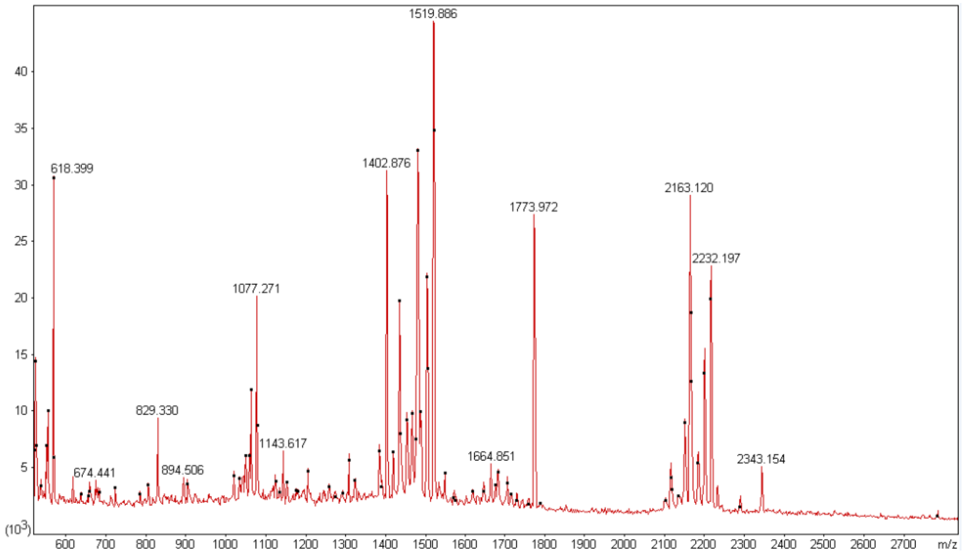
Protein name: **Thiamine thiazole synthase, chloroplastic**

PFF Mascot score: [133] **Sequence coverage %: [8]**

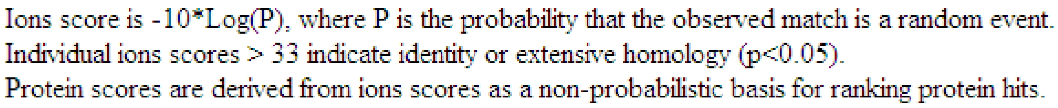
Matched peptides No.: **[2]** p value: **6.7e-006**

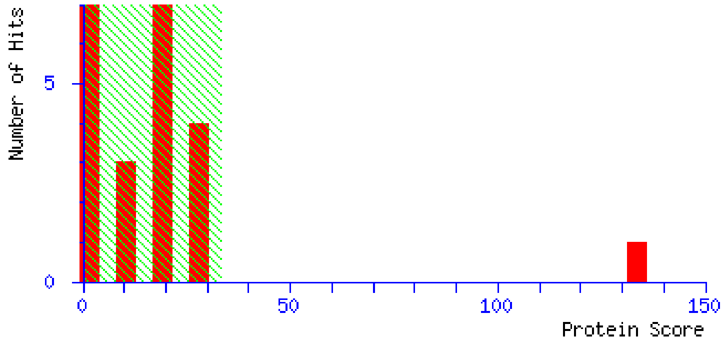
Calculated Mr: **37625** Calculated *p*I: **6.07**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **48**

NCBI accession No.: **cassava4.1_013135m|PACid:17983192**

Plant species: ***Manihot esculenta***

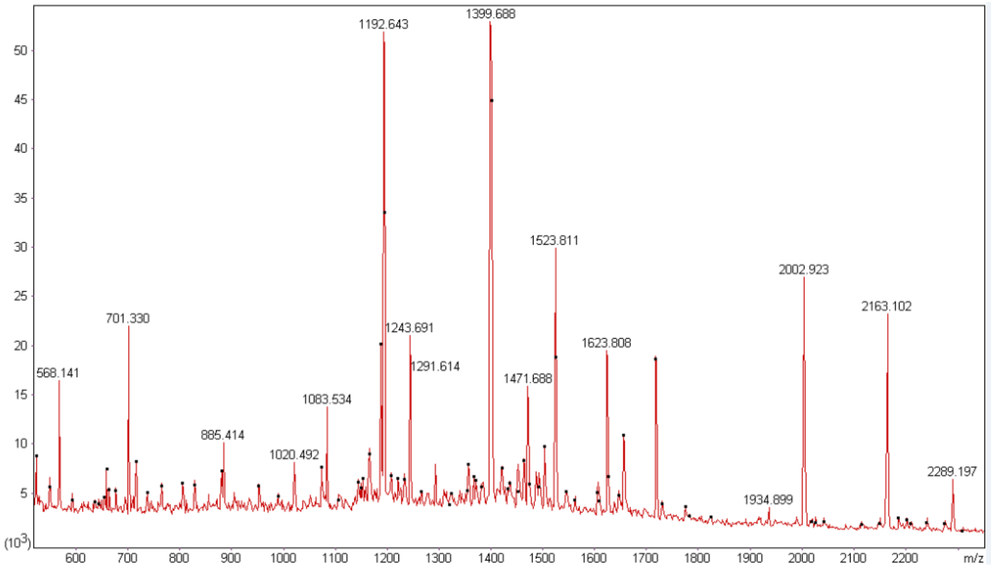
Protein name： **Alpha-soluble NSF attachment protein 2**

PFF Mascot score: [209] **Sequence coverage %: [12]**

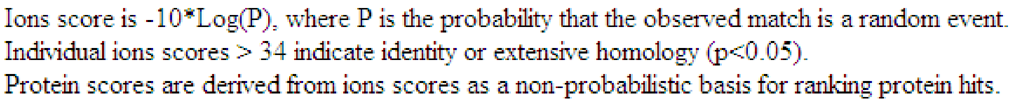
Matched peptides No.: **[3]** p value: **9.1e-007**

Calculated Mr: **32780** Calculated *p*I: **5.13**

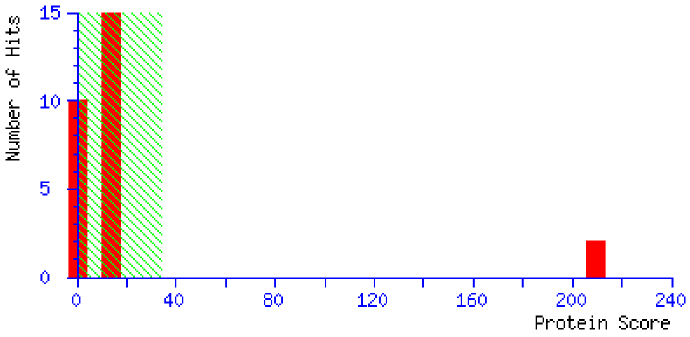
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **49**

NCBI accession No.: **cassava4.1_014185m|PACid:17964106**

Plant species: ***Manihot esculenta***

Protein name： **Ferritin-4, chloroplastic**

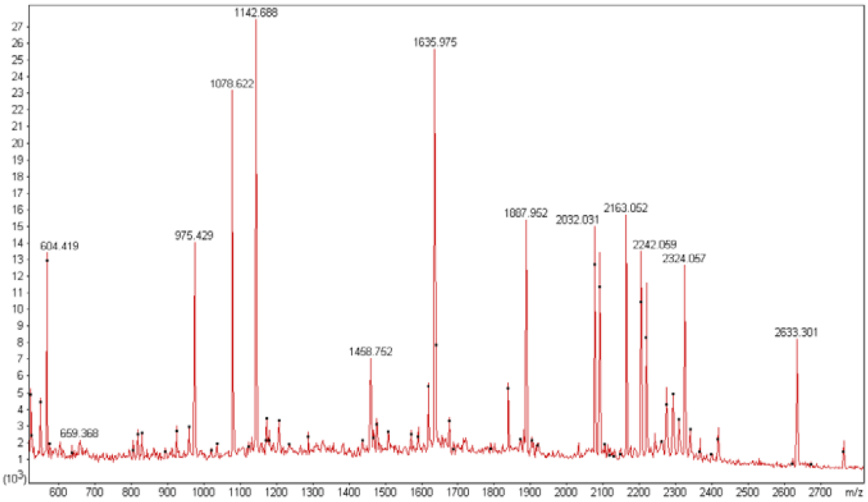
Mascot score: **125**

Sequence coverage %: **61**　　p value: **2.3e-008**

Matched peptides No.: **18**　　Total peptides No.: **68**

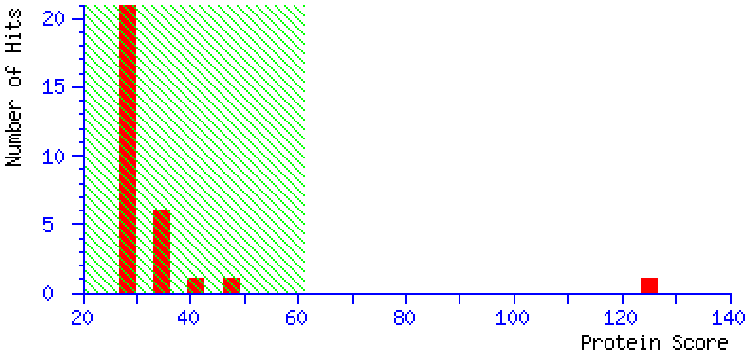
Calculated Mr: **29470**　　Calculated *p*I: **5.30**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **50**

NCBI accession No.: **cassava4.1_014410m|PACid:17965277**

Plant species: ***Manihot esculenta***

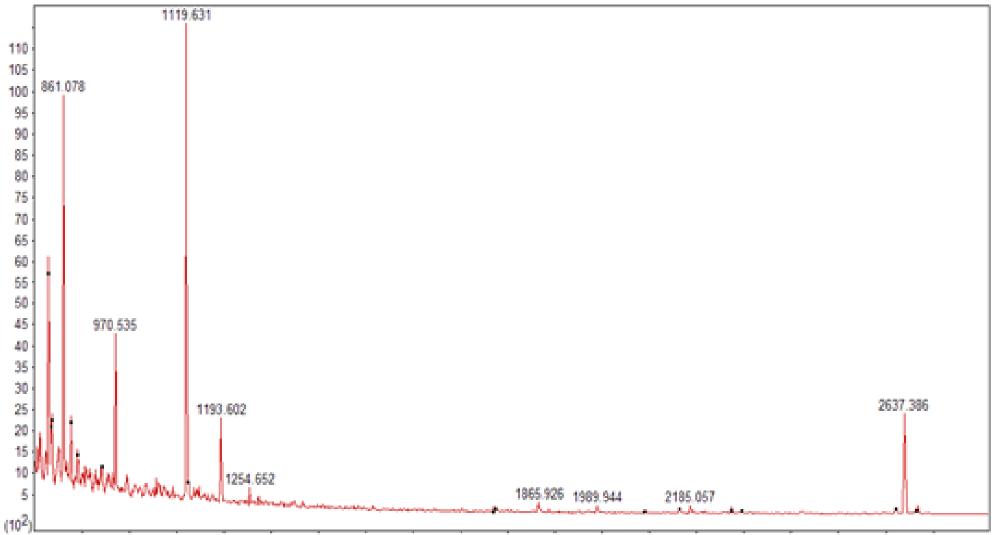
Protein name： **20 kDa chaperonin, chloroplastic**

PFF Mascot score: **[172]** Sequence coverage %: **[21]**

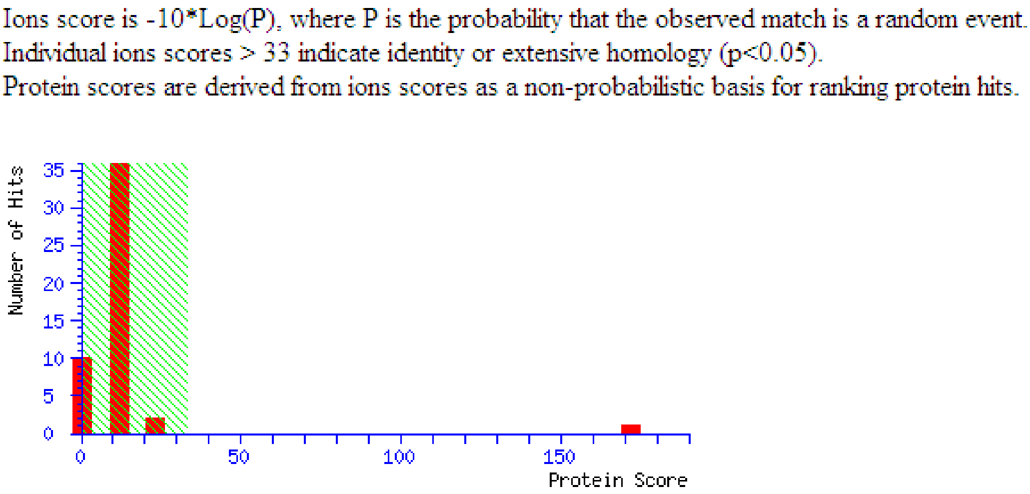
Matched peptides No.: **[3]** p value: **5e-005**

Calculated Mr: **26695** Calculated *p*I: **7.79**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Spot No.: **51**

NCBI accession No.: **cassava4.1_014643m|PACid:17991662**

Plant species: ***Manihot esculenta***

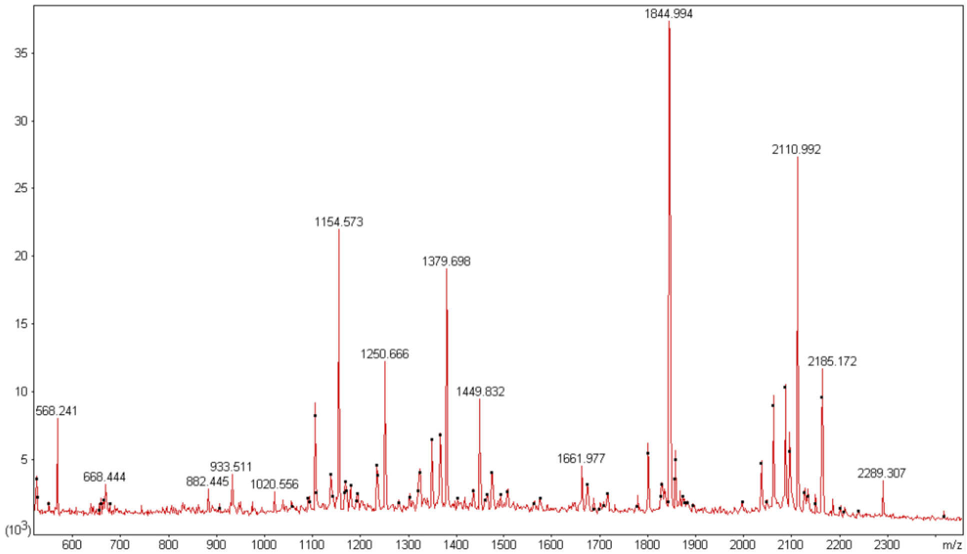
Protein name: **L-ascorbate peroxidase 1, cytosolic**

Mascot score: **82** p value: **0.00046**

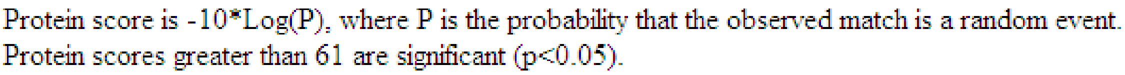
Sequence coverage %: **40** Matched peptides No.: **13**

Calculated Mr: **27766** Calculated *p*I: **5.31**

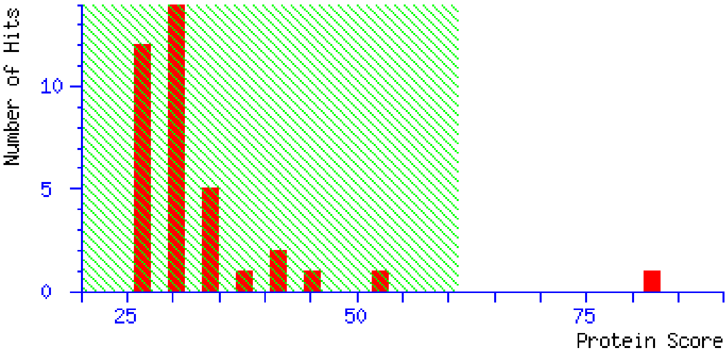
Annotated PMF **spectra:**



Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **52**

NCBI accession No.: **cassava4.1_014643m|PACid:17991662**

Plant species: ***Manihot esculenta***

Protein name： **L-ascorbate peroxidase 1, cytosolic**

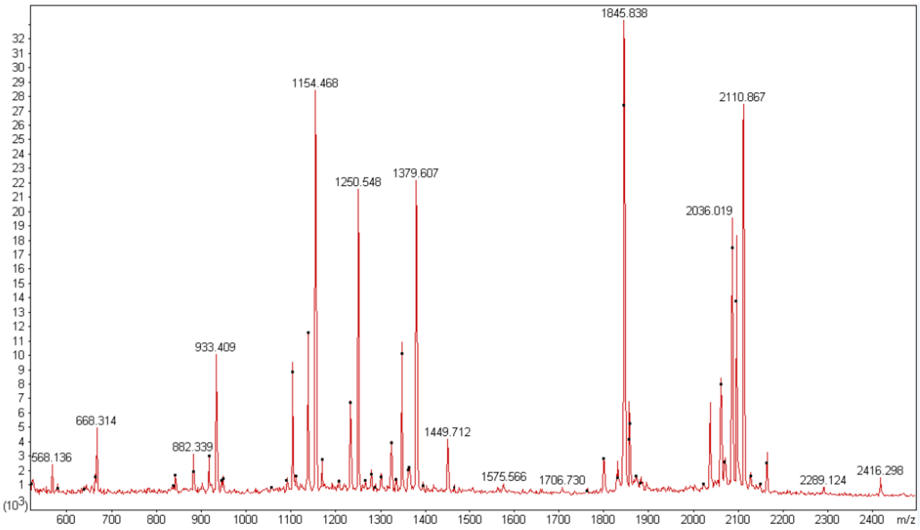
Mascot score: **133**　　　p value: **`3.7e-009`**

Sequence coverage %: **50**

Matched peptides No.: **17**　　　　　　Total peptides No.: **52**

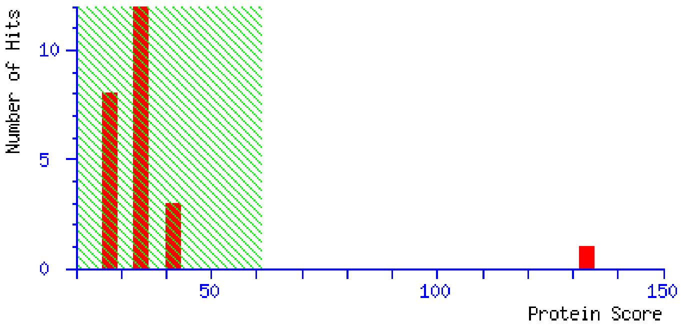
Calculated Mr: **27766**　　　　　　　Calculated *p*I: **5.31**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **53**

NCBI accession No.: **cassava4.1_009779m|PACid:17990964**

Plant species: ***Manihot esculenta***

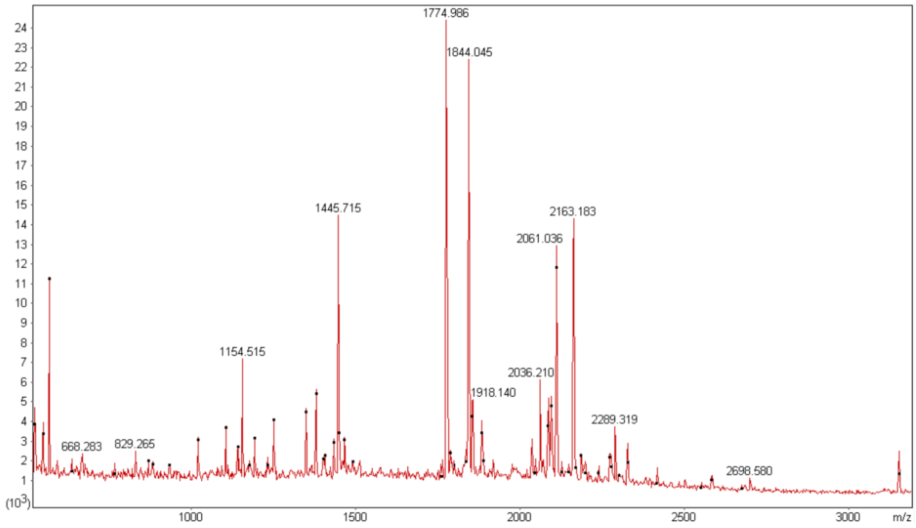
Protein name： **Actin-7**

PFF Mascot score: [96] **Sequence coverage %:** [7]

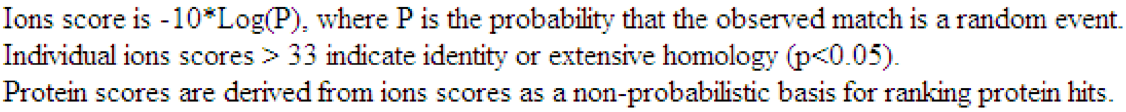
Matched peptides No.: [**2**] p value: **0.00065**

Calculated Mr: 41897 Calculated *p*I: **5.31**

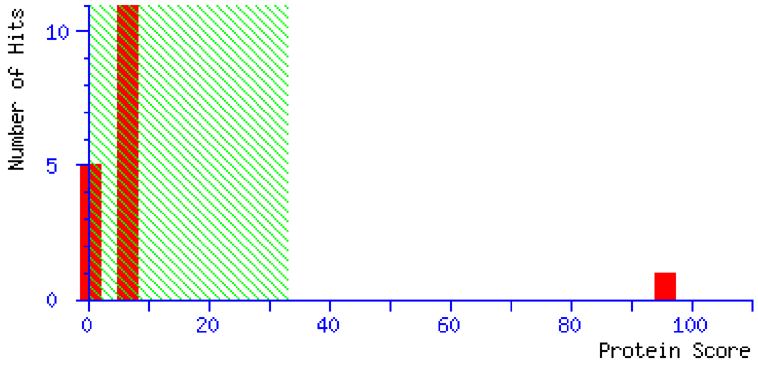
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **54**

NCBI accession No.: **cassava4.1_017771m|PACid:17966880**

Plant species: ***Manihot esculenta***

Protein name：**ATP synthase subunit d, mitochondrial**

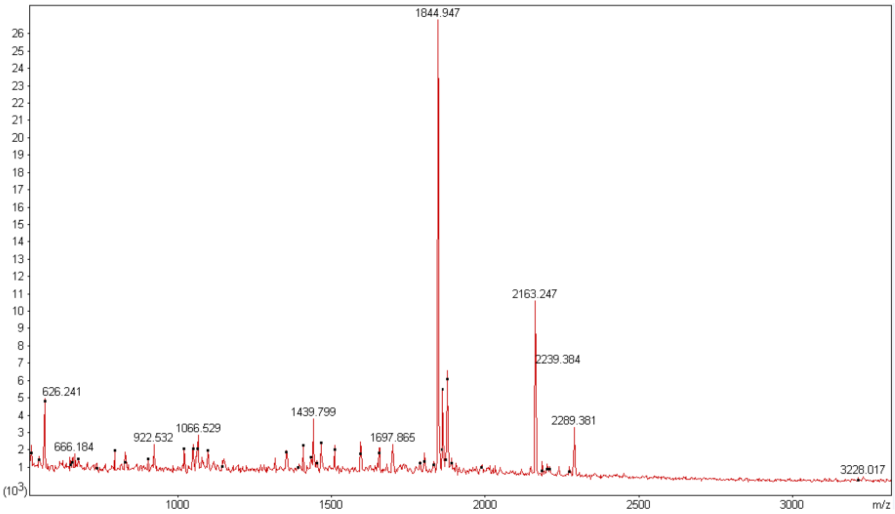
Mascot score: **113**   p value: **`3.7e-007`**

Sequence coverage %: **57**

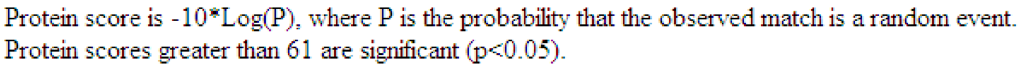
Matched peptides No.: **13**   Total peptides No.: **39**

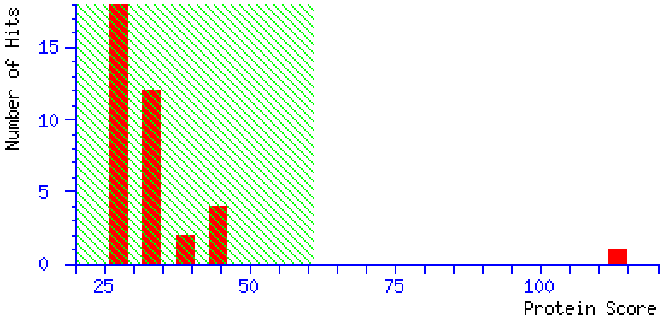
Calculated Mr: **19663**   Calculated *p*I: **5.11**

Annotated PMF **spectra:**



Probability Based Mowse Score:


Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **55**

NCBI accession No.: **cassava4.1_017771m|PACid:17966880**

Plant species: ***Manihot esculenta***

Protein name: **ATP synthase subunit d, mitochondrial**

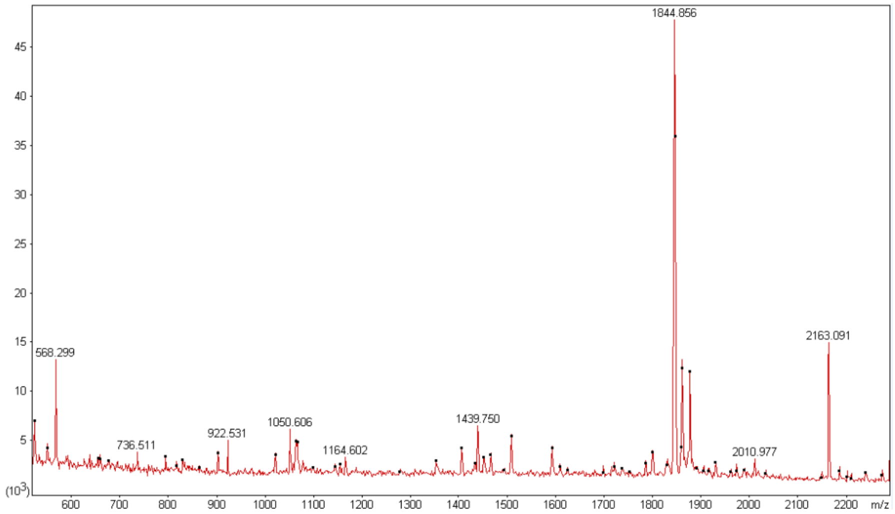
Mascot score: **184** p value: **`2.9e-014`**

Sequence coverage %: **70**

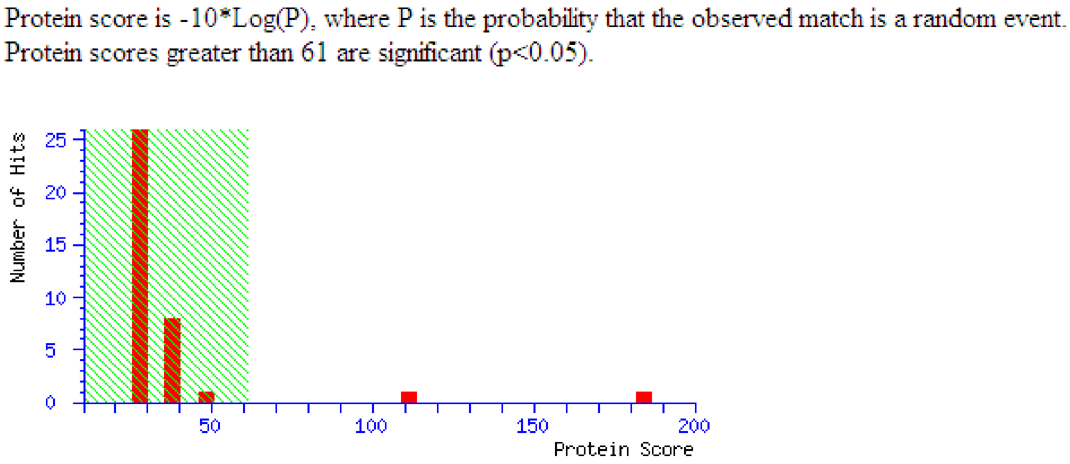
Matched peptides No.: 19 Total peptides No.: **50**

Calculated Mr: **19663** Calculated *p*I: **5.11**

Annotated PMF **spectra:**



Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).

Spot No.: **56**

NCBI accession No.: **cassava4.1_015349m|PACid:17959817**

Plant species: ***Manihot esculenta***

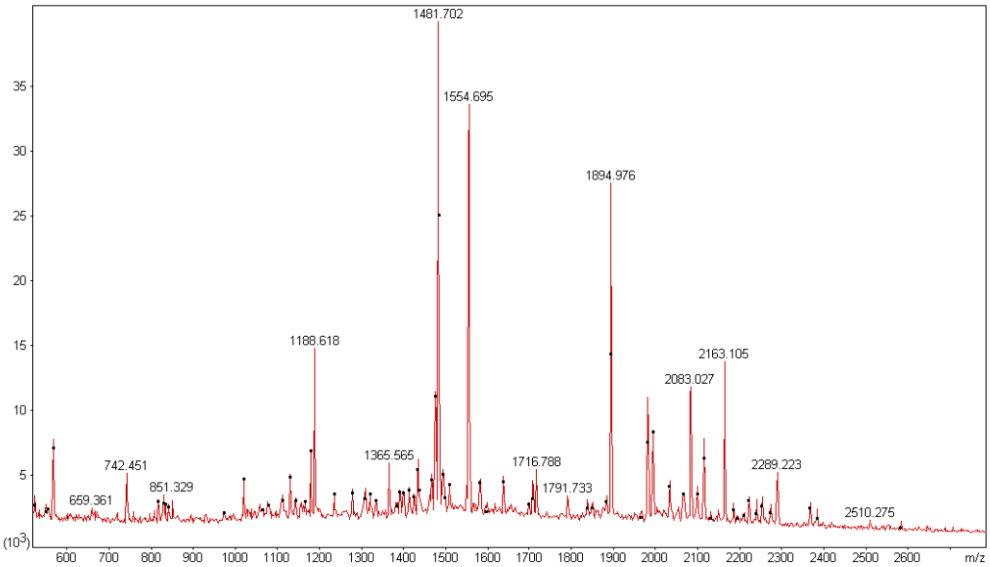
Protein name： **Proteasome subunit beta type**

PFF Mascot score: [137] **Sequence coverage %:** [11]

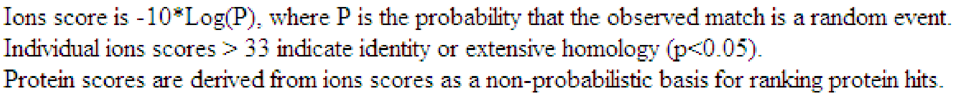
Matched peptides No.: **[2]** p value: **9.5e-006**

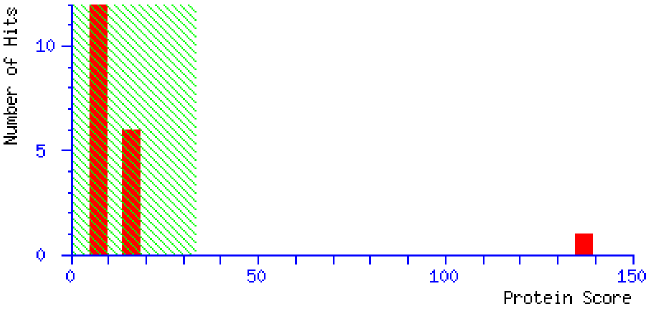
Calculated Mr: **24988** Calculated *p*I: **5.51**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **57**

NCBI accession No.: **cassava4.1_017832m|PACid:17961591**

Plant species: ***Manihot esculenta***

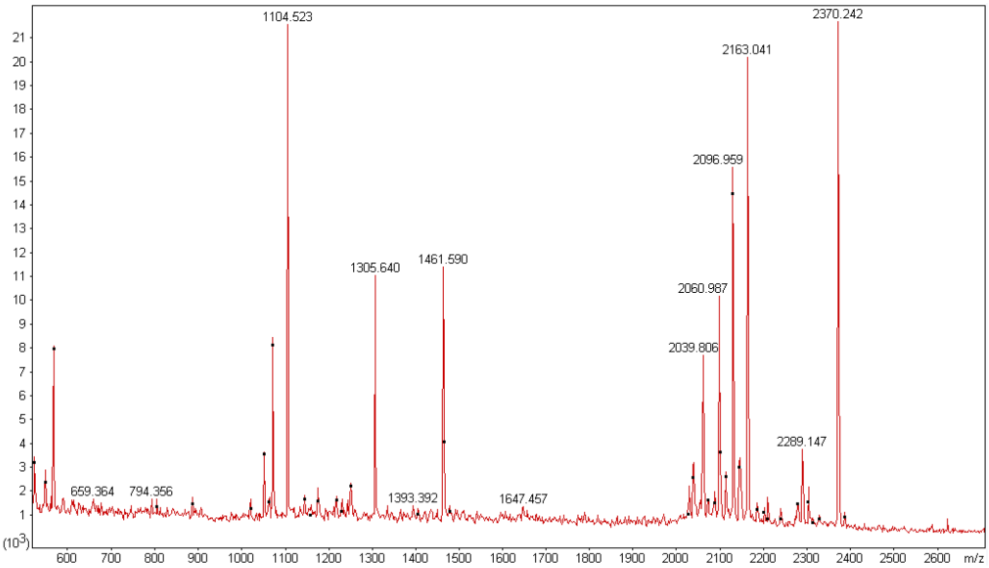
Protein name: **regulator of ribonuclease activity a**

PFF Mascot score: [133] **Sequence coverage %: [16]**

Matched peptides No.: **[2]** p value: **8.1e-007**

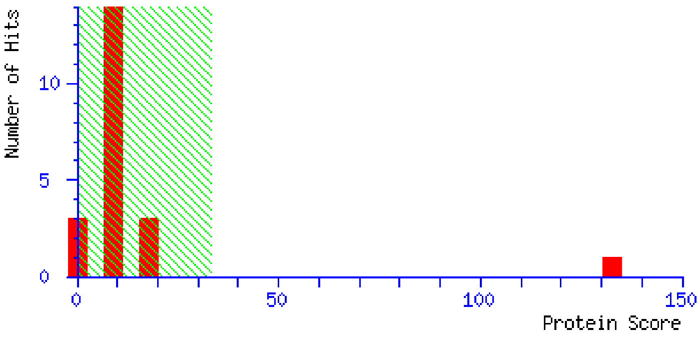
Calculated Mr: 18015 Calculated *p*I: **5.39**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **58**

NCBI accession No.: **cassava4.1_018059m|PACid:17963195**

Plant species: ***Manihot esculenta***

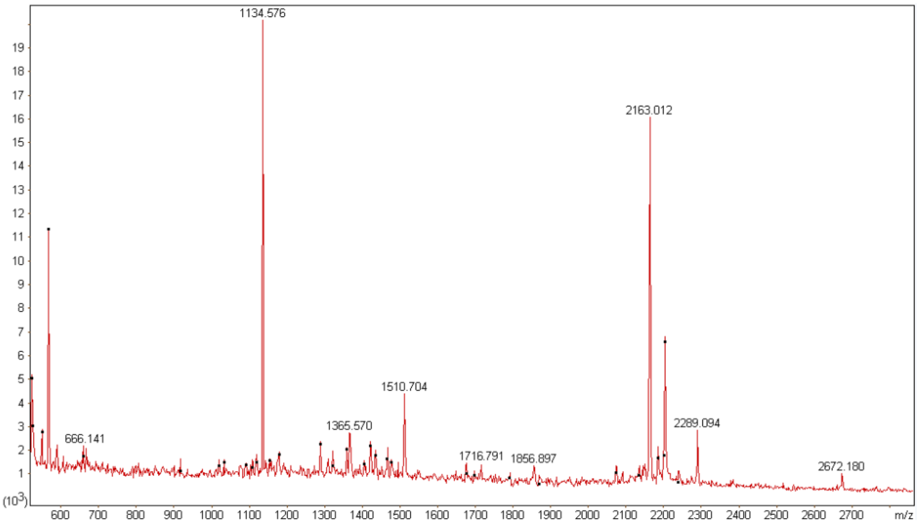
Protein name：**Eukaryotic translation initiation factor 5A-2**

PFF Mascot score: [66] **Sequence coverage %:** [**18**]

Matched peptides No.: [**2**] p value: **0.00026**

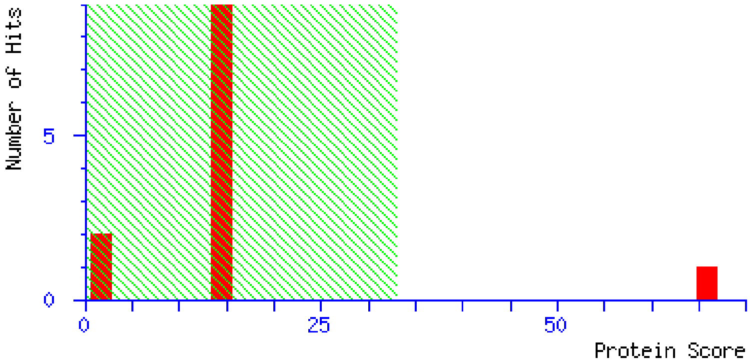
Calculated Mr: **17706** Calculated *p*I: **5.60**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **59**

NCBI accession No.: **cassava4.1_018026m|PACid:17990511**

Plant species: ***Manihot esculenta***

Protein name：**Eukaryotic translation initiation factor 5A-2**

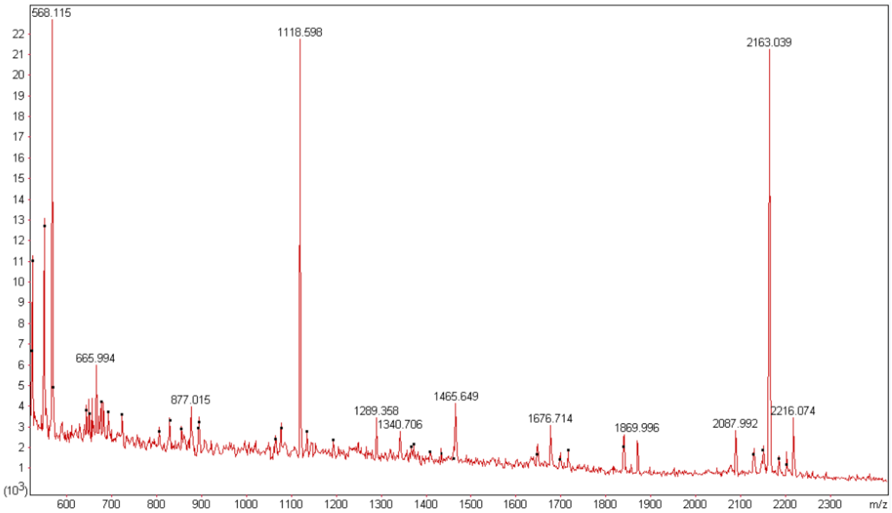
Mascot score: **72** p value: **0.041**

Sequence coverage %: **44**

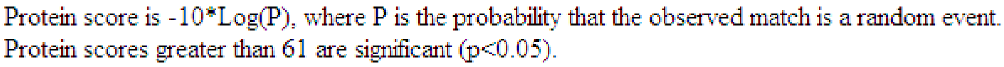
Matched peptides No.: **7** Total peptides No.: **33**

Calculated Mr: **17805** Calculated *p*I: **5.60**

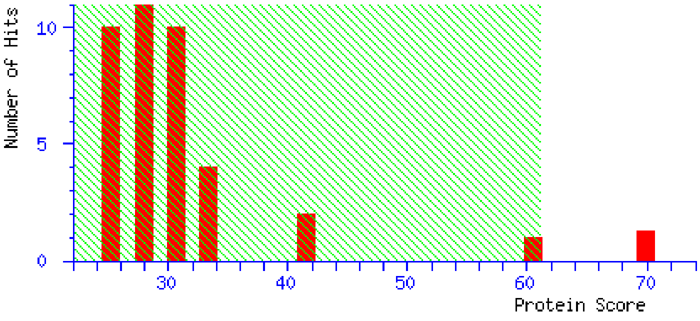
Annotated PMF **spectra:**



Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **60**

NCBI accession No.: **cassava4.1_018158m|PACid:17970560**

Plant species: ***Manihot esculenta***

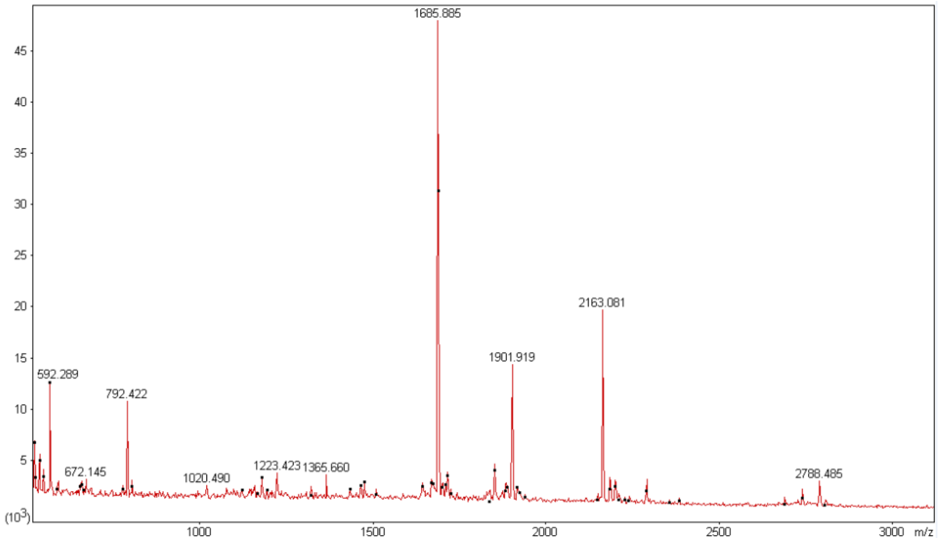
Protein name： **heat-shock protein, putative**

PFF Mascot score: [196] **Sequence coverage %:** [**19]**

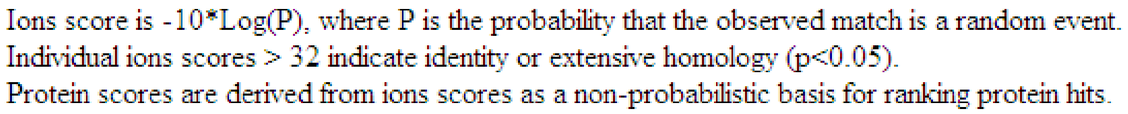
Matched peptides No.: [**2]** p value: **4.4e-011**

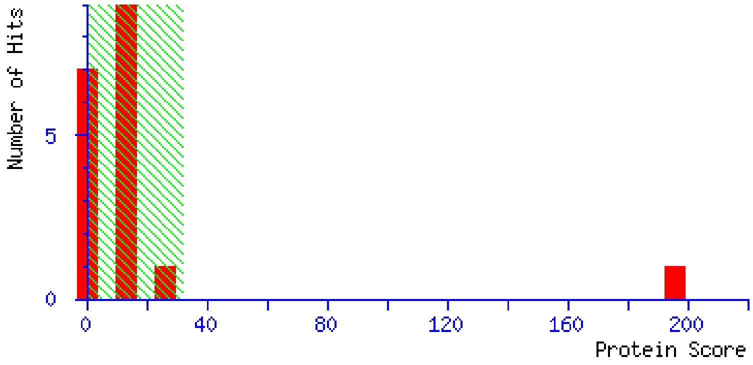
Calculated Mr: **17672** Calculated *p*I: **5.78**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 32 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **61**

NCBI accession No.: **cassava4.1_018737m|PACid:17986123**

Plant species: ***Manihot esculenta***

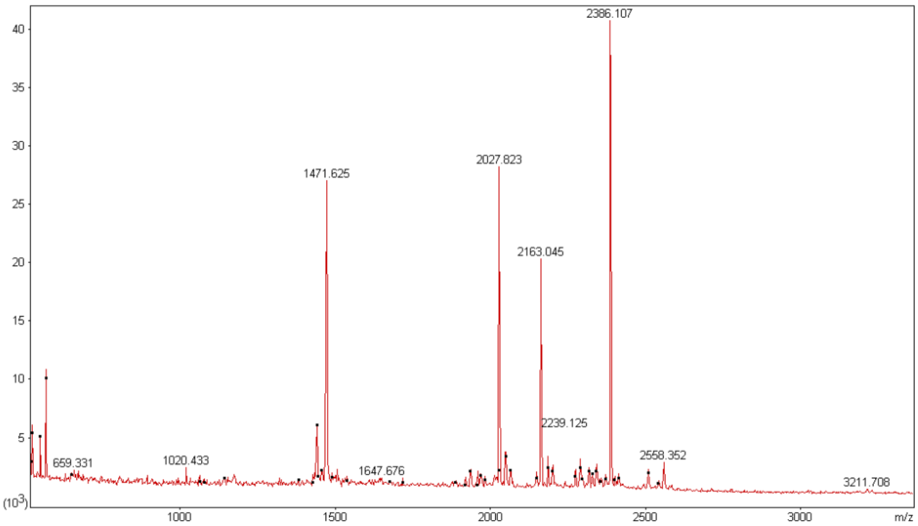
Protein name： **Actin-depolymerizing factor 3**

PFF Mascot score: [112]   Sequence coverage %: [11]

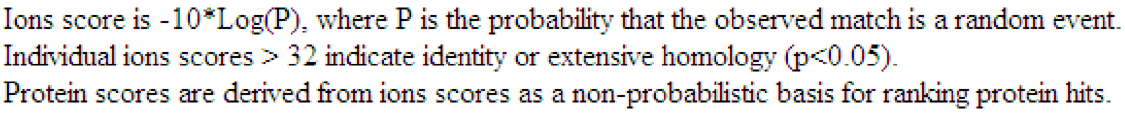
Matched peptides No.: **[3]**   p value: **5.3e-010**

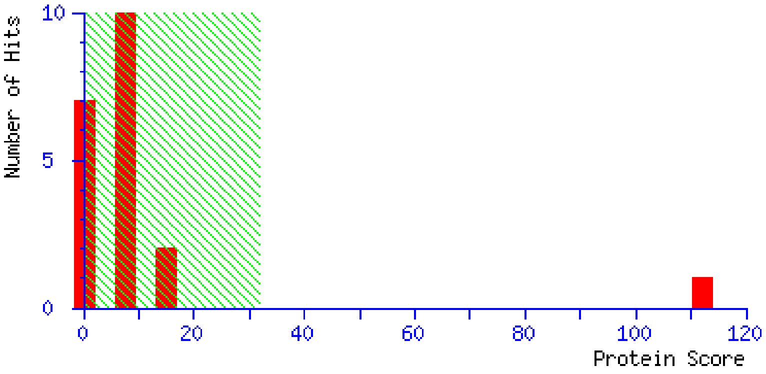
Calculated Mr: **16253**   Calculated *p*I: **6.60**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 32 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **62**

NCBI accession No.: **cassava4.1_017871m|PACid:17980723**

Plant species: ***Manihot esculenta***

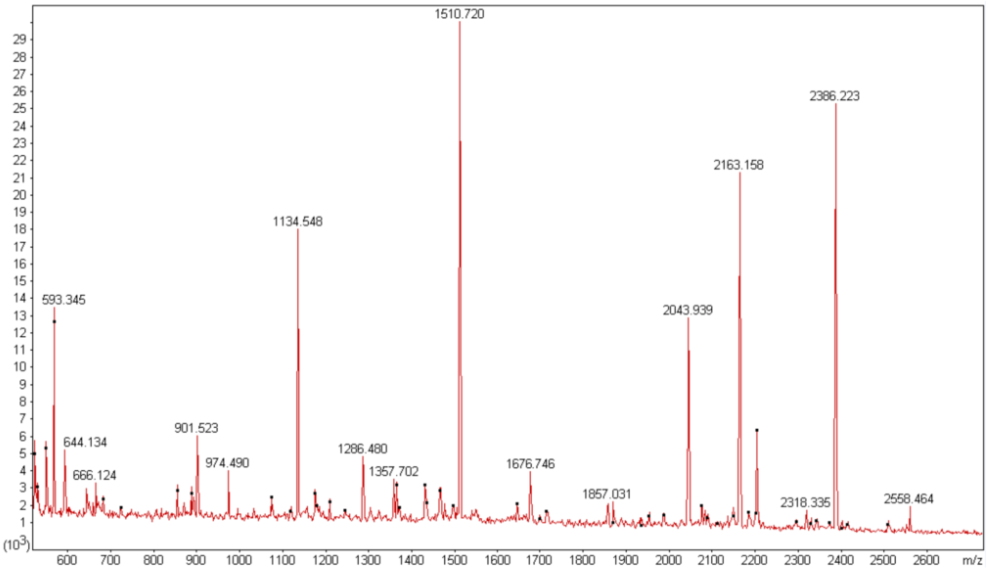
Protein name： **class I heat shock protein**

PFF Mascot score: [95] **Sequence coverage %: [8]**

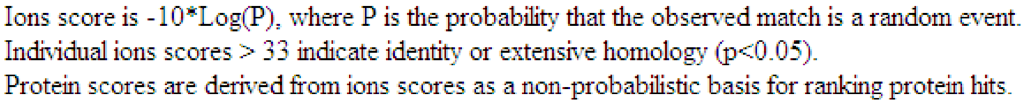
Matched peptides No.: **[2]** p value: **3.7e-008**

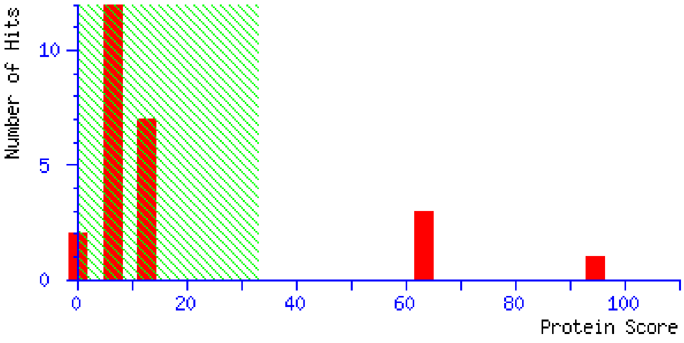
Calculated Mr: 18750 Calculated *p*I: **7.93**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **63**

NCBI accession No.: **cassava4.1_018026m|PACid:17990511**

Plant species: ***Manihot esculenta***

Protein name： **Eukaryotic translation initiation factor 5A-2**

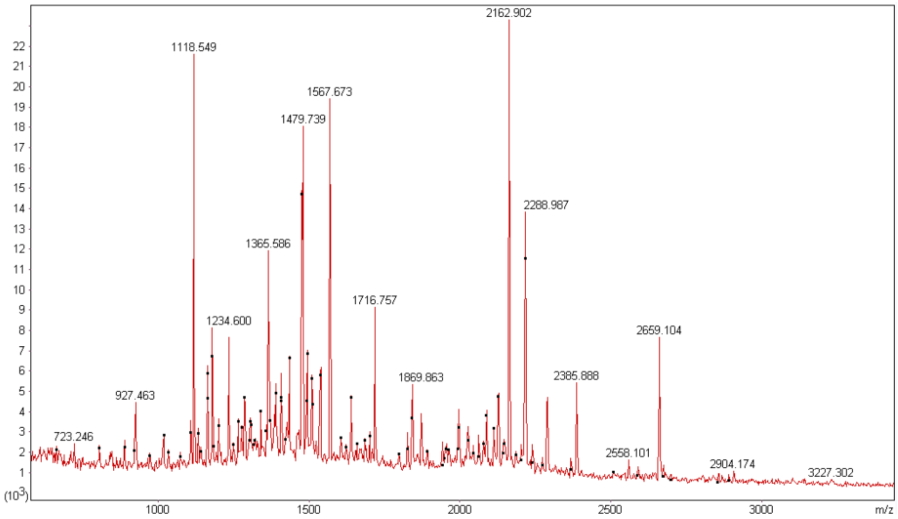
Mascot score: **82**

Sequence coverage %: **73**   p value: **0.00045**

Matched peptides No.: **11**   Total peptides No.: **76**

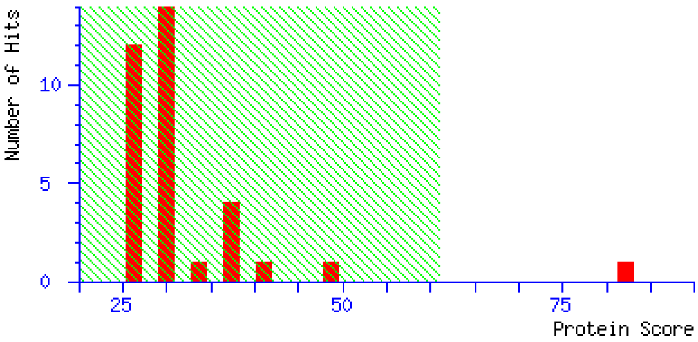
Calculated Mr: **17805**   Calculated *p*I: **5.60**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **64**

NCBI accession No.: **cassava4.1_017973m|PACid:17985926**

Plant species: ***Manihot esculenta***

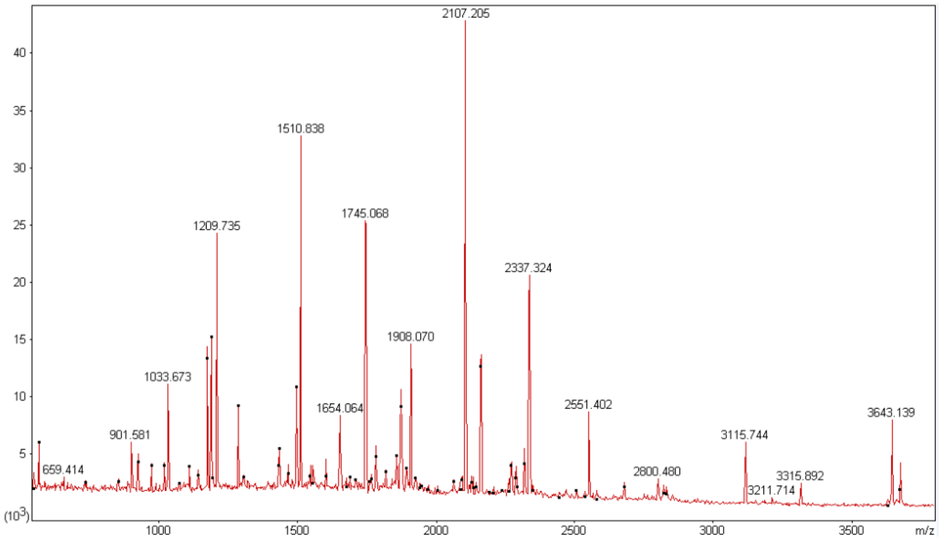
Protein name：**Peroxiredoxin-2B**

PFF Mascot score: [**180**] Sequence coverage %: **[22]**

Matched peptides No.: [**10**] p value: 2e-013

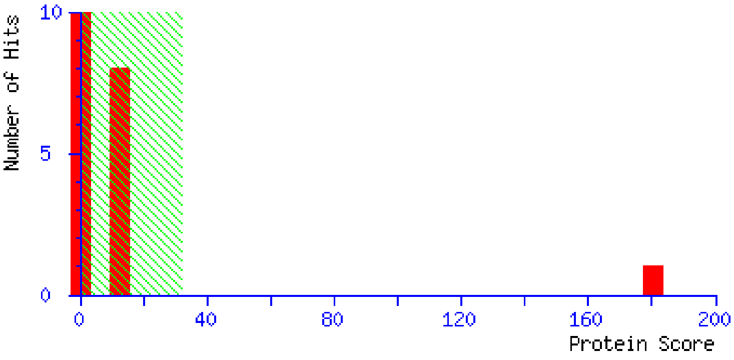
Calculated Mr: **17433** Calculated *p*I: **5.70**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 32 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **65**

NCBI accession No.: **cassava4.1_017871m|PACid:17980723**

Plant species: ***Manihot esculenta***

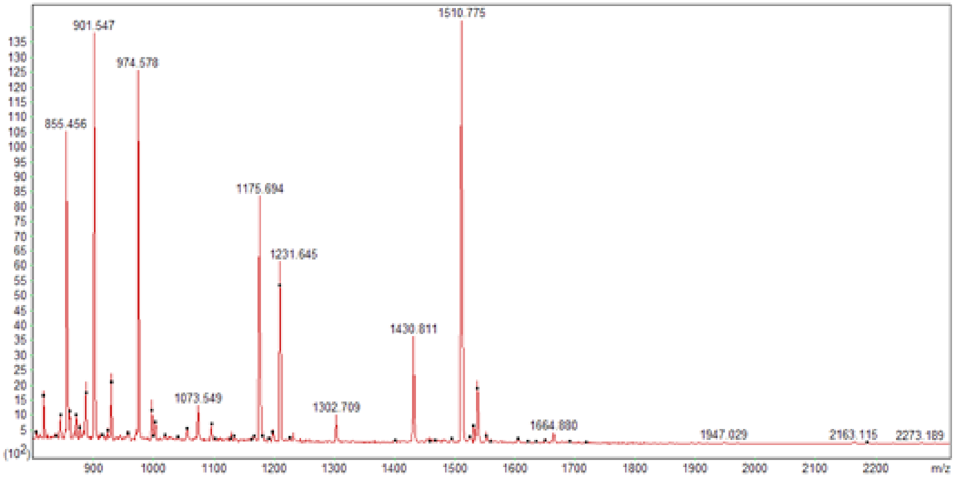
Protein name：**18.1 kDa class I heat shock protein**

PFF Mascot score: **[164]**　　　Sequence coverage %: **[25]**

Matched peptides No.: **[5]**　　　p value: **0.00017**

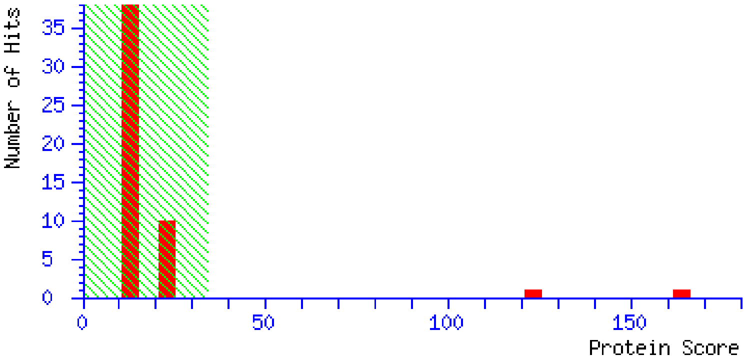
Calculated Mr: **18750**　　　Calculated p*I*: **7.93**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **66**

NCBI accession No.: **cassava4.1_018294m|PACid:17966054**

Plant species: ***Manihot esculenta***

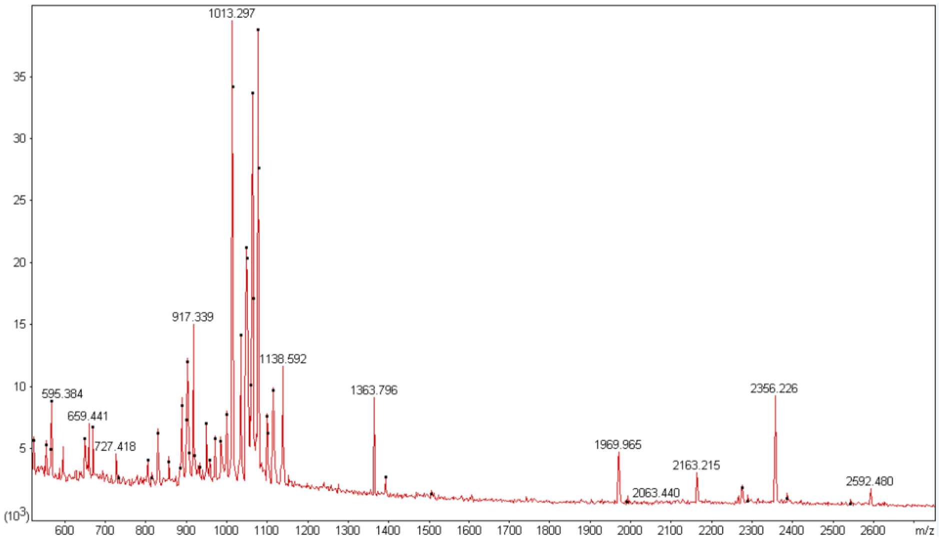
Protein name： **Superoxide dismutase [Cu-Zn] 1**

PFF Mascot score: [80] Sequence coverage %: [8]

Matched peptides No.: **[2]** p value: **1.3e-006**

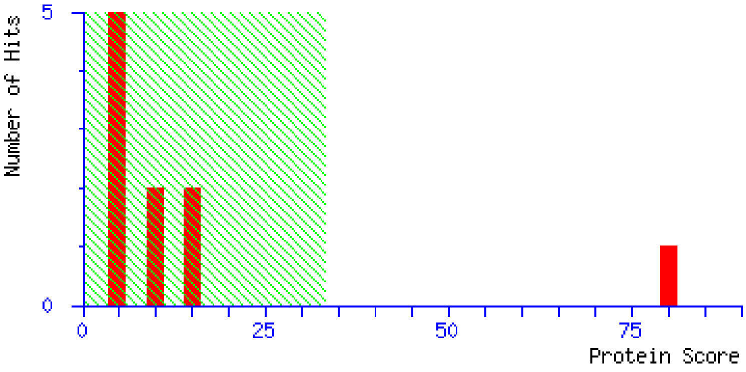
Calculated Mr: **15416** Calculated *p*I: **5.85**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **67**

NCBI accession No.: **cassava4.1_018422m|PACid:17961678**

Plant species: ***Manihot esculenta***

Protein name: Actin-depolymerizing factor 3

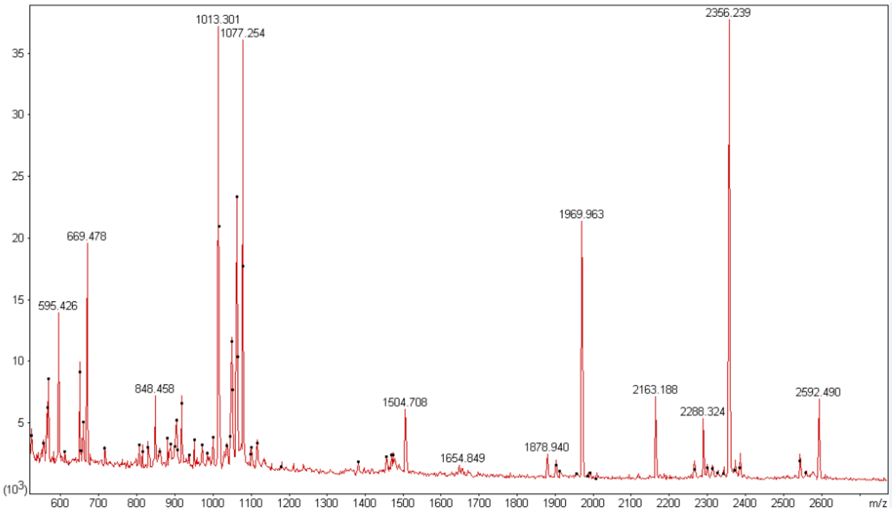
PFF Mascot score: [147]

Sequence coverage %: [14]

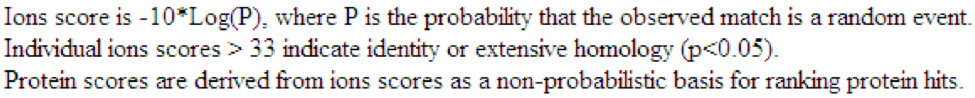
Matched peptides No.: **[3]** p value: **1.5e-013**

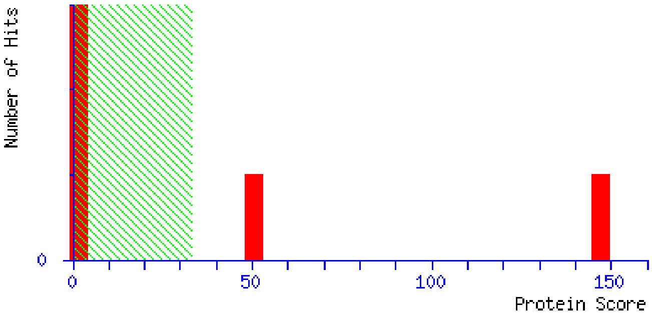
Calculated Mr: **17512** Calculated *p*I: 8. 39

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **68**

NCBI accession No.: **cassava4.1_018338m|PACid:17992346**

Plant species: ***Manihot esculenta***

Protein name：**Ubiquitin-conjugating enzyme E2 variant 1C**

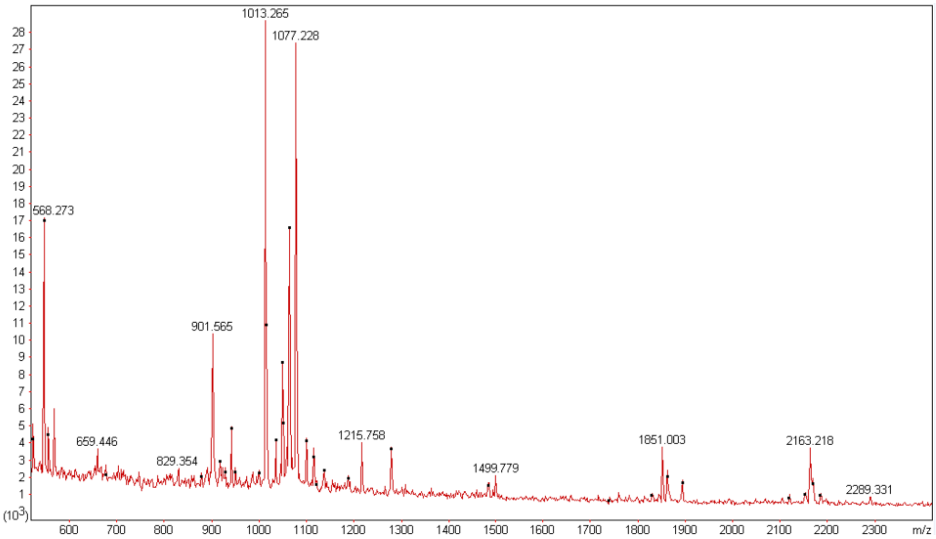
Mascot score: **119**

Sequence coverage %: **72** p value: **9.2e-008**

Matched peptides No.: **12** Total peptides No.: **37**

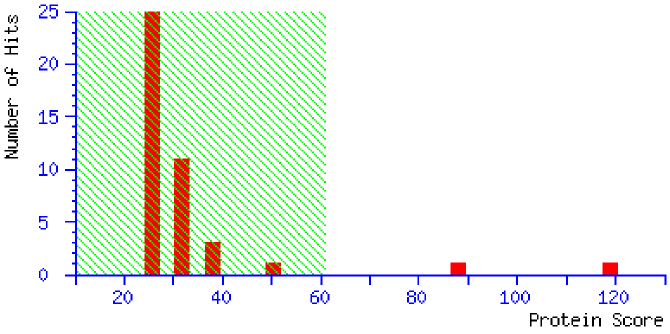
Calculated Mr: **17236** Calculated *p*I: **5.73**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **69**

NCBI accession No.: **cassava4.1_018010m|PACid:17970081**

Plant species: ***Manihot esculenta***

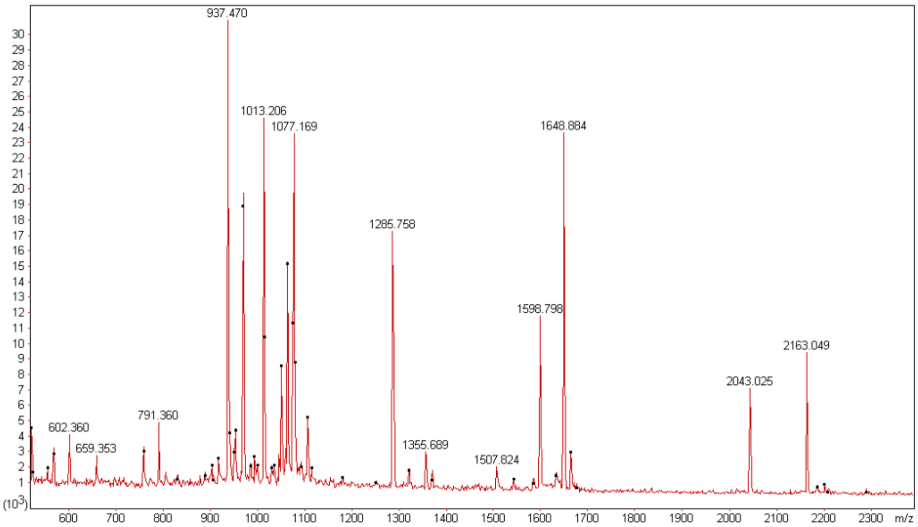
Protein name： **AT3g53990/F5K20_290**

PFF Mascot score: [195] **Sequence coverage %: [21]**

Matched peptides No.: **[3]** p value: **5.2e-006**

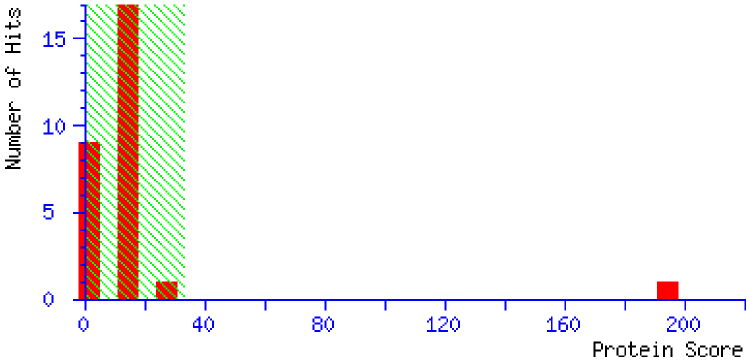
Calculated Mr: **18044** Calculated *p*I: **6.14**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **70**

NCBI accession No.: **cassava4.1_015272m|PACid:17960181**

Plant species: ***Manihot esculenta***

Protein name： **Superoxide dismutase [Mn] 1, mitochondrial**

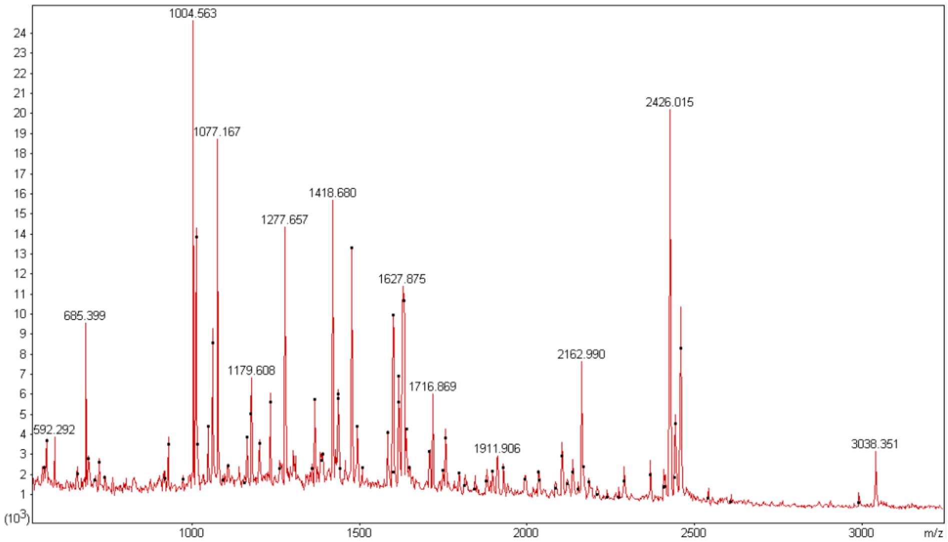
Mascot score: **139**

Sequence coverage %: **54** p value: **`9.2e-010`**

Matched peptides No.: **16** Total peptides No.:**67**

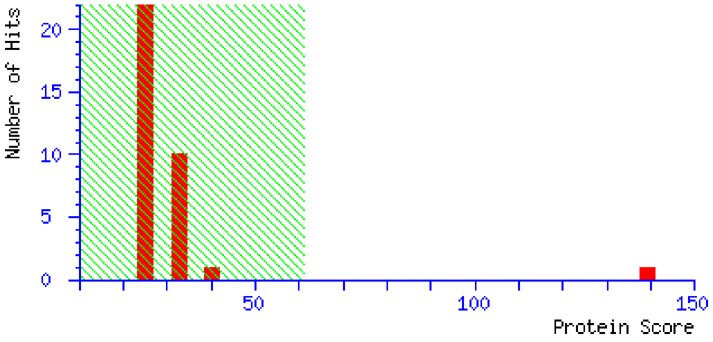
Calculated Mr: **25905** Calculated *p*I: **7.82**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: 71

NCBI accession No.: cassava4.1_013840m|PACid:17968262

Plant species: ***Manihot esculenta***

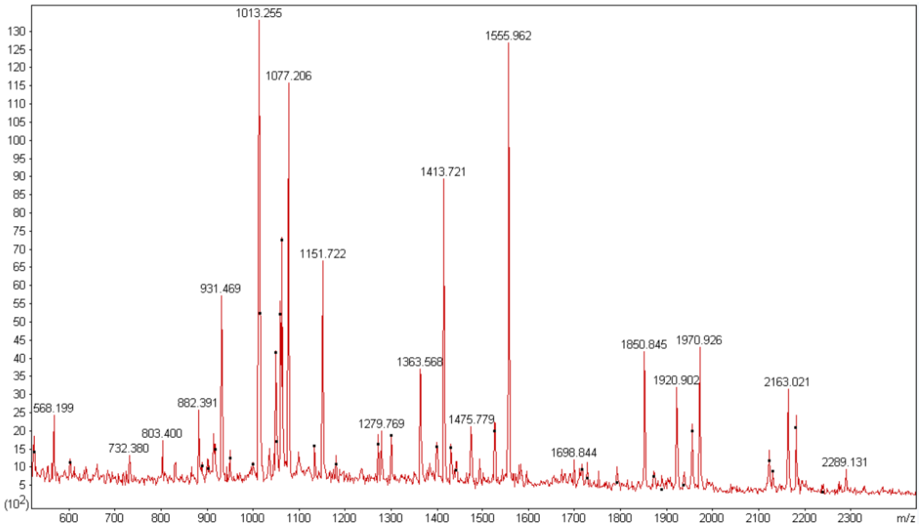
Protein name： **Proteasome subunit alpha type-2-A**

PFF Mascot score: [99] **Sequence coverage %: [7]**

Matched peptides No.: **[2]** p value: **0.0001**

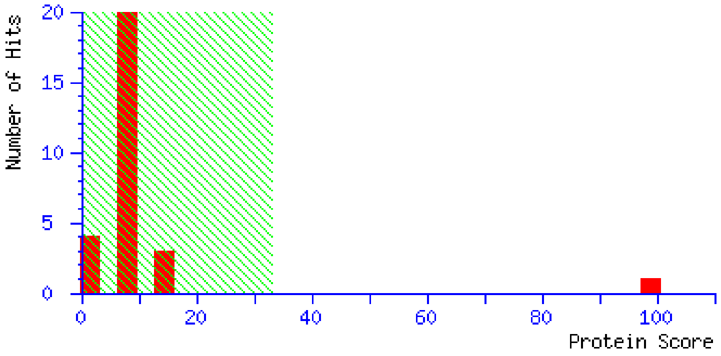
Calculated Mr: **29845** Calculated *p*I: **6.13**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **72**

NCBI accession No.: **cassava4.1_013784m|PACid:17965032**

Plant species: ***Manihot esculenta***

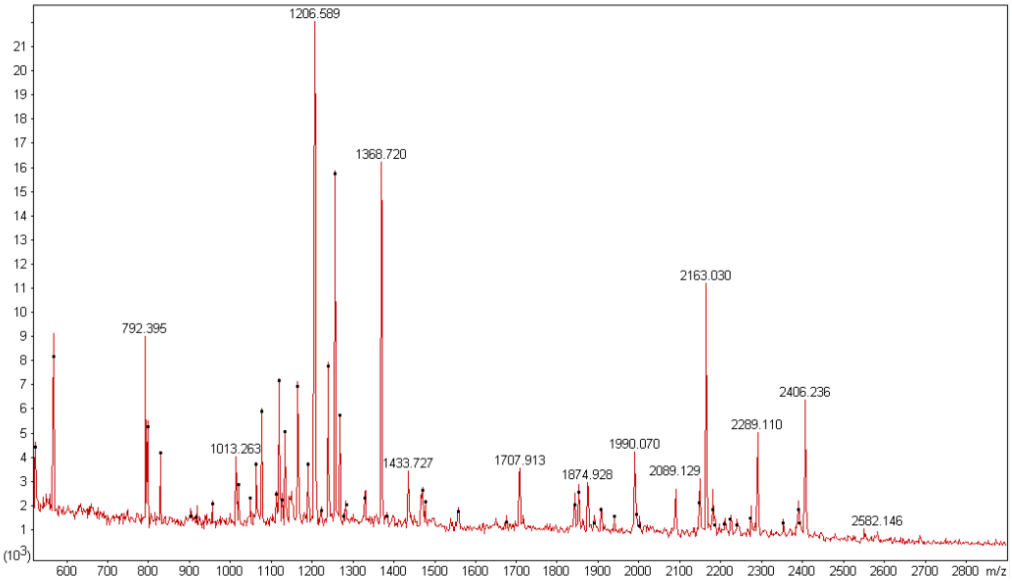
Protein name： **Superoxide dismutase [Fe] 2, chloroplastic**

PFF Mascot score: [94] **Sequence coverage %: [11]**

Matched peptides No.: **[3]** p value: **0.0079**

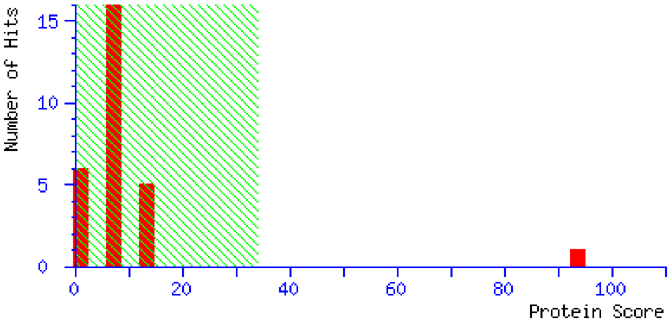
Calculated Mr: **30888** Calculated *p*I: **6.67**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **73**

NCBI accession No.: **cassava4.1_014423m|PACid:17980868**

Plant species: ***Manihot esculenta***

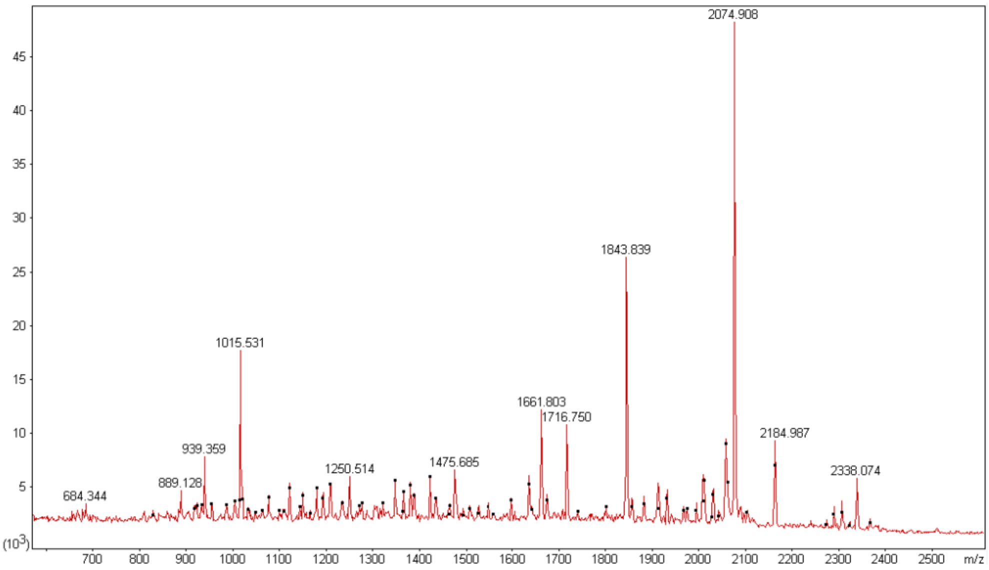
Protein name： **L-ascorbate peroxidase 1, cytosolic**

PFF Mascot score: [234] **Sequence coverage %:** [**17]**

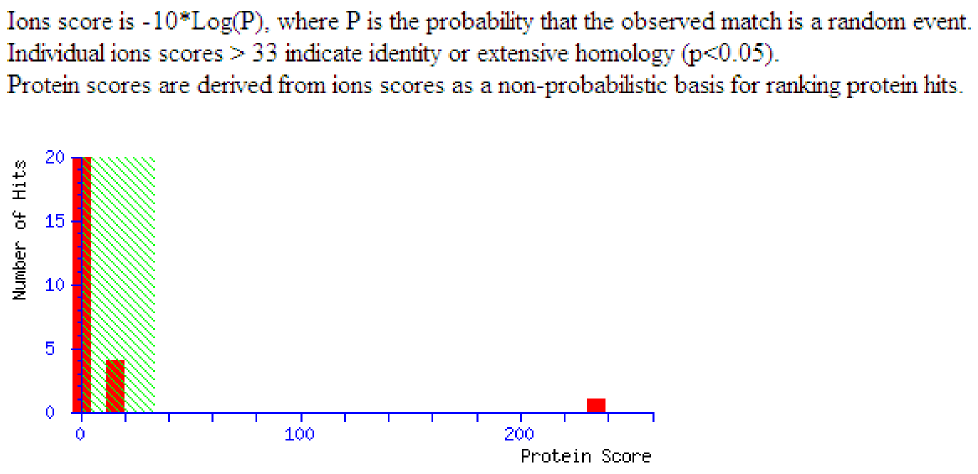
Matched peptides No.: **[3]** p value: **1.1e-010**

Calculated Mr: **28235** Calculated *p*I: **6.09**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Spot No.: **74**

NCBI accession No.: **cassava4.1_014432m|PACid:17967798**

Plant species: ***Manihot esculenta***

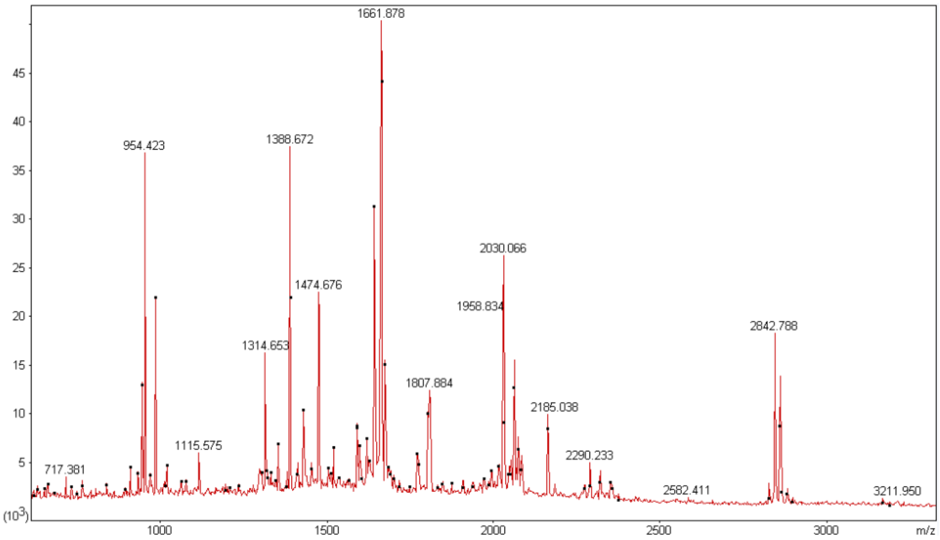
Protein name：**Triosephosphate isomerase, cytosolic**

PFF Mascot score: [194] **Sequence coverage %: [16]**

Matched peptides No.: **[3]** p value: **9.9e-006**

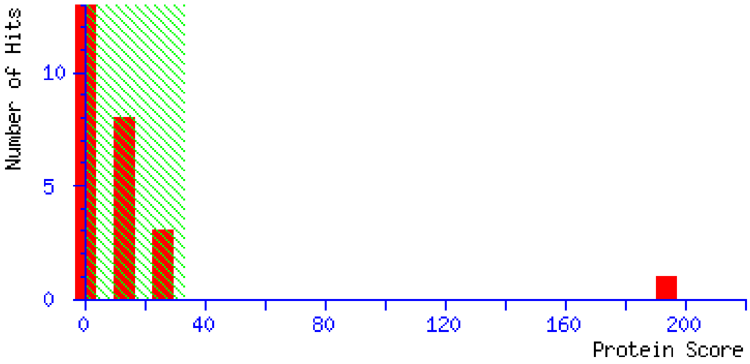
Calculated Mr: **27729** Calculated *p*I: **5.77**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **75**

NCBI accession No.: **cassava4.1_014799m|PACid:17972994**

Plant species: ***Manihot esculenta***

Protein name: **Proteasome subunit alpha type-6-A**

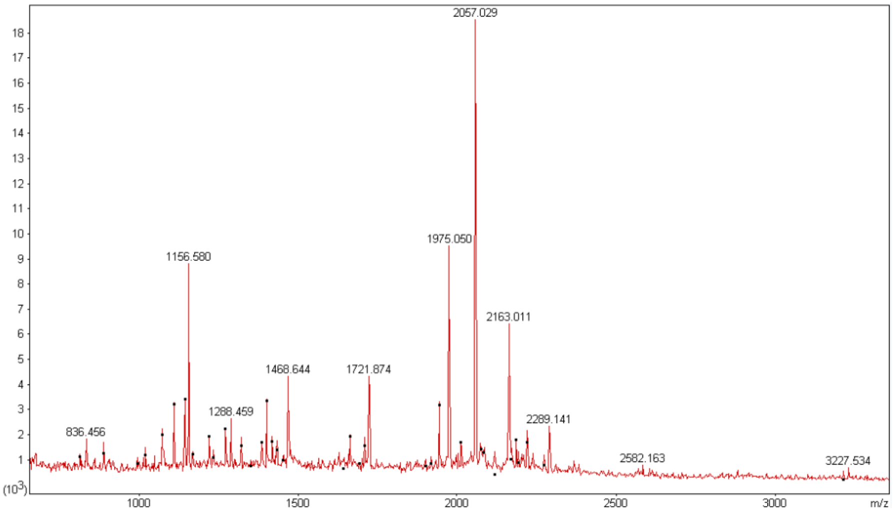
Mascot score: **131**

Sequence coverage %: **52**   p value: **`5.8e-009`**

Matched peptides No.: **14**   Total peptides No.: **35**

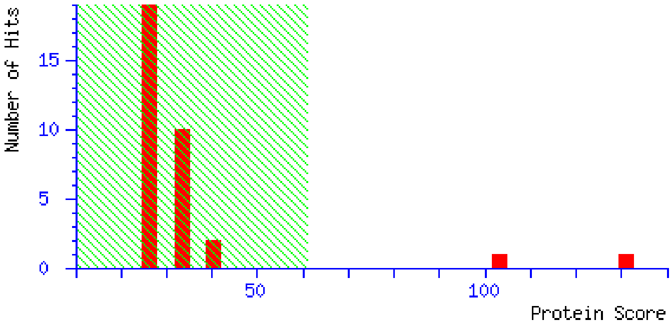
Calculated Mr: **27642**   Calculated *p*I: **6.19**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **76**

NCBI accession No.: **cassava4.1_010620m|PACid:17987783**

Plant species Manihot esculenta

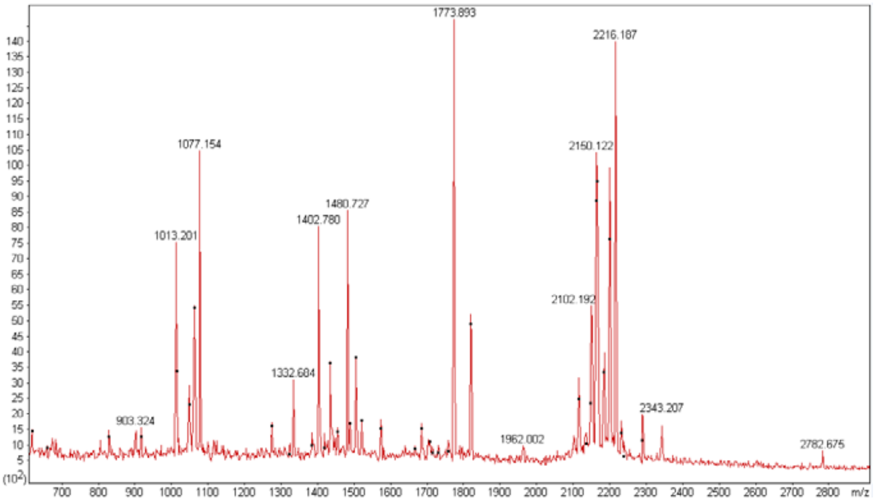
Protein name：**Thiamine thiazole synthase, chloroplastic**

PFF Mascot score: [162] **Sequence coverage %:** [8]

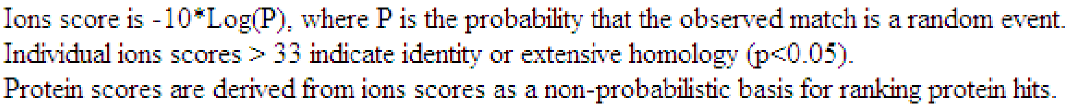
Matched peptides No.: **[2]** p value: **1.8e-007**

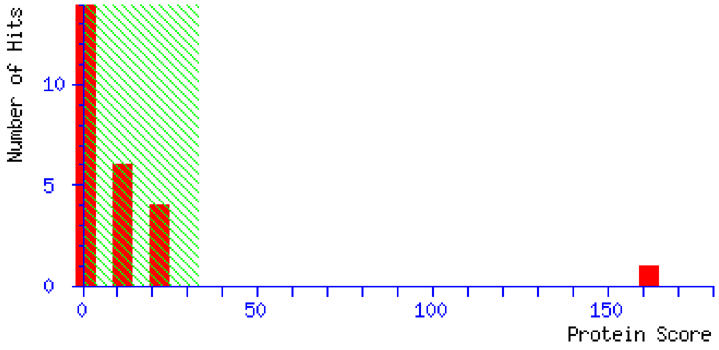
Calculated Mr: 37625 Calculated *p*I: **6.07**

Annotated PMF **spectra:**



Probability Based Mowse Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **77**

NCBI accession No.: **cassava4.1_010971m|PACid:17987784**

Plant species: ***Manihot esculenta***

Protein name： **Thiamine thiazole synthase, chloroplastic**

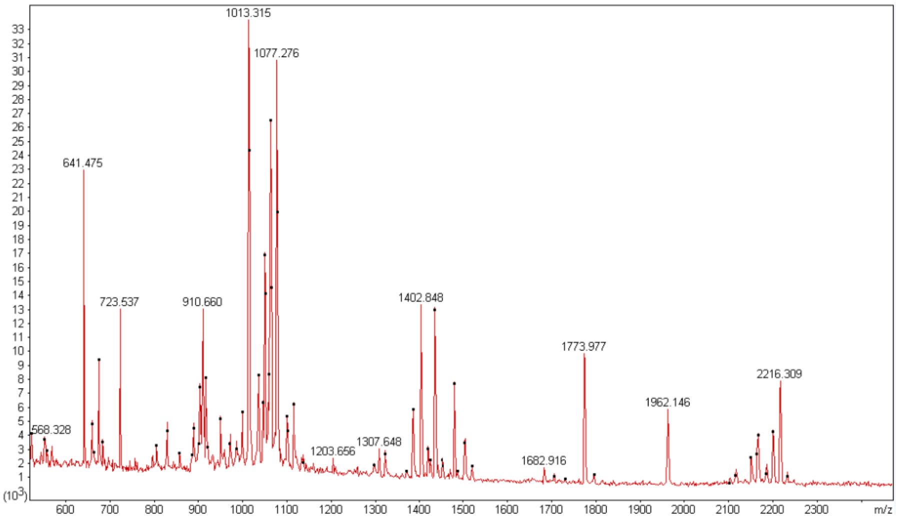
Mascot score: **88**

Sequence coverage %: **38**　　p value: **0.00011**

Matched peptides No.: **17**　　Total peptides No.: **70**

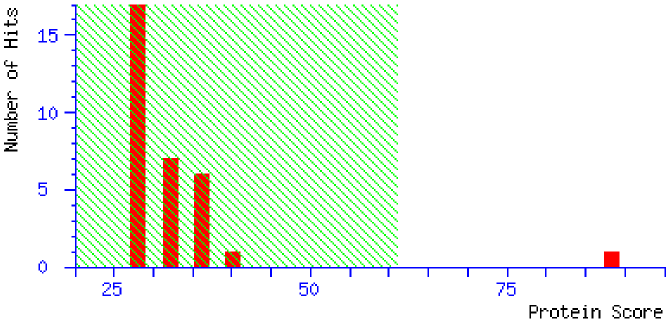
Calculated Mr: **36908**　　Calculated *p*I: **7.10**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **78**

NCBI accession No.: **cassava4.1_009245m|PACid:17963775**

Plant species: ***Manihot esculenta***

Protein name：**S-adenosylmethionine synthase 1**

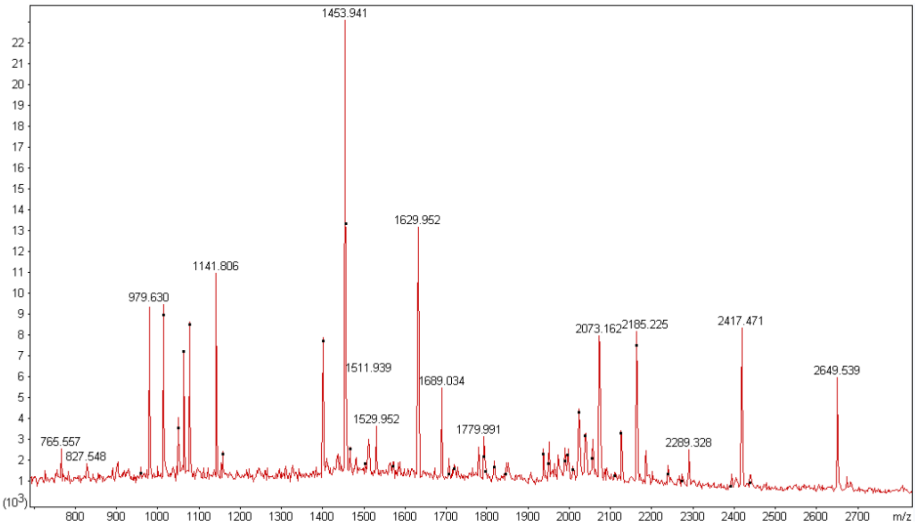
Mascot score: **119**

Sequence coverage %: **55**　　　p value: **9.2e-008**

Matched peptides No.: **16**　　　Total peptides No.: **54**

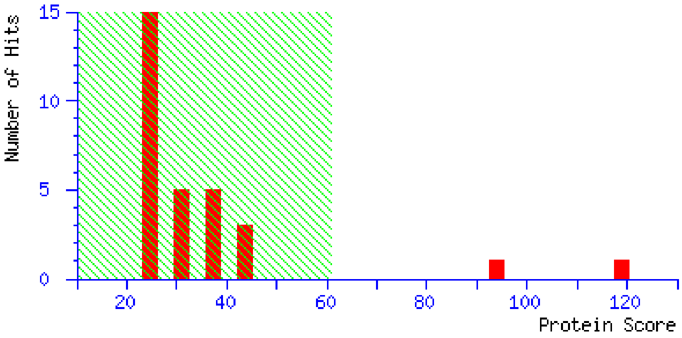
Calculated Mr: **43709**　　　Calculated *p*I: **5.68**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **79**

NCBI accession No.: **cassava4.1_011550m|PACid:17993466**

Plant species: ***Manihot esculenta***

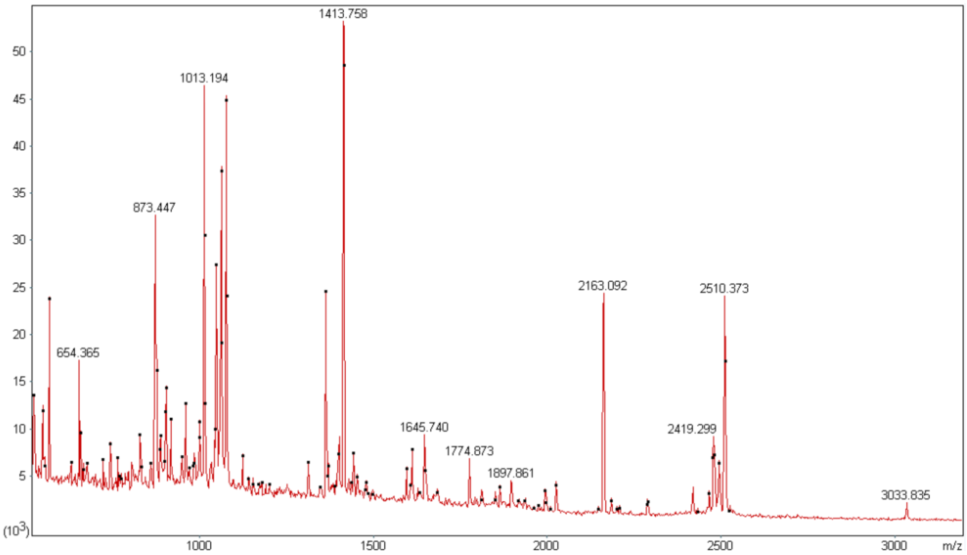
Protein name：**predicted protein** Mascot score: **108**

Sequence coverage %: **50** p value: **`1.2e-006`**

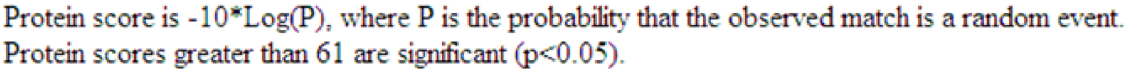
Matched peptides No.: **17** Total peptides No.: **67**

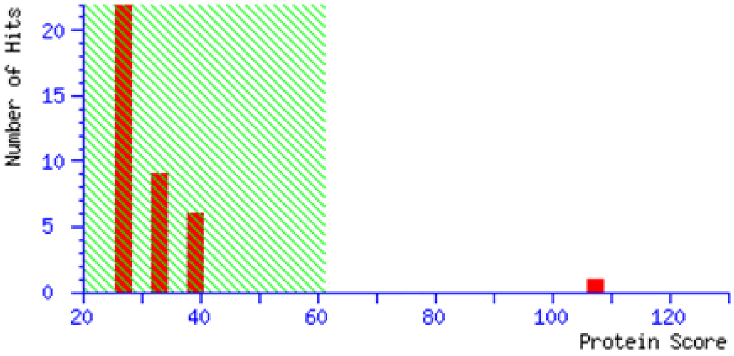
Calculated Mr: **36178** Calculated *p*I: **6.09**

Annotated PMF **spectra:**



Probability Based Mowse Score:


Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **80**

NCBI accession No.: **cassava4.1_009410m|PACid:17973470**

Plant species: ***Manihot esculenta***

Protein name：**UDP-D-apiose/UDP-D-xylose synthase 1**

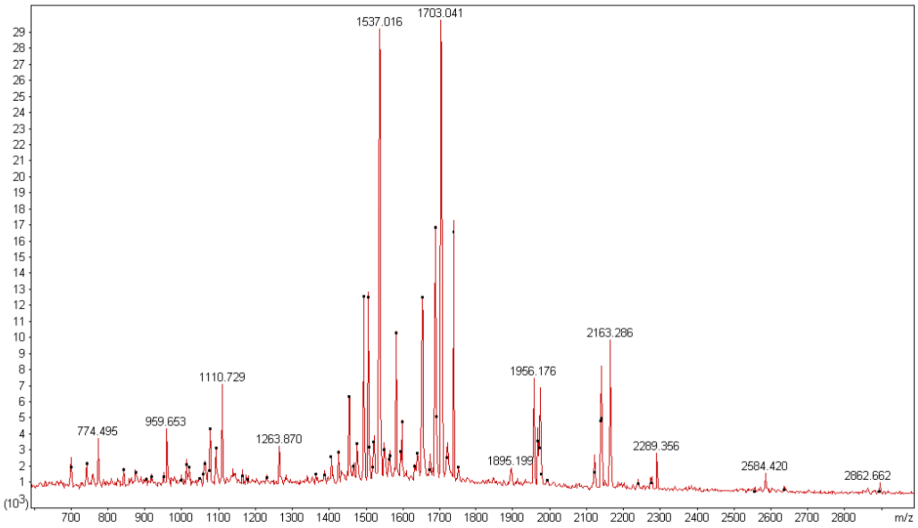
Mascot score: **163**

Sequence coverage %: **51**　　p value: **3.7e-012**

Matched peptides No.: **24**　　Total peptides No.: **73**

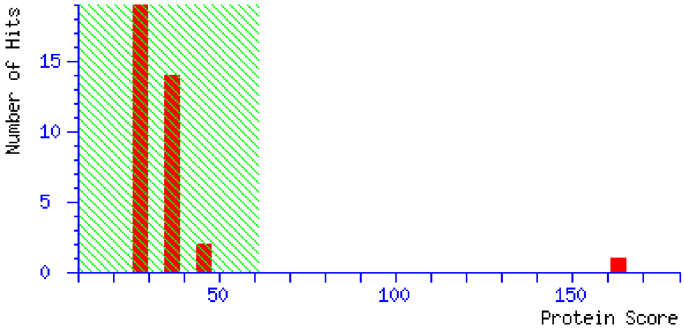
Calculated Mr: **43967**　　Calculated *p*I: **6.03**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **81**

NCBI accession No.: **cassava4.1_008604m|PACid:17979400**

Plant species: ***Manihot esculenta***

Protein name：**Cytosolic isocitrate dehydrogenase [NADP]**

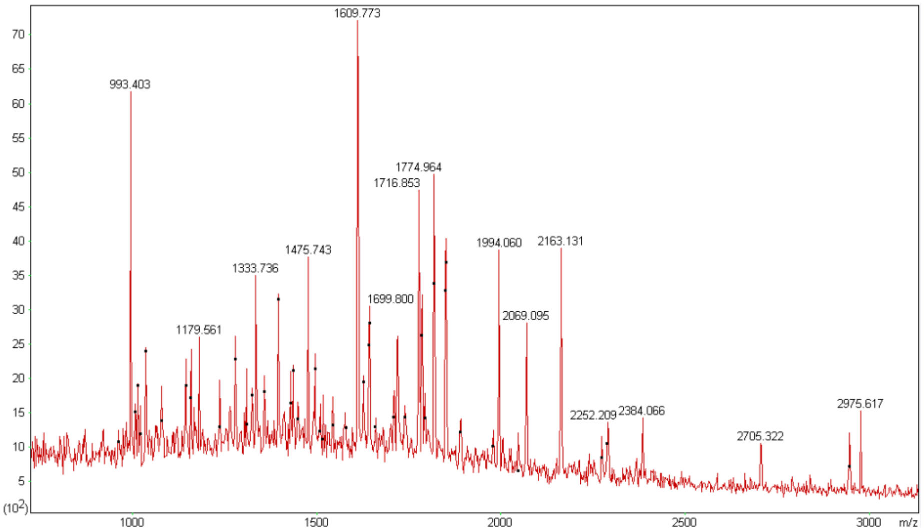
Mascot score: **115**

Sequence coverage %: **45** p value: **2.3e-007**

Matched peptides No.: **17** Total peptides No.: **49**

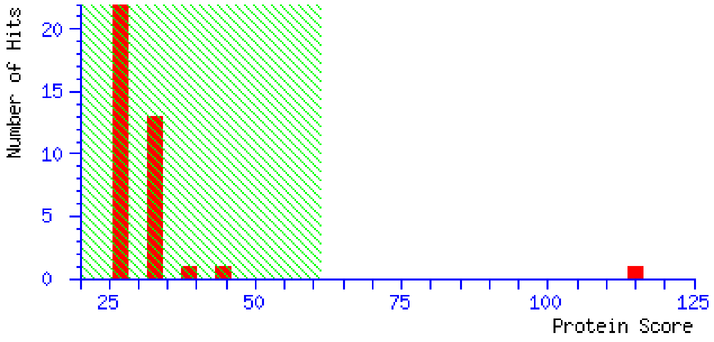
Calculated Mr: **46844** Calculated *p*I: **6.07**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **82**

NCBI accession No.: **cassava4.1_009808m|PACid:17965663**

Plant species: ***Manihot esculenta***

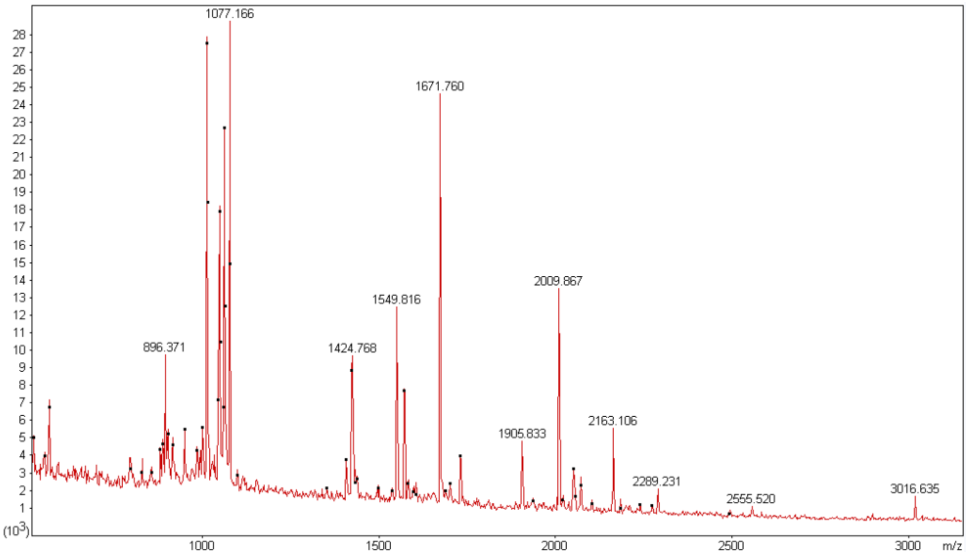
Protein name： **GDP-mannose 3,5-epimerase** Mascot score: **76**

Sequence coverage %: **41** p value: **0.002**

Matched peptides No.: **14** Total peptides No.: **58**

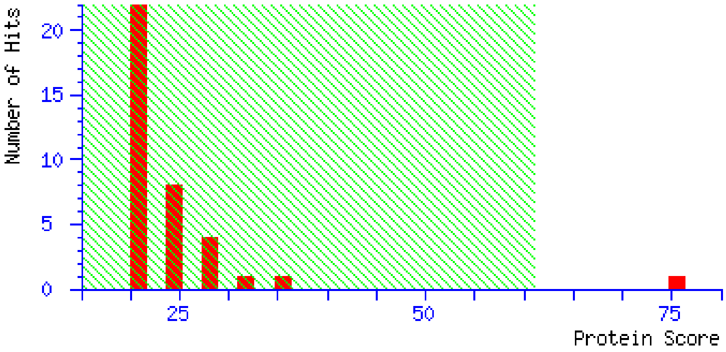
Calculated Mr: **42843** Calculated *p*I: **6.05**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **83**

NCBI accession No.: **cassava4.1_007673m|PACid:17979089**

Plant species: ***Manihot esculenta***

Protein name： **Bifunctional enolase 2/transcriptional activator**

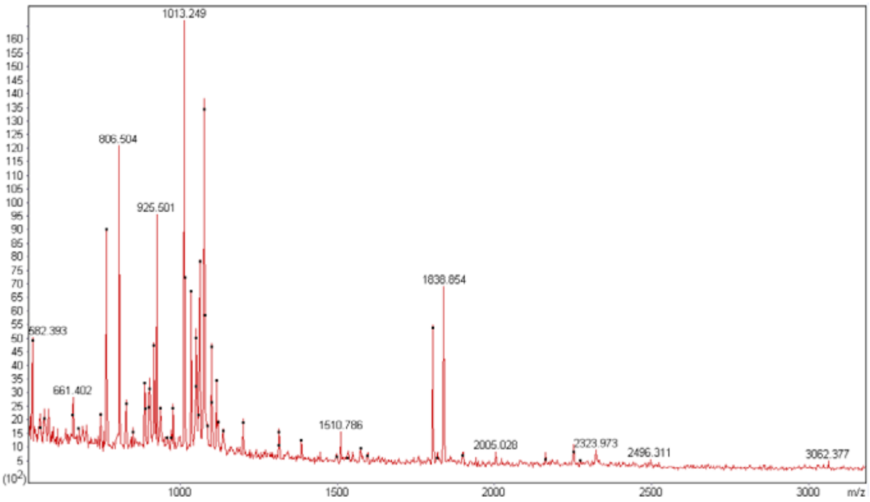
Mascot score: **124**

Sequence coverage %: **42** p value: **2.9e-008**

Matched peptides No.: **17** Total peptides No.: **57**

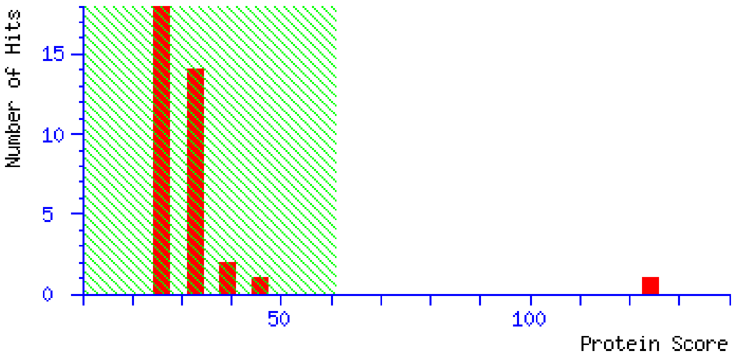
Calculated Mr: **48058** Calculated *p*I: **5.86**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **84**

NCBI accession No.: **cassava4.1_007678m|PACid:17961094**

Plant species: ***Manihot esculenta***

Protein name：**Bifunctional enolase 2/transcriptional activator**

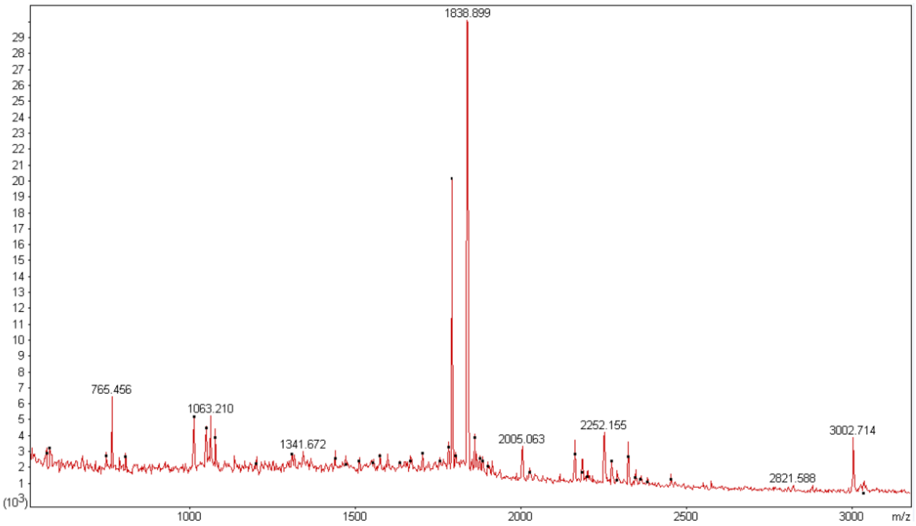
Mascot score: **100**

Sequence coverage %: **46** p value: **0.0000073**

Matched peptides No.: **14** Total peptides No.: **45**

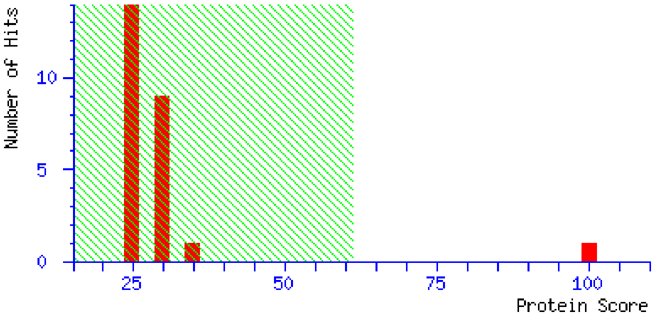
Calculated Mr: **47854** Calculated *p*I: **5.86**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **85**

NCBI accession No.: **cassava4.1_033530m|PACid:17973804**

Plant species: ***Manihot esculenta***

Protein name： **ATP synthase F1 subunit 1**

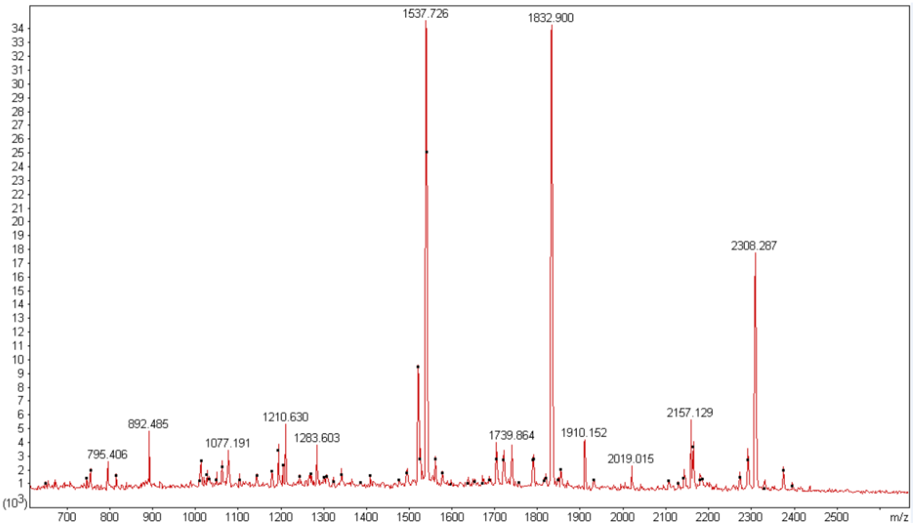
Mascot score: **151** p value: **1.3e-09**

Sequence coverage %: **42**

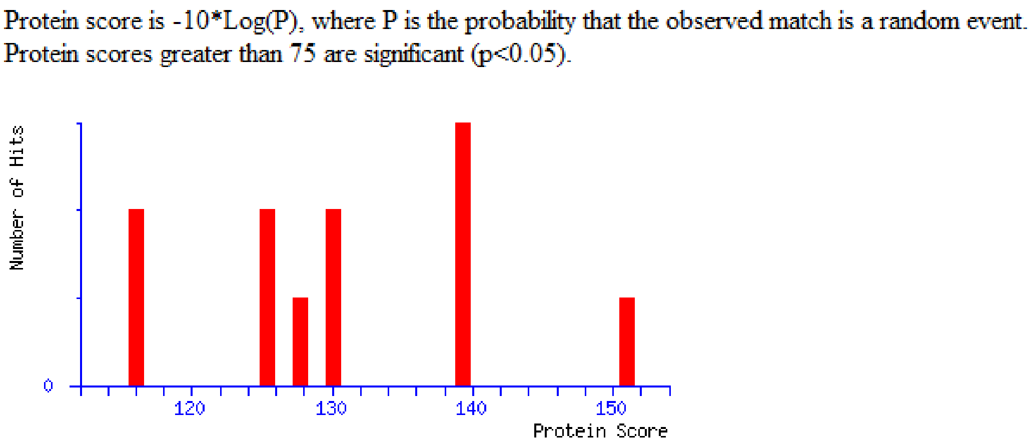
Matched peptides No.: **20** Total peptides No.: **56**

Calculated Mr: **55536** Calculated *p*I: **6.02**

Annotated PMF **spectra:**



Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 75 are significant (p<0.05).

Spot No.: **86**

NCBI accession No.: **cassava4.1_004164m|PACid:17985770**

Plant species: ***Manihot esculenta***

Protein name： **malic enzyme, putative**

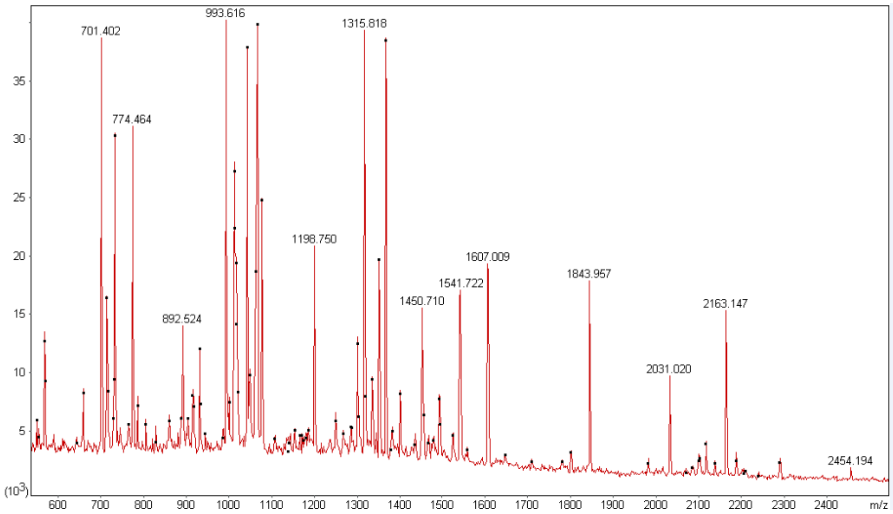
Mascot score: **177**

Sequence coverage %: **47**　　p value: **1.5e-013**

Matched peptides No.: **33**　　Total peptides No.: **90**

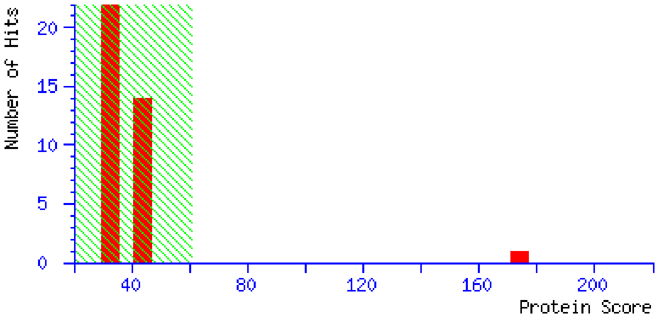
Calculated Mr: **65246**　　Calculated *p*I: **6.03**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **87**

NCBI accession No.: **cassava4.1_007673m|PACid:17979089**

Plant species: ***Manihot esculenta***

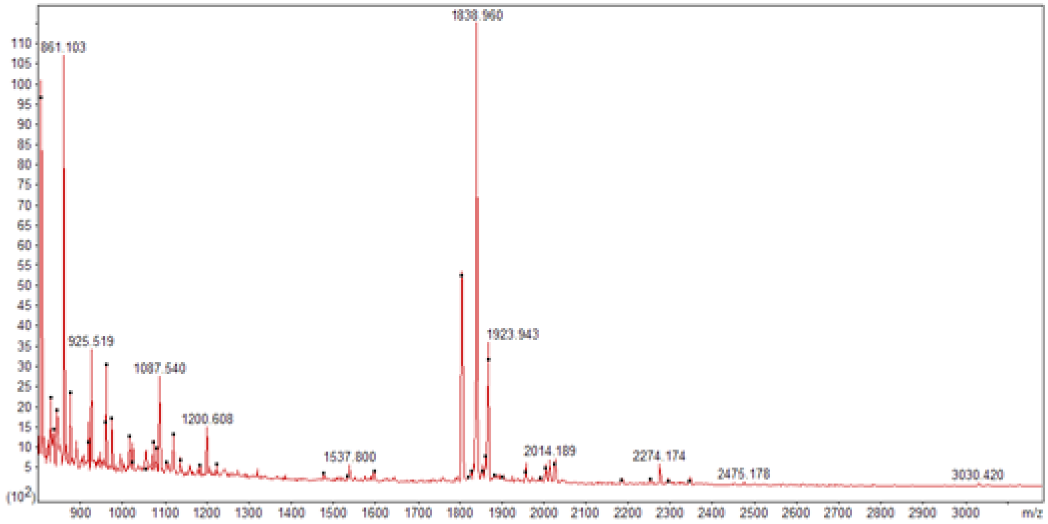
Protein name：**Bifunctional enolase 2/transcriptional activator**

PFF Mascot score: **[150]** Sequence coverage %: **[7]**

Matched peptides No.: **[2]** p value: **1e-013**

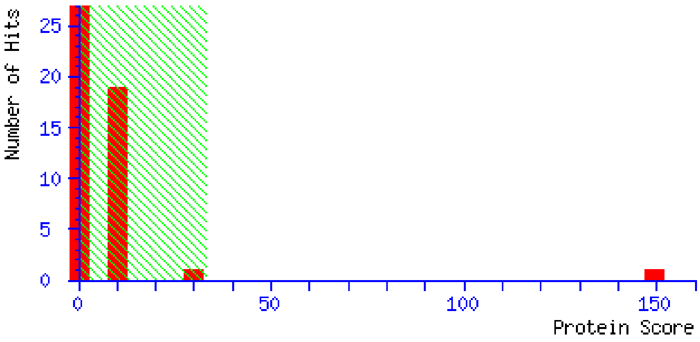
Calculated Mr: **48058** Calculated *p*I: **5.86**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **88**

NCBI accession No.: **cassava4.1_007678m|PACid:17961094**

Plant species: ***Manihot esculenta***

Protein name：**Bifunctional enolase 2/transcriptional activator**

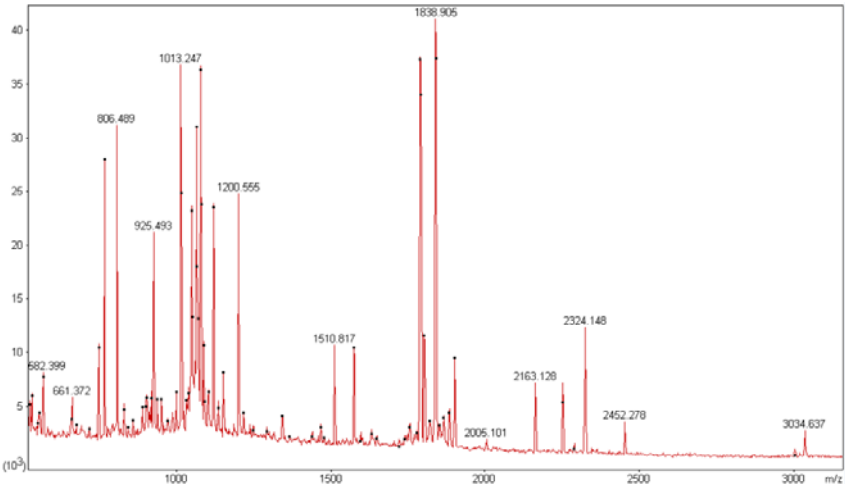
Mascot score: **160**

Sequence coverage %: **62**　　p value: **7.3e-012**

Matched peptides No.: **25**　　Total peptides No.: **78**

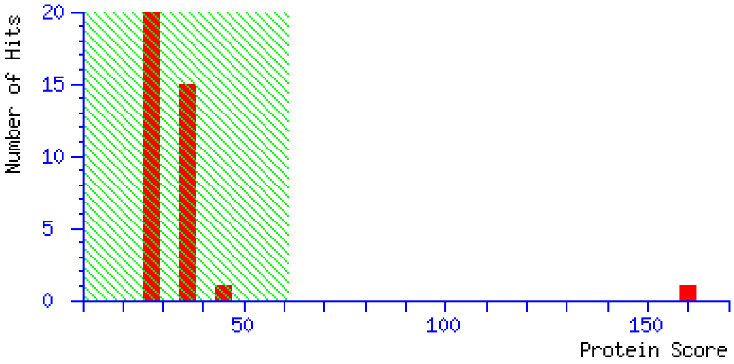
Calculated Mr: **47854**　　Calculated *p*I: **5.86**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **89**

NCBI accession No.: **cassava4.1_003677m|PACid:17968299**

Plant species: ***Manihot esculenta***

Protein name： **V-type proton ATPase catalytic subunit A**

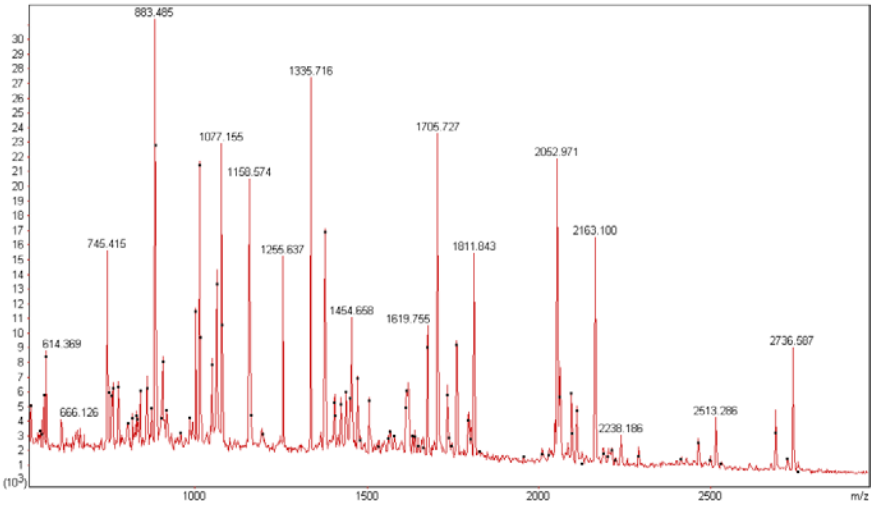
Mascot score: **234**

Sequence coverage %: **61** p value: **2.9e-019**

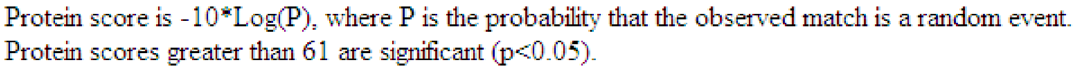
Matched peptides No.: **41** Total peptides No.: **95**

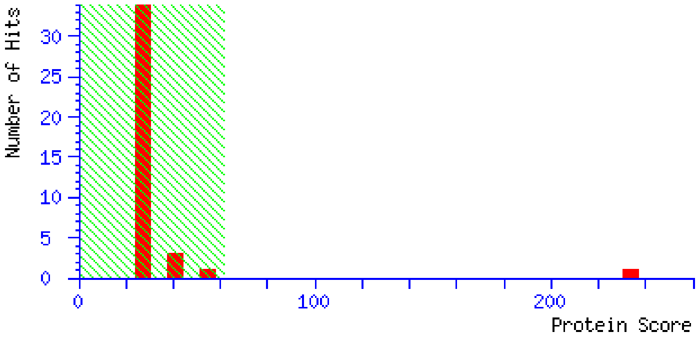
Calculated Mr: **68989** Calculated *p*I: **5.29**

Annotated PMF **spectra:**



Probability Based Mowse Score:


Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **90**

NCBI accession No.: **cassava4.1_003676m|PACid:17974360**

Plant species: ***Manihot esculenta***

Protein name： **V-type proton ATPase catalytic subunit A**

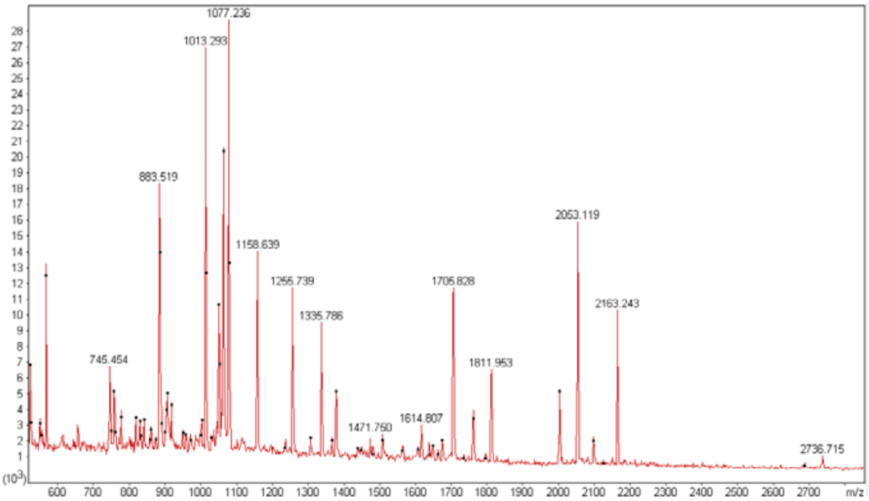
Mascot score: **194**

Sequence coverage %: **49**   p value: **2.9e-015**

Matched peptides No.: **30**   Total peptides No.: **68**

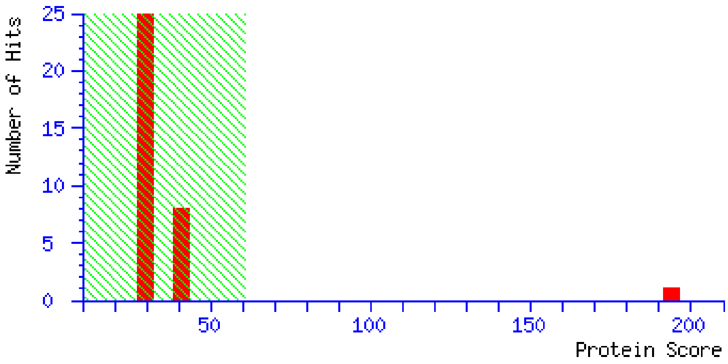
Calculated Mr: **68956**   Calculated *p*I: **5.34**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **91**

NCBI accession No.: **cassava4.1_005518m|PACid:17993865**

Plant species: ***Manihot esculenta***

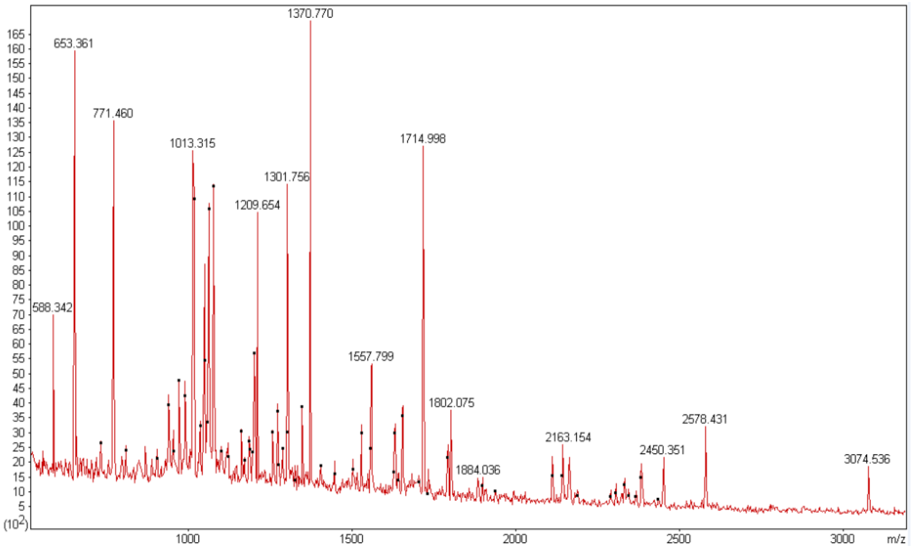
Protein name： **Glucose-1-phosphate adenylyltransferase small subunit, chloroplastic** Mascot score: **81**

Sequence coverage %: **34** p value: **0.00053**

Matched peptides No.: **16** Total peptides No.: **63**

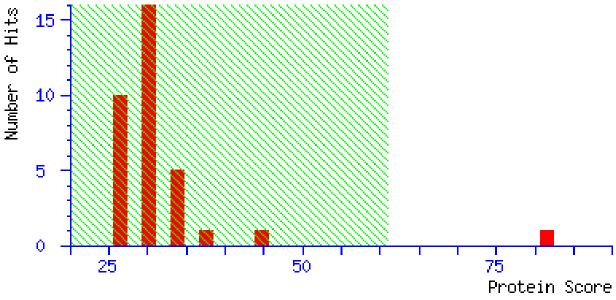
Calculated Mr: **57581** Calculated *p*I: **6.69**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **92**

NCBI accession No.: **cassava4.1_004164m|PACid:17985770**

Plant species: ***Manihot esculenta***

Protein name： **malic enzyme, putative**

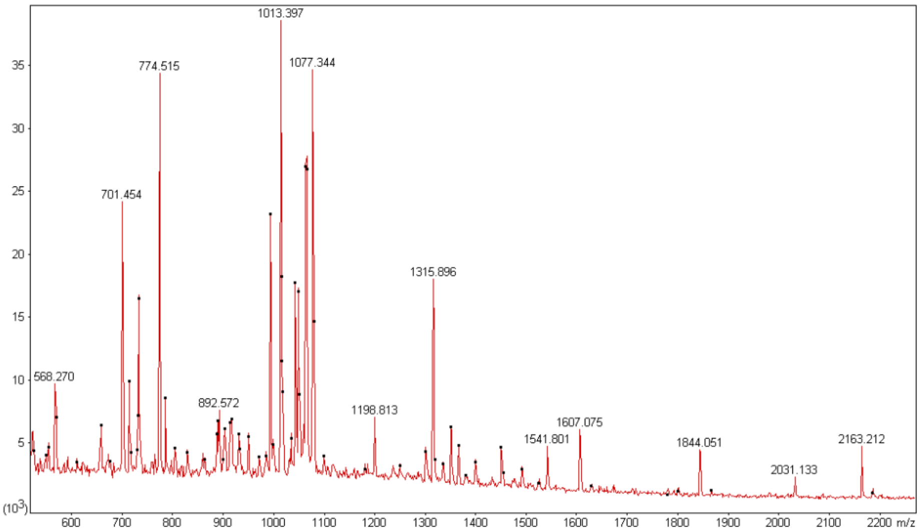
Mascot score: **154**

Sequence coverage %: **35**   p value: **2.9e-11**

Matched peptides No.: **26**   Total peptides No.: **66**

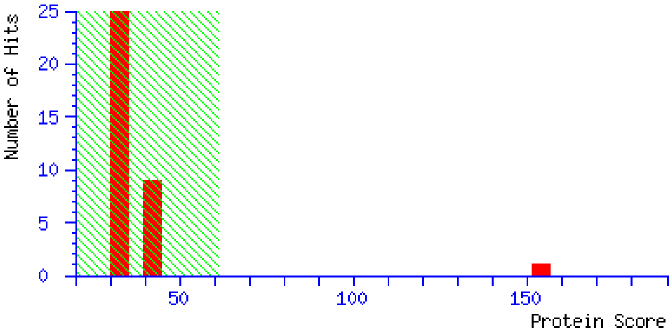
Calculated Mr: **65246**   Calculated *p*I: **6.03**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **93**

NCBI accession No.: **cassava4.1_014432m|PACid:17967798**

Plant species: ***Manihot esculenta***

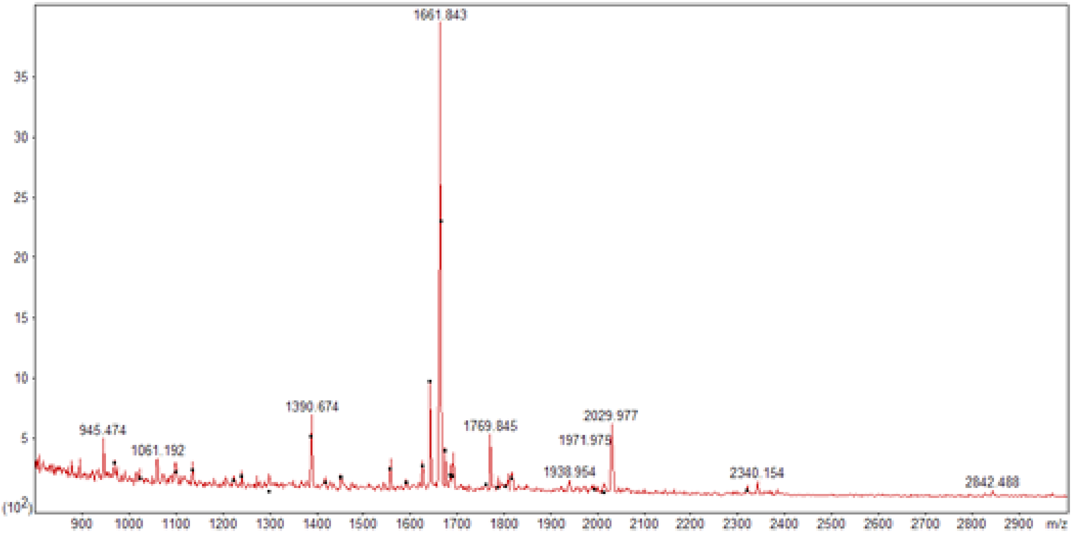
Protein name：**Triosephosphate isomerase, cytosolic**

PFF Mascot score: **[114]**　　　Sequence coverage %: **[23]**

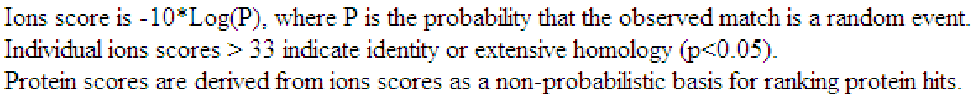
Matched peptides No.: **[4]**　　　p value: **2e-005**

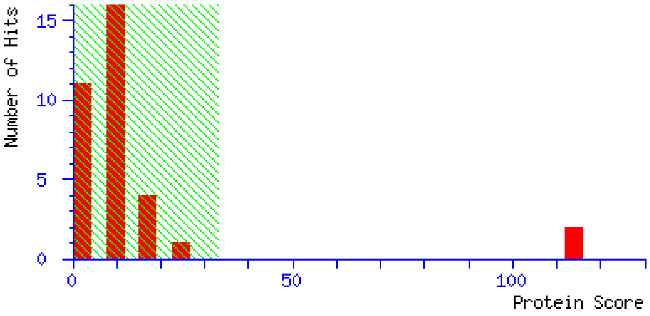
Calculated Mr: 27729　　　Calculated *p*I: **5.77**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **94**

NCBI accession No.: **cassava4.1_002466m|PACid:17978799**

Plant species: ***Manihot esculenta***

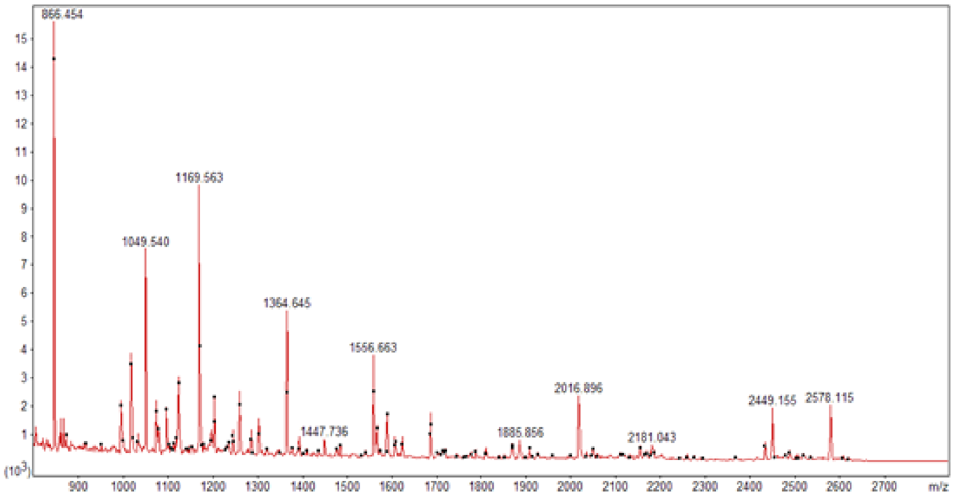
Protein name：**Alpha-glucan phosphorylase 1**

PFF Mascot score: **[278]** Sequence coverage %: **[12]**

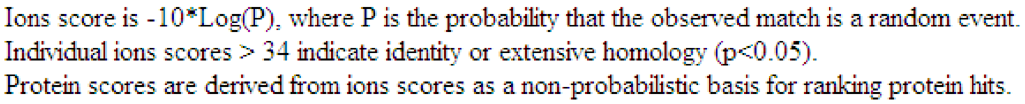
Matched peptides No.: **[7]** p value: **1.1e-007**

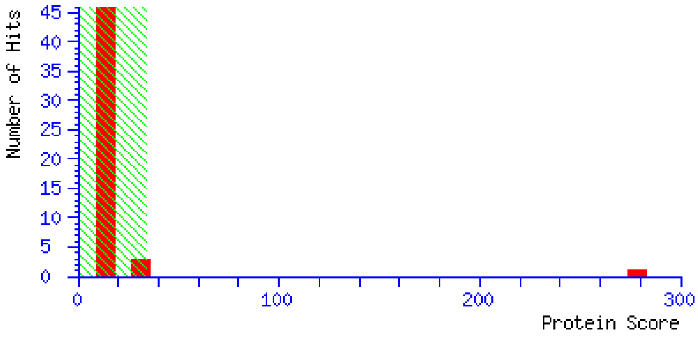
Calculated Mr: 81918 Calculated *p*I: **8.50**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **95**

NCBI accession No.: **cassava4.1_009779m|PACid:17990964**

Plant species: ***Manihot esculenta***

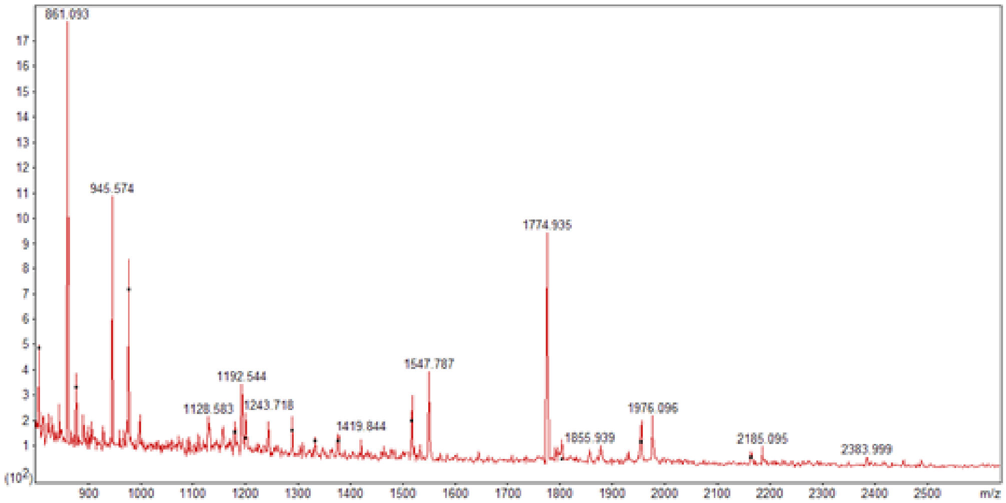
Protein name：**Actin-7**

PFF Mascot score: **[108]** Sequence coverage %: **[9]**

Matched peptides No.: **[3]** p value: **9.7e-0086**

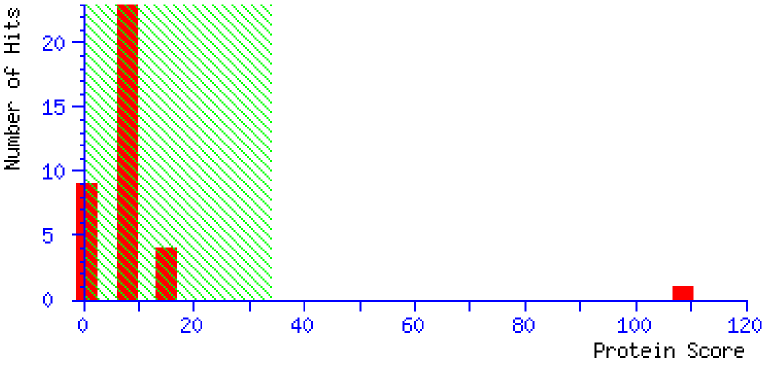
Calculated Mr: 41897 Calculated *p*I: **5.31**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **96**

NCBI accession No.: **cassava4.1_009779m|PACid:17990964**

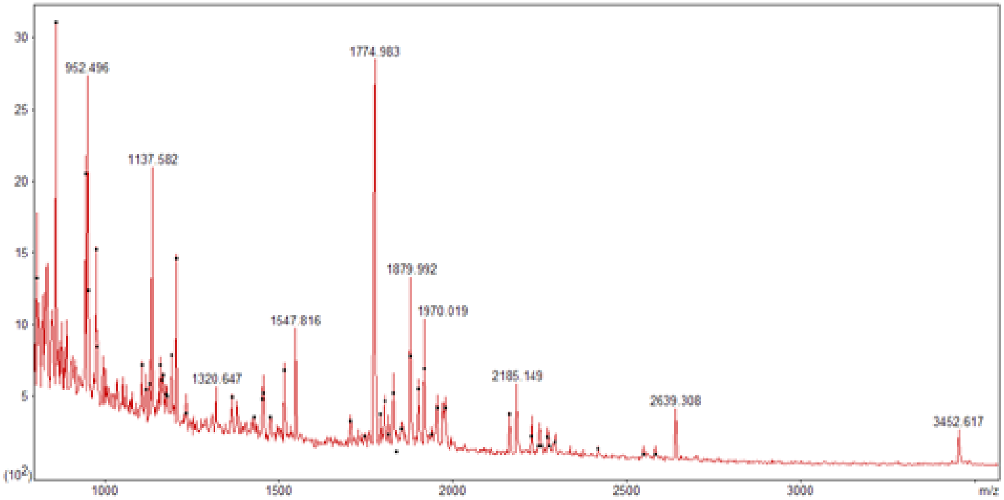
Plant species: ***Manihot esculenta***Protein name： **Actin-7**

PFF Mascot score: **[77]** Sequence coverage %: **[6]**

Matched peptides No.: **[2]** p value: **0.00032**

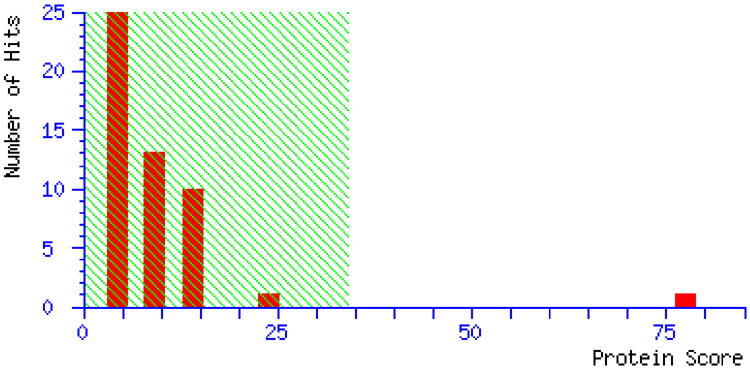
Calculated Mr: 41897 Calculated *p*I: **5.31**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **97**

NCBI accession No.: **cassava4.1_011729m|PACid:17989246**

Plant species: ***Manihot esculenta***

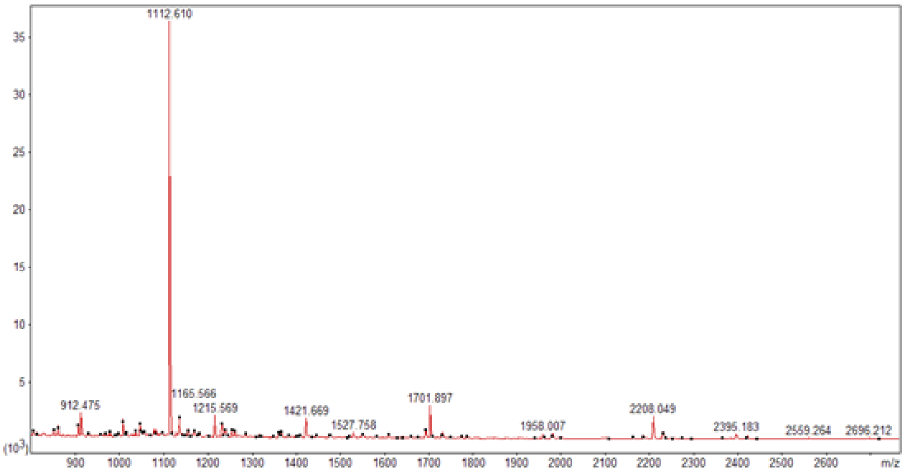
Protein name：**nitrile-specifier protein 5-like**

PFF Mascot score: **[165]** Sequence coverage %: **[24]**

Matched peptides No.: **[7]** p value: **0.00081**

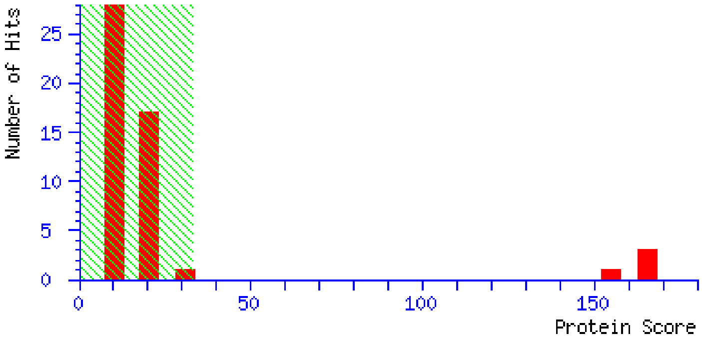
Calculated Mr: 35840 Calculated *p*I: **5.49**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **98**

NCBI accession No.: **cassava4.1_016053m|PACid:17985673**

Plant species: ***Manihot esculenta***

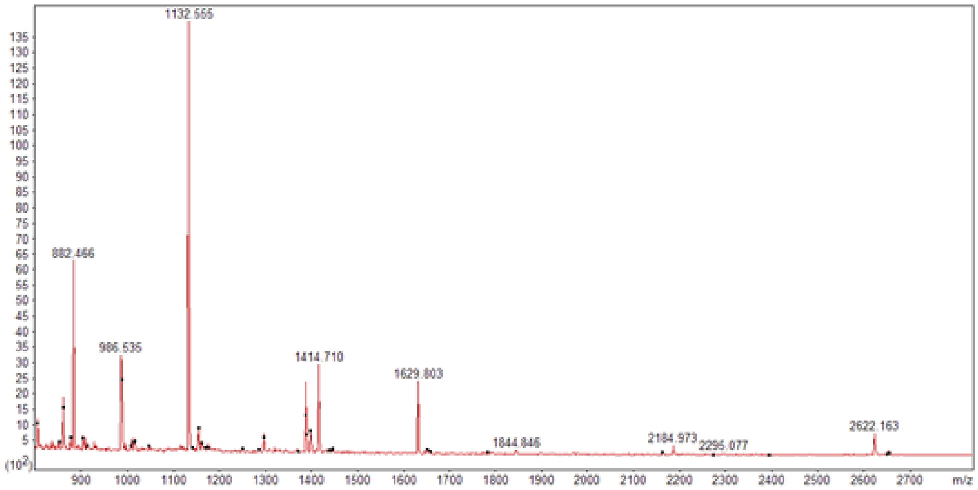
Protein name：**Abscisic acid receptor PYR1**

PFF Mascot score: **[190]** Sequence coverage %: **[28]**

Matched peptides No.: **[4]** p value: **2.2e-006**

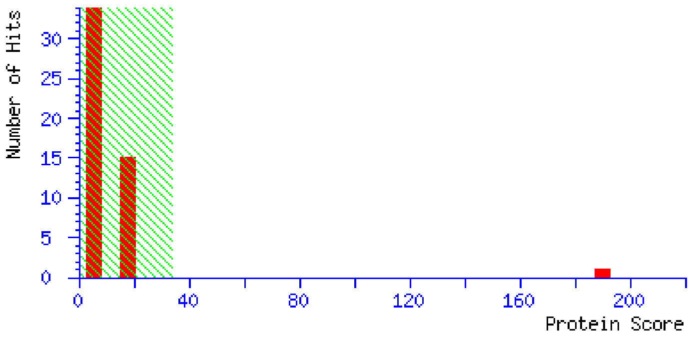
Calculated Mr: 23981 Calculated *p*I: **5.26**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **99**

NCBI accession No.: **cassava4.1_012016m|PACid:17981009**

Plant species: ***Manihot esculenta***

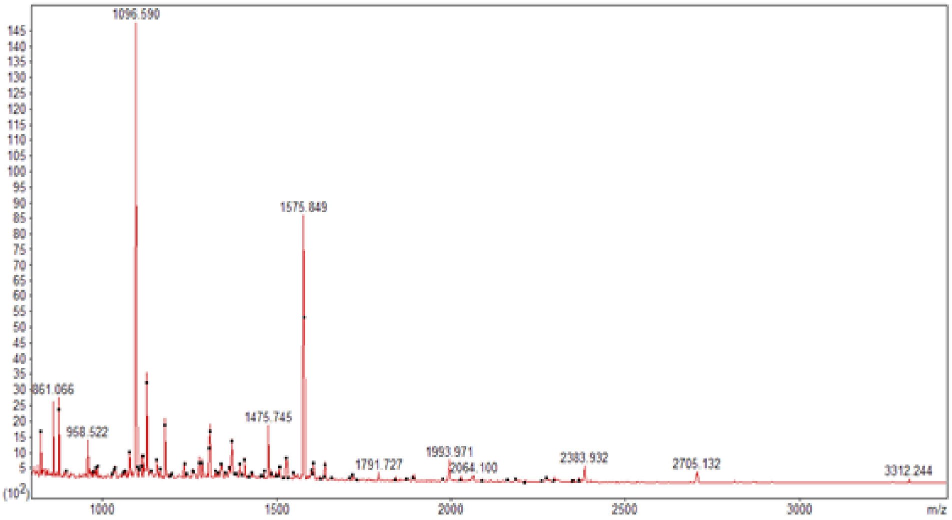
Protein name：**Triosephosphate isomerase, chloroplastic**

PFF Mascot score: **[210]** Sequence coverage %: **[15]**

Matched peptides No.: **[4]** p value: **1.5e-007**

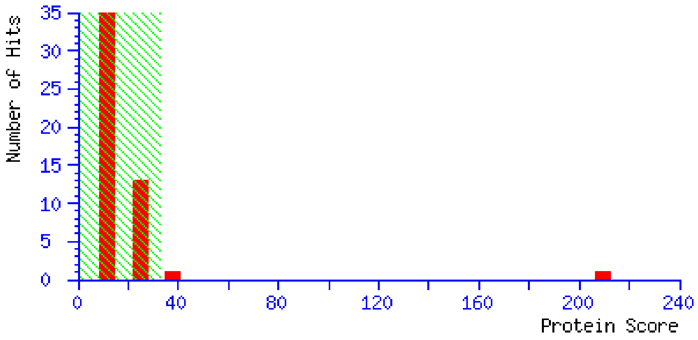
Calculated Mr: 34643 Calculated *p*I: **6.96**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **100**

NCBI accession No.: **cassava4.1_013157m|PACid:17980169**

Plant species: ***Manihot esculenta***

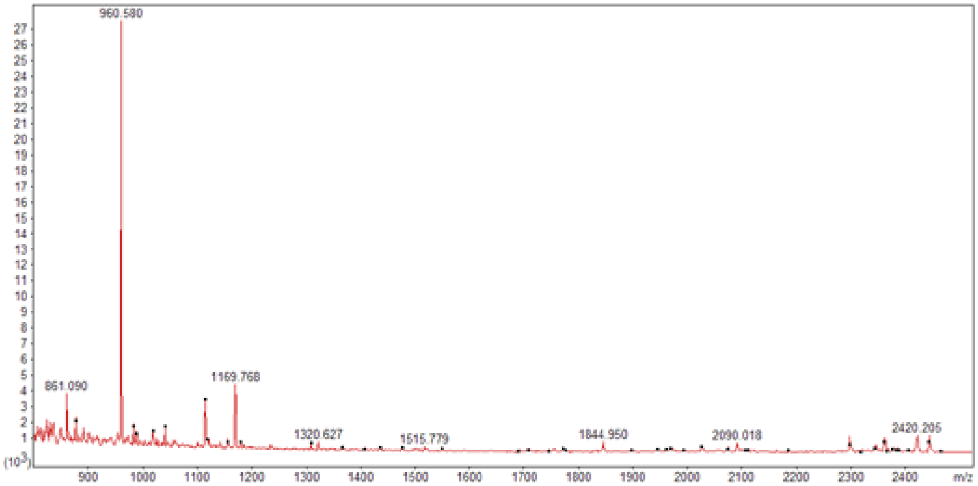
Protein name：**Dienelactone hydrolase domain-containing protein**

PFF Mascot score: **[161]** Sequence coverage %: **[17]**

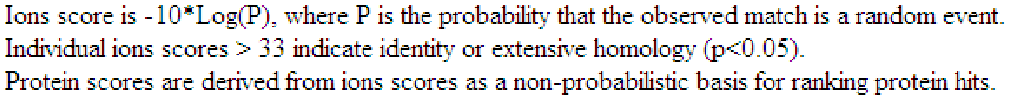
Matched peptides No.: **[3]** p value: **1.6e-009**

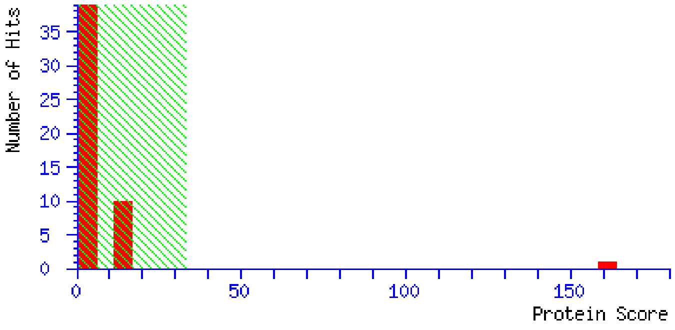
Calculated Mr: 31535 Calculated *p*I: **6.54**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **101**

NCBI accession No.: **cassava4.1_016210m|PACid:17989119**

Plant species: ***Manihot esculenta***

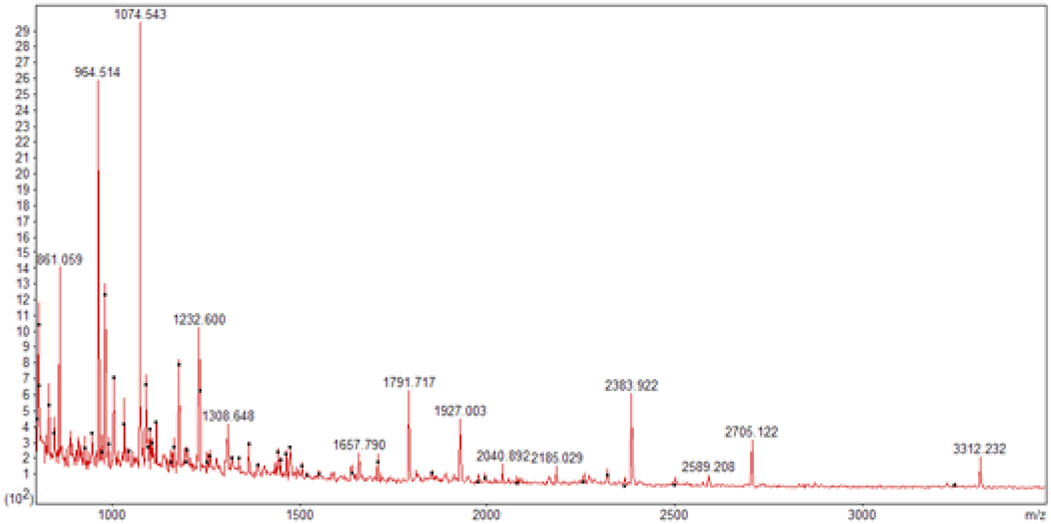
Protein name： **UMP-CMP kinase 3**

PFF Mascot score: **[67]** Sequence coverage %: **[8]**

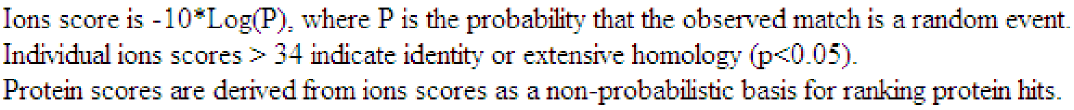
Matched peptides No.: **[2]** p value: **0.0035**

Calculated Mr: 23568 Calculated *p*I: **5.34**

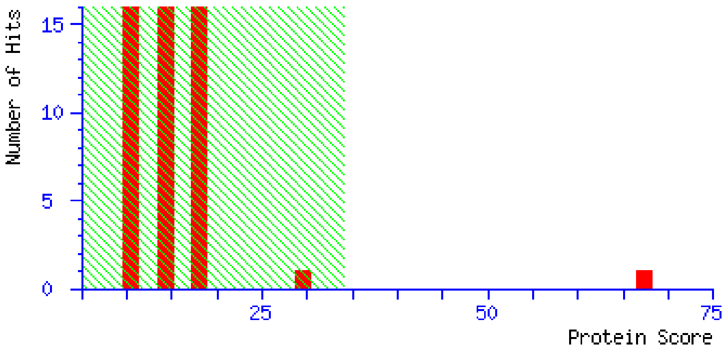
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **102**

NCBI accession No.: **cassava4.1_009779m|PACid:17990964**

Plant species: ***Manihot esculenta***

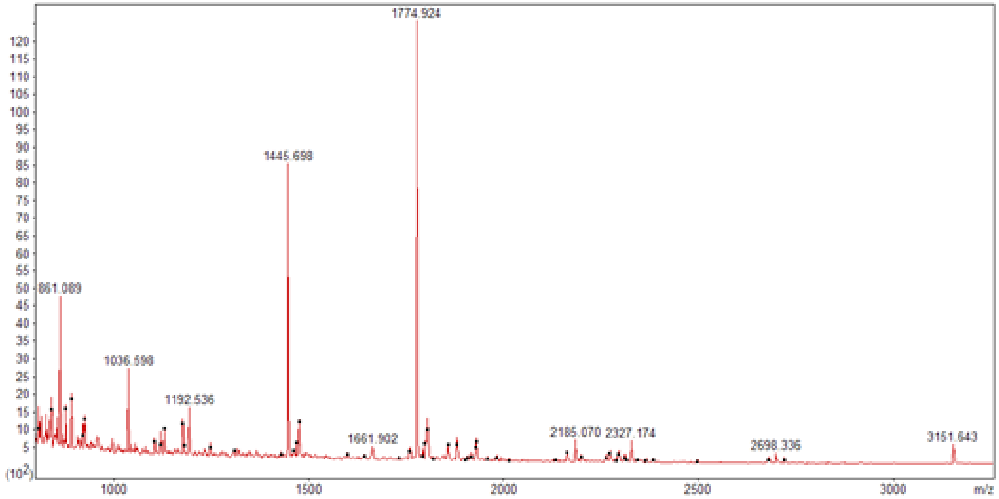
Protein name： **Actin-7**

PFF Mascot score: **[189]** Sequence coverage %: **[24]**

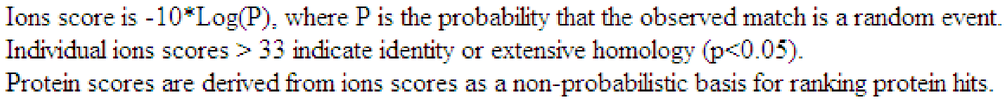
Matched peptides No.: **[5]** p value: **1.6e-007**

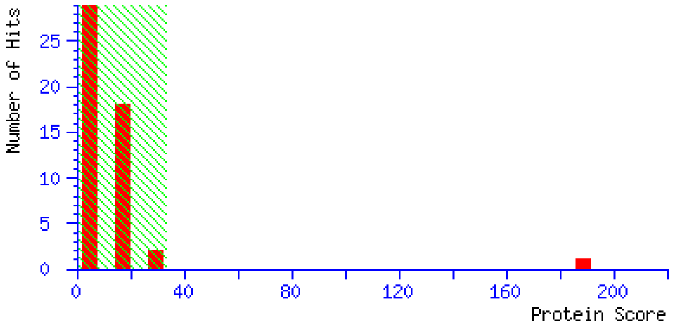
Calculated Mr: 41897 Calculated *p*I: **5.31**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **103**

NCBI accession No.: **cassava4.1_016465m|PACid:17964780**

Plant species: ***Manihot esculenta***

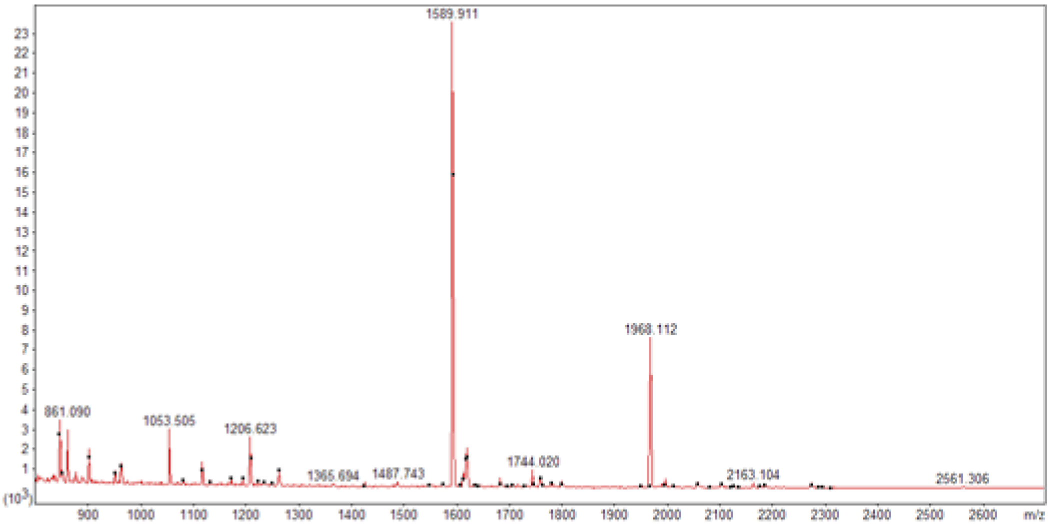
Protein name：**Proteasome subunit beta type-3-A**

PFF Mascot score: **[158]** Sequence coverage %: **[11]**

Matched peptides No.: **[2]** p value: **1.1e-008**

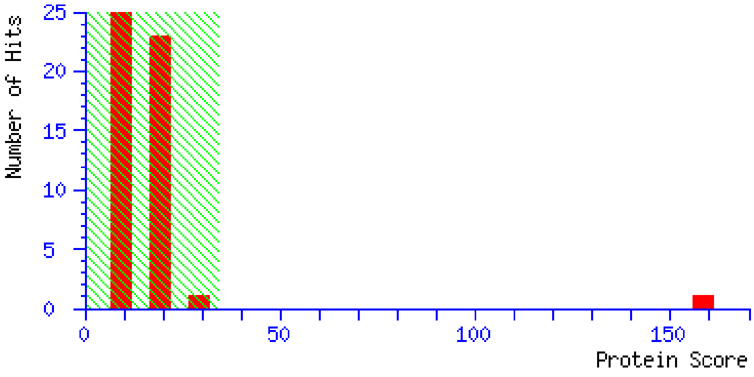
Calculated Mr: 23143 Calculated *p*I: **5.33**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **104**

NCBI accession No.: **cassava4.1_018289m|PACid:17961715**

Plant species: ***Manihot esculenta***

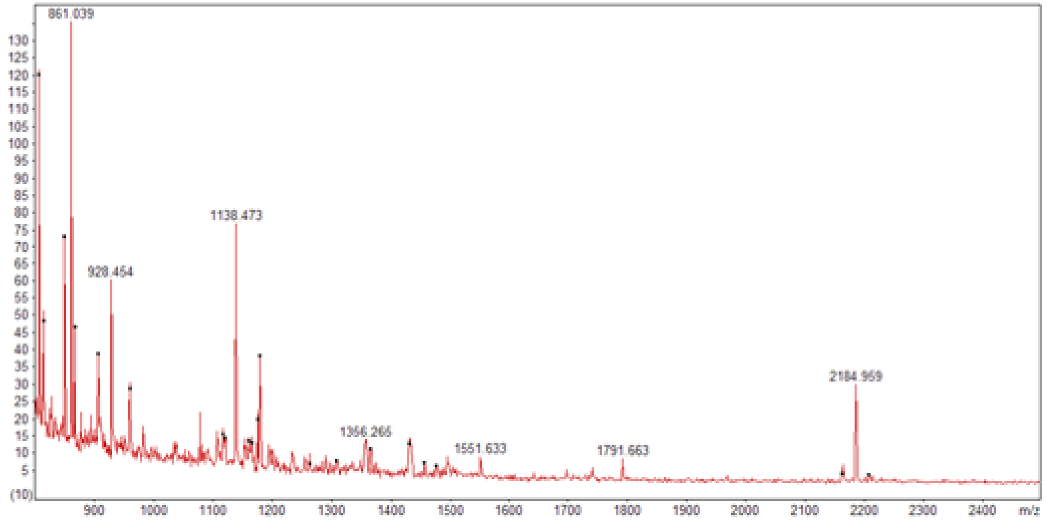
Protein name： **Superoxide dismutase [Cu-Zn] 1**

PFF Mascot score: **[61]**　　　Sequence coverage %: **[6]**

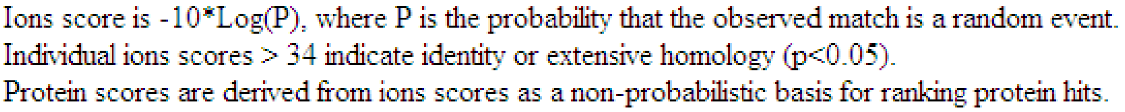
Matched peptides No.: **[2]**　　　p value: **0.00011**

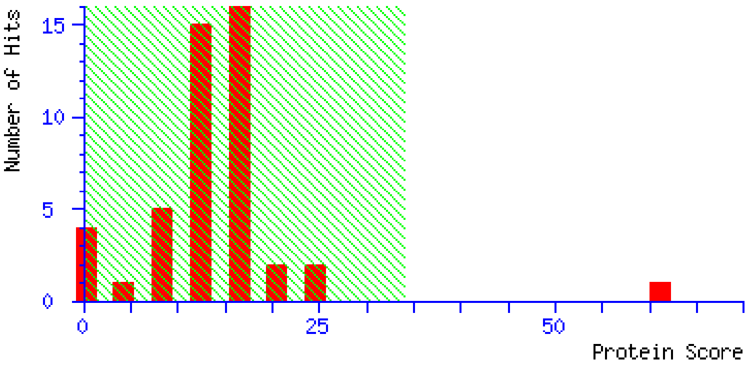
Calculated Mr: **15219**　　　Calculated *p*I: **5.42**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **105**

NCBI accession No.: **cassava4.1_017871m|PACid:17980723**

Plant species: ***Manihot esculenta***

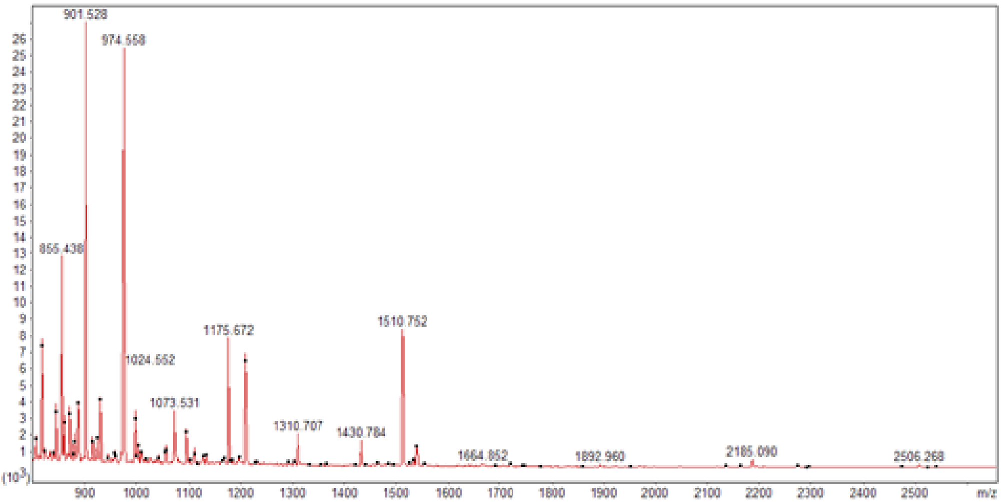
Protein name：**18.1 kDa class I heat shock protein**

PFF Mascot score: **[142]** Sequence coverage %: **[23]**

Matched peptides No.: **[5]** p value: **0.00014**

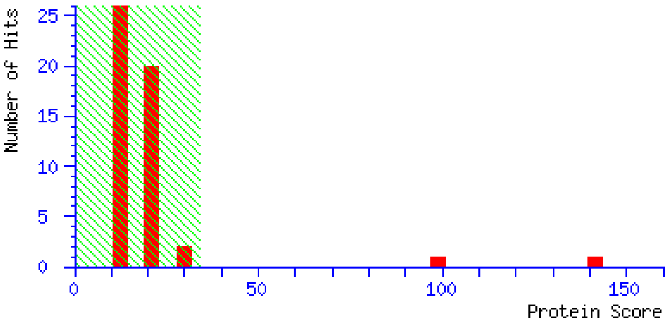
Calculated Mr: **18750** Calculated *p*I: **7.93**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **106**

NCBI accession No.: **cassava4.1_018294m|PACid:17966054**

Plant species: ***Manihot esculenta***

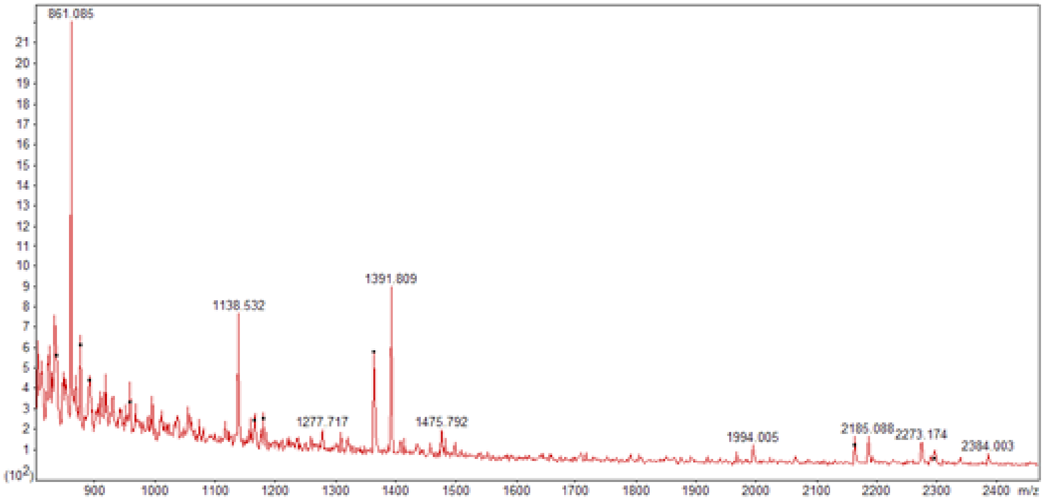
Protein name：**Superoxide dismutase [Cu-Zn] 1**

PFF Mascot score: **[130]** Sequence coverage %: **[23]**

Matched peptides No.: **[3]** p value: **0.00011**

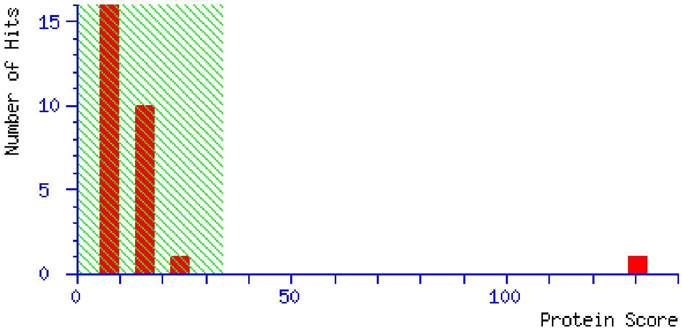
Calculated Mr: 15416 Calculated *p*I: **5.85**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **107**

NCBI accession No.: **cassava4.1_016175m|PACid:17993085**

Plant species: ***Manihot esculenta***

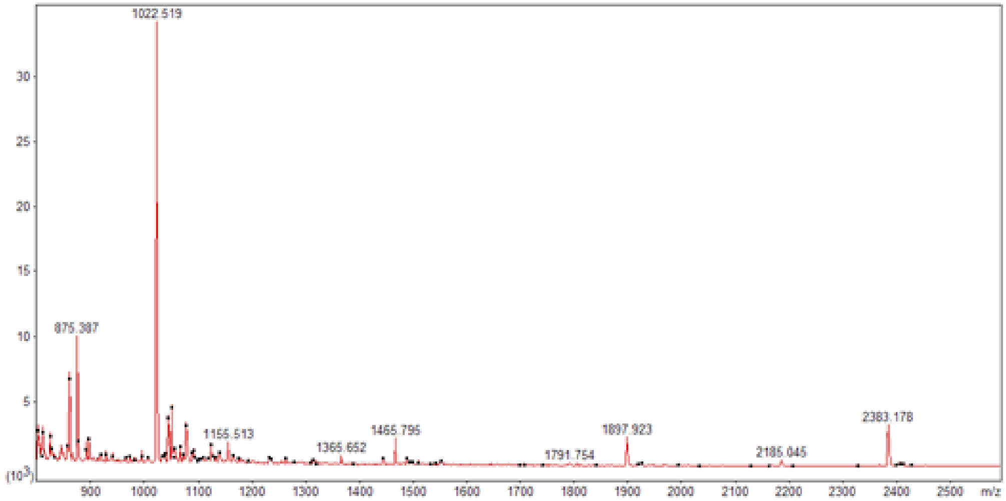
Protein name： **glutathione S-transferase GST, putative**

PFF Mascot score: **[257]** Sequence coverage %: **[27]**

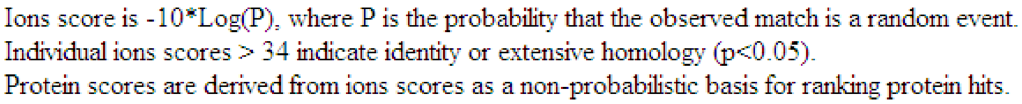
Matched peptides No.: **[5]** p value: **1.9e-009**

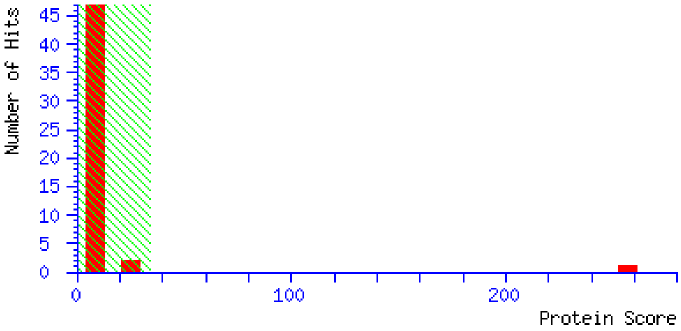
Calculated Mr: 24372 Calculated *p*I: **6.25**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **108**

NCBI accession No.: **cassava4.1_014432m|PACid:17967798**

Plant species: ***Manihot esculenta***

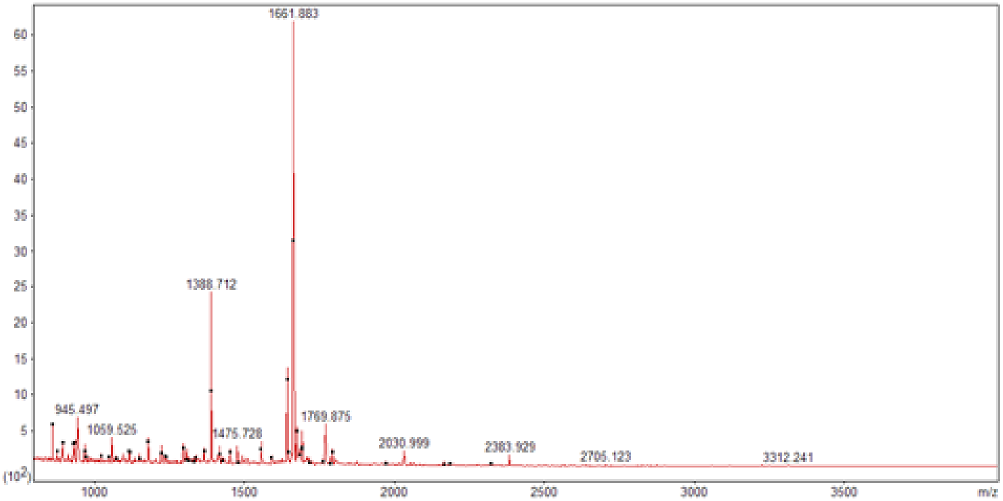
Protein name：**Triosephosphate isomerase, cytosolic**

PFF Mascot score: **[166]** Sequence coverage %: **[16]**

Matched peptides No.: **[3]** p value: **0.00021**

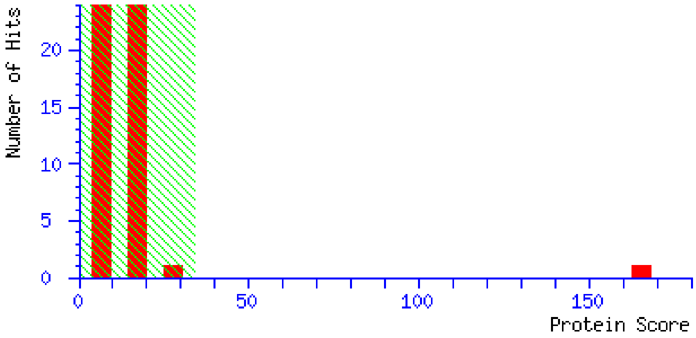
Calculated Mr: **27729** Calculated *p*I: **5.77**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **109**

NCBI accession No.: **cassava4.1_011868m|PACid:17990035**

Plant species: ***Manihot esculenta***

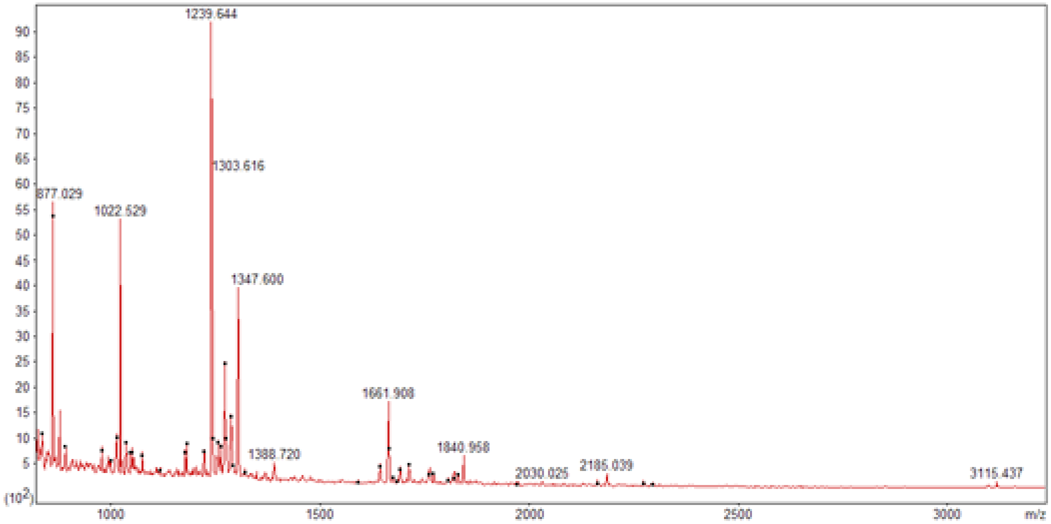
Protein name： **6-phosphogluconolactonase**

PFF Mascot score: **[77]** Sequence coverage %: **[5]**

Matched peptides No.: **[2]** p value: **0.0018**

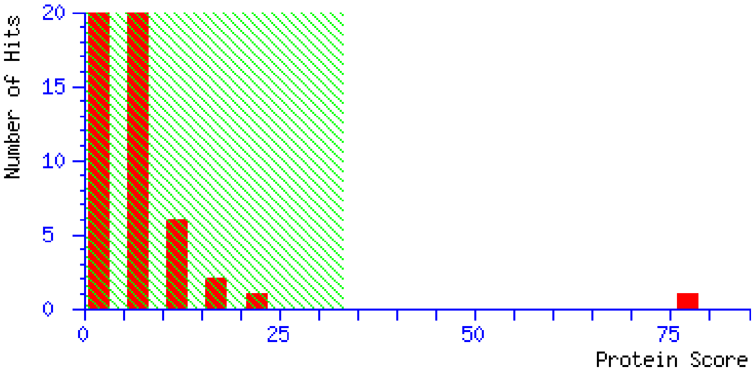
Calculated Mr: **35492** Calculated *p*I: **8.07**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **110**

NCBI accession No.: **cassava4.1_014432m|PACid:17967798**

Plant species: ***Manihot esculenta***

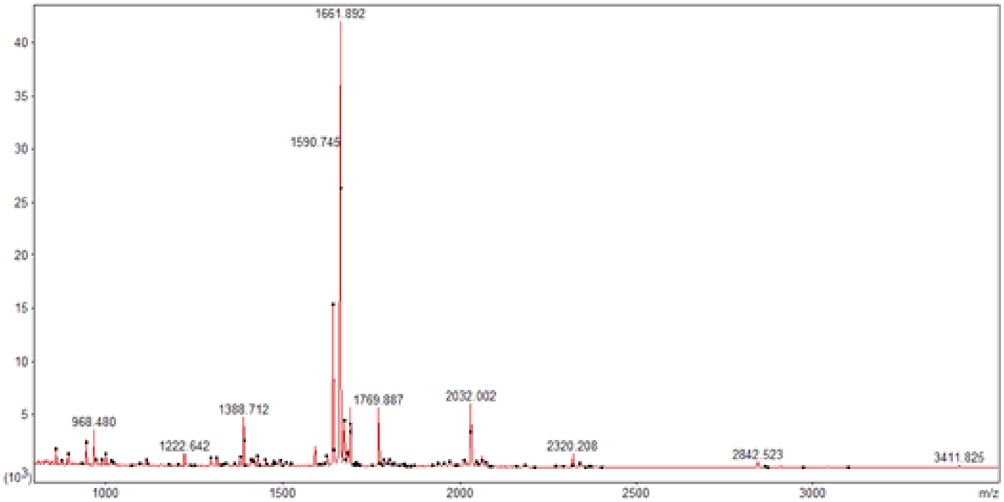
Protein name：**Triosephosphate isomerase, cytosolic**

PFF Mascot score: **[298]** Sequence coverage %: **[31]**

Matched peptides No.: **[7]** p value: **2.3e-006**

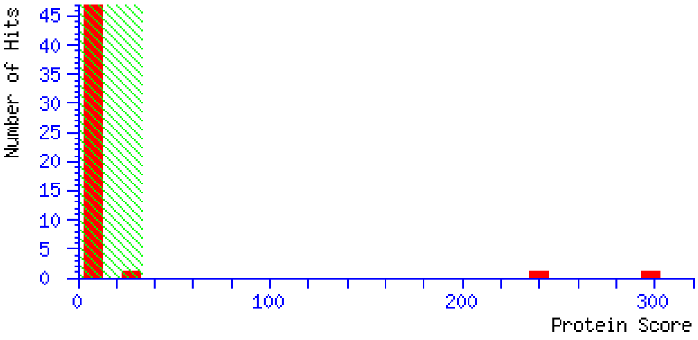
Calculated Mr: 27729 Calculated *p*I: **5.77**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **111**

NCBI accession No.: **cassava4.1_021183m|PACid:17971835**

Plant species: ***Ricinus communis***

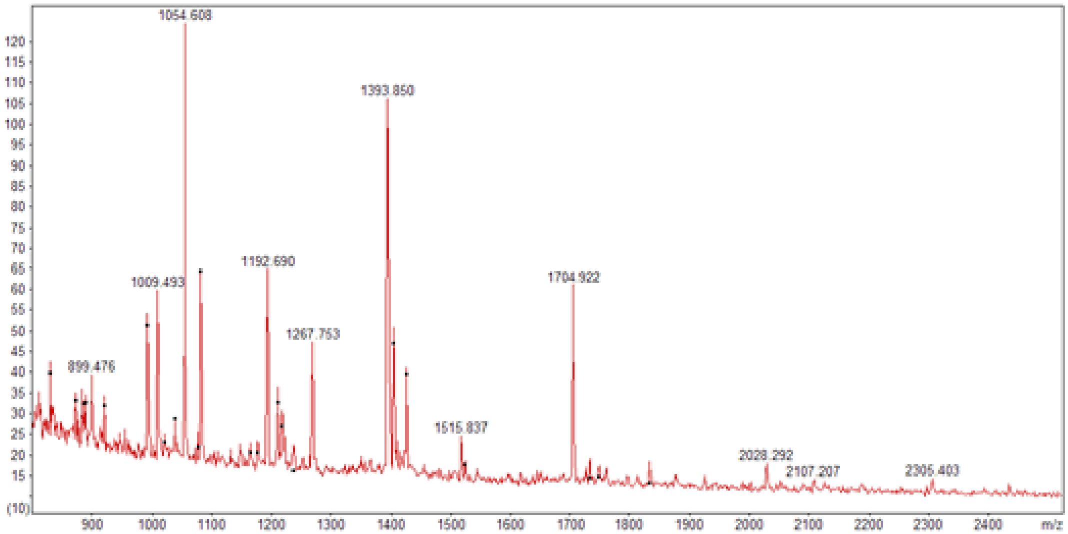
Protein name：**annexin**

PFF Mascot score: **[298]** Sequence coverage %: **[21]**

Matched peptides No.: **[6]** p value: **0.000000042**

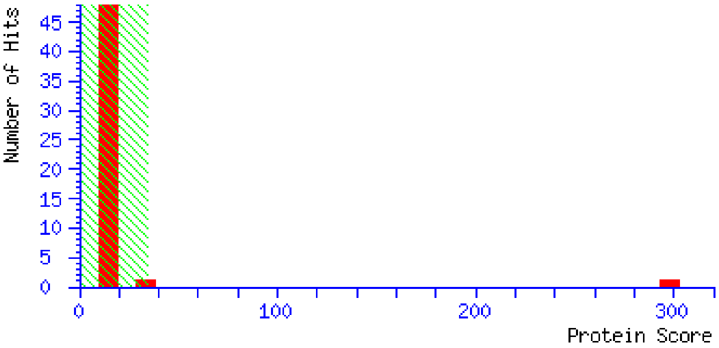
Calculated Mr: 33276 Calculated *p*I: **6.04**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **112**

NCBI accession No.: **cassava4.1_010344m|PACid:17990491**

Plant species: ***Manihot esculenta***

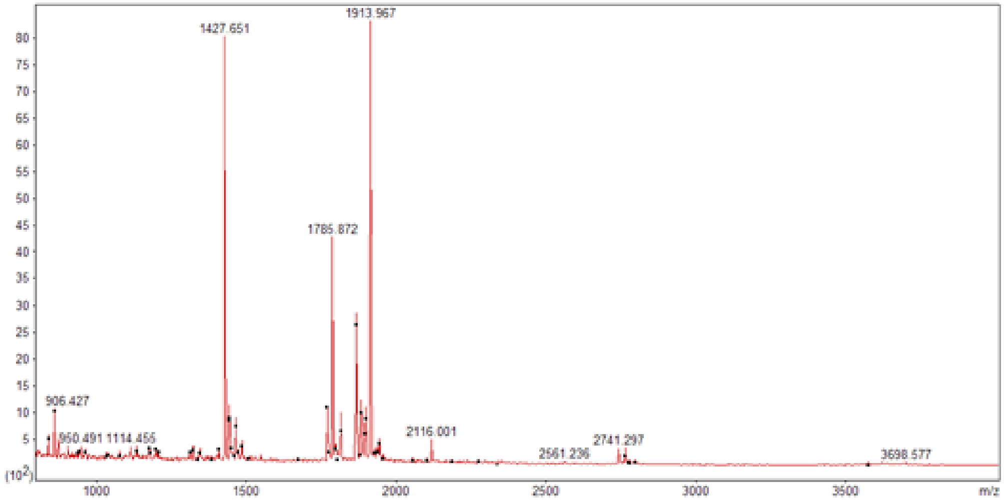
Protein name： **alcohol dehydrogenase, putative**

PFF Mascot score: **[343]** Sequence coverage %: **[8]**

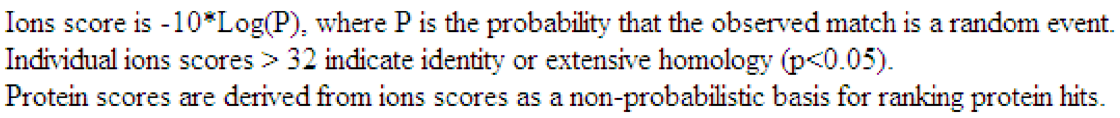
Matched peptides No.: **[2]** p value: **3.9e-011**

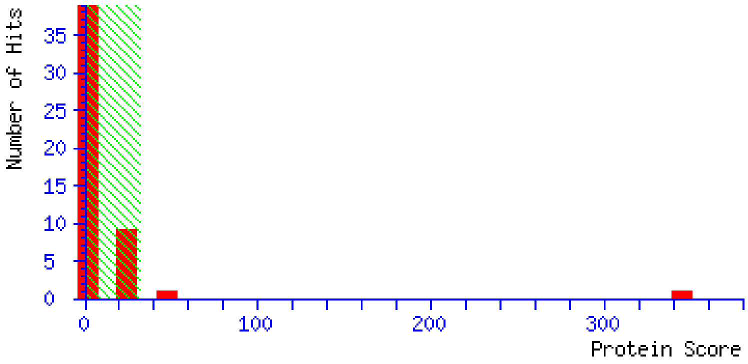
Calculated Mr: 39515 Calculated *p*I: **6.15**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 32 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **113**

NCBI accession No.: **cassava4.1_009779m|PACid:17990964**

Plant species: ***Manihot esculenta***

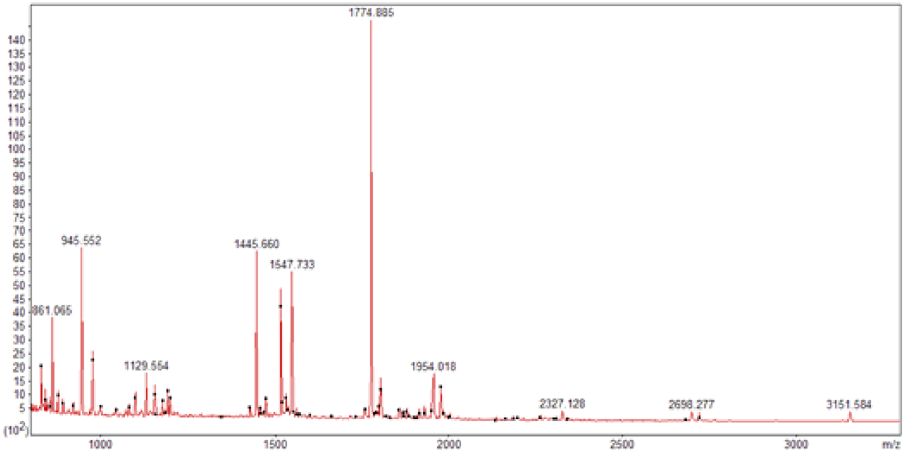
Protein name：**Actin-7**

PFF Mascot score: **[440]** Sequence coverage %: **[36]**

Matched peptides No.: **[9]** p value: **2.9e-012**

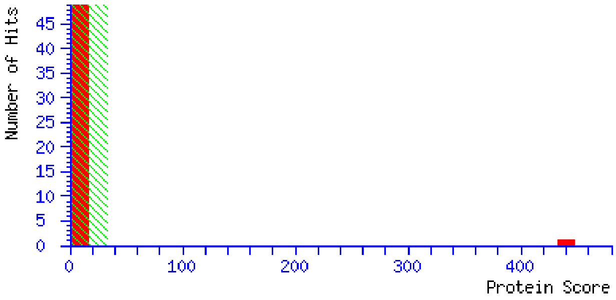
Calculated Mr: 41897 Calculated *p*I: **5.31**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **114**

NCBI accession No.: **cassava4.1_010105m|PACid:17962148**

Plant species: ***Manihot esculenta***

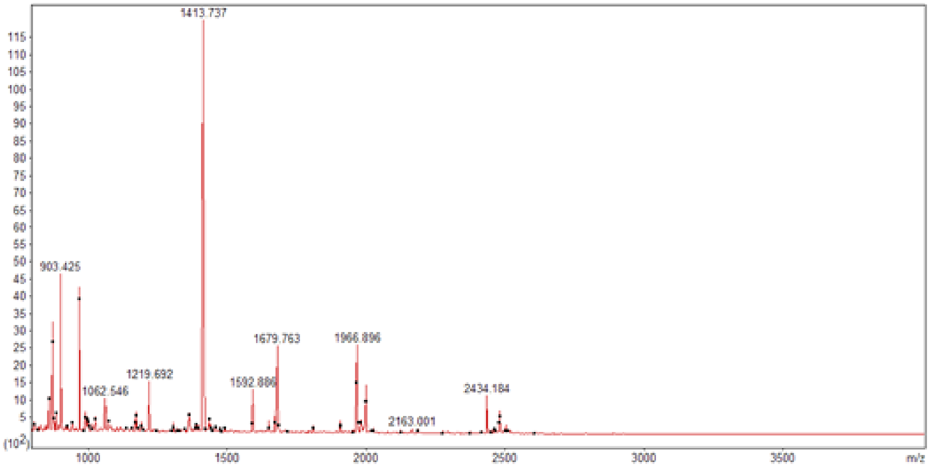
Protein name： **Malate dehydrogenase, cytoplasmic 1**

PFF Mascot score: **[349]** Sequence coverage %: **[20]**

Matched peptides No.: **[6]** p value: **1.4e-006**

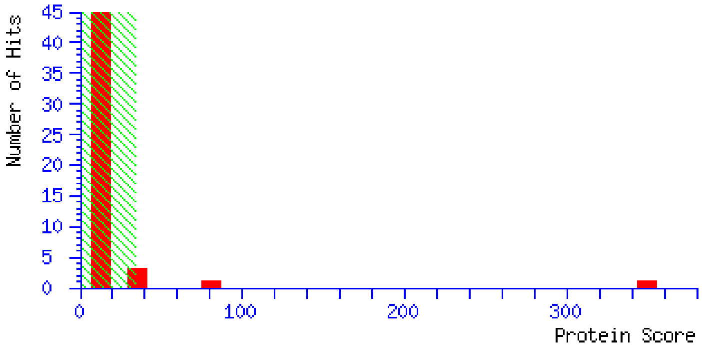
Calculated Mr: 40924 Calculated *p*I: **7.08**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **115**

NCBI accession No.: **cassava4.1_004280m|PACid:17986008**

Plant species: ***Manihot esculenta***

Protein name：**Leucine aminopeptidase 3, chloroplastic**

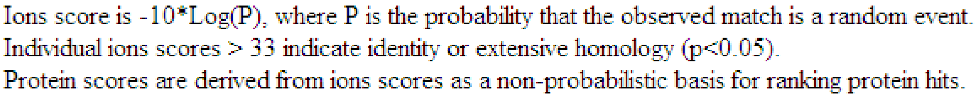
PFF Mascot score: **[399]**　　　Sequence coverage %: **[9]**

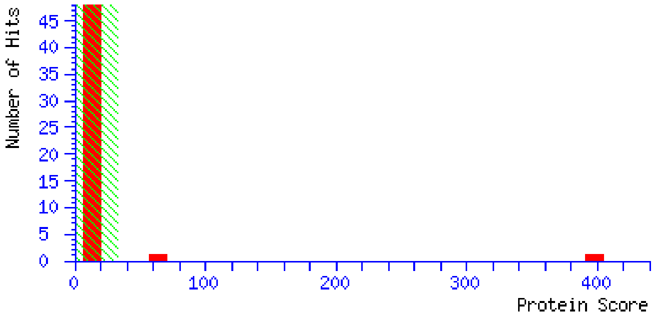
Matched peptides No.: **[4]**　　　p value: **2.5e-010**

Calculated Mr: 61349　　　Calculated *p*I: **6.69**

Annotated PMF **spectra:**

PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **116**

NCBI accession No.: **cassava4.1_007673m|PACid:17979089**

Plant species: ***Manihot esculenta***

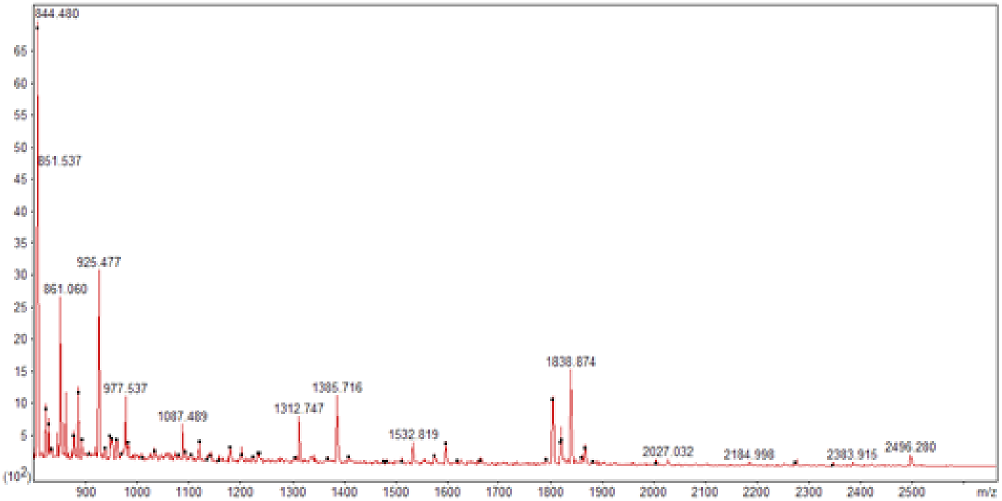
Protein name：**Bifunctional enolase 2/transcriptional activator**

PFF Mascot score: **[173]** Sequence coverage %: **[9]**

Matched peptides No.: **[4]** p value: **1.3e-008**

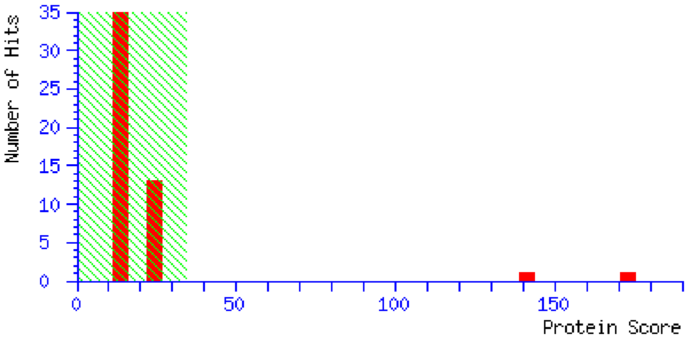
Calculated Mr: **48058** Calculated *p*I: **5.86**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **117**

NCBI accession No.: **cassava4.1_006024m|PACid:17974163**

Plant species: ***Manihot esculenta***

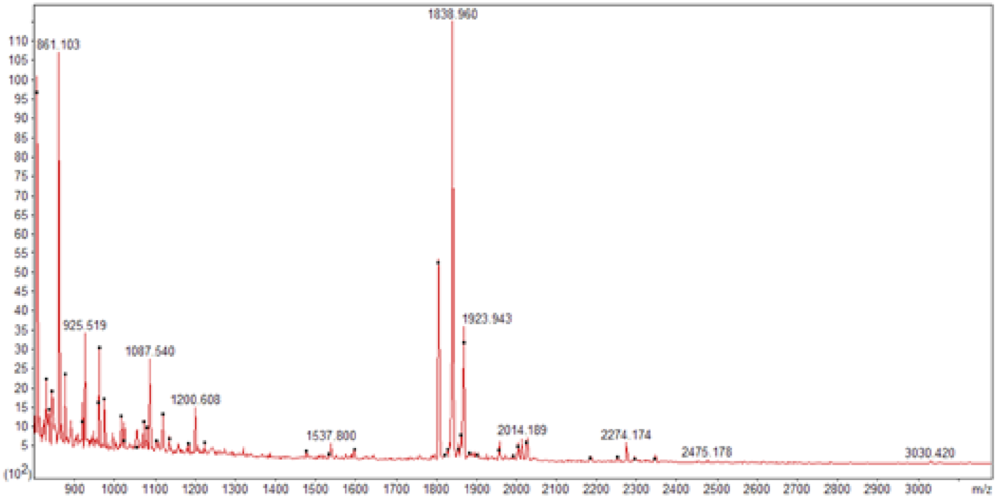
Protein name：**Betaine aldehyde dehydrogenase 1, chloroplastic**

PFF Mascot score: **[345]** Sequence coverage %: **[18]**

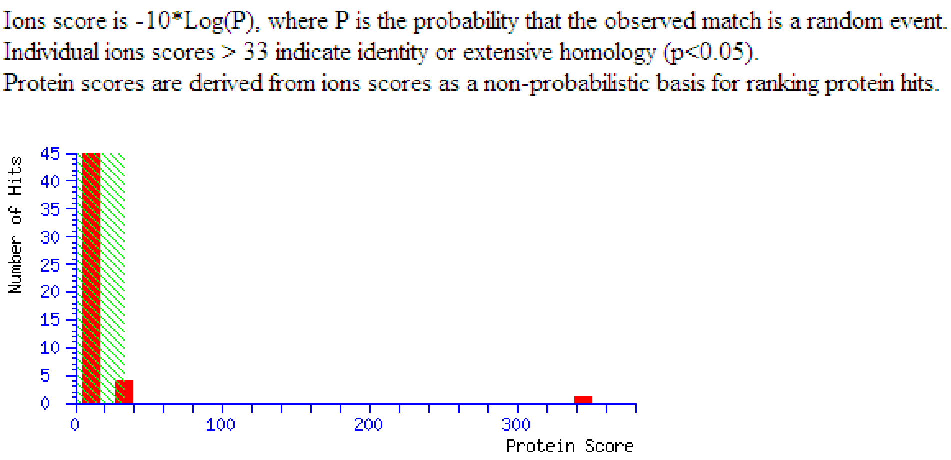
Matched peptides No.: **[5]** p value: **6.9e-013**

Calculated Mr: 55678 Calculated *p*I: **5.48**

Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Spot No.: **118**

NCBI accession No.: **cassava4.1_005314m|PACid:17981128**

Plant species: ***Manihot esculenta***

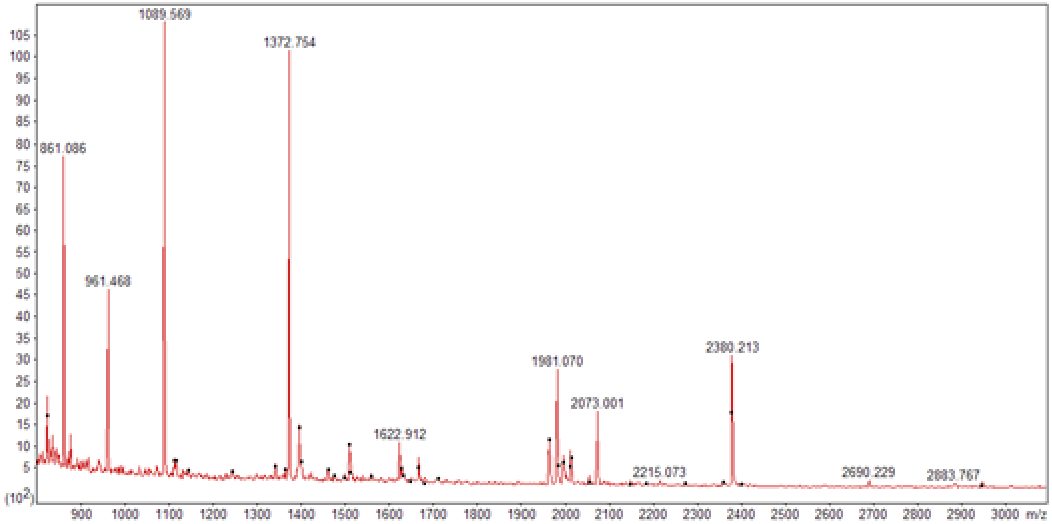
Protein name：**Ketol-acid reductoisomerase, chloroplastic**

PFF Mascot score: **[214]** Sequence coverage %: **[9]**

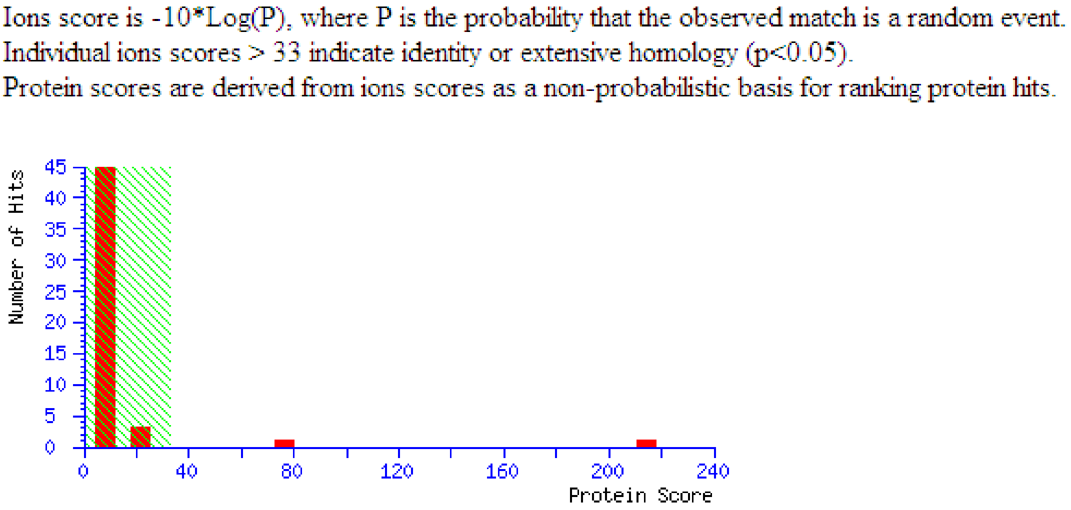
Matched peptides No.: **[4]** p value: **9.6e-005**

Calculated Mr: **58515** Calculated *p*I: **5.50**

Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Supplemental Figure S3:
Supplemental spectra and MALDI TOF/TOF MS/MS identification information

Annotated spectra for the 80 proteins on DIGE gels identified by PMF and PFF.

CID: collision induced dissociation

MALDI TOF:

matrix assisted laser desorption/ionization time of flight

MS: mass spectrometry

PMF: peptide mass fingerprinting

PFF: peptide fragment fingerprinting

Spot No.: **2**

NCBI accession No.: **cassava4.1_004263m|PACid:17968763**

Protein name：**Chaperonin 60 subunit alpha 1, chloroplastic**

Plant species: ***Manihot esculenta***

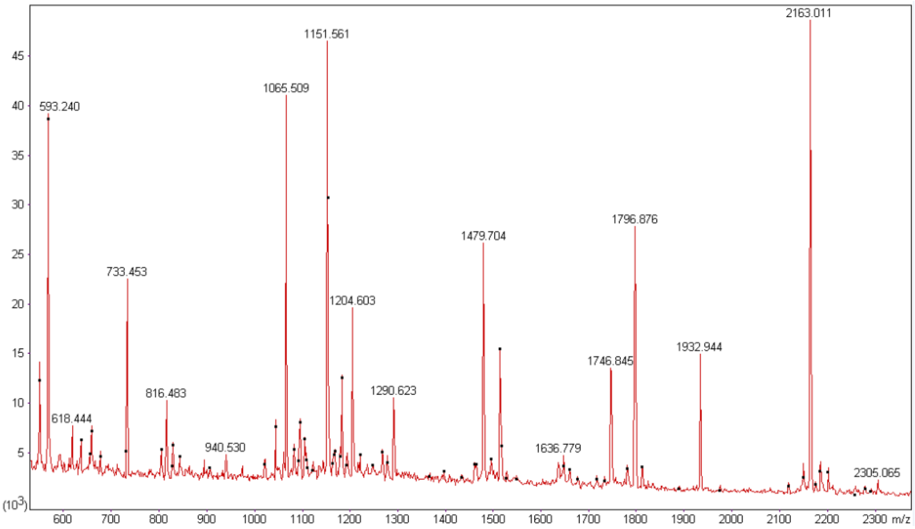
Mascot score: **215**

Sequence coverage %: **47** p value: **2.3e-017**

Matched peptides No.: **29** Total peptides No.: **64**

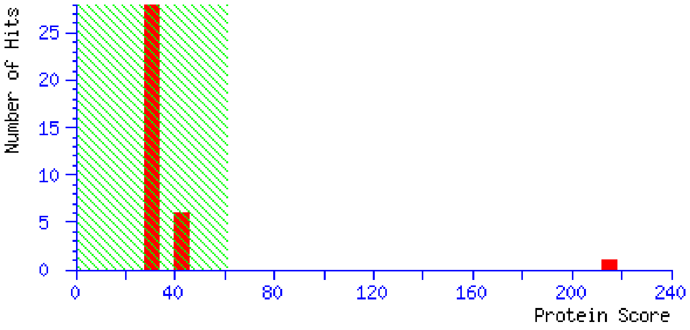
Calculated Mr: **62302** Calculated *p*I: **5.34**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **5**

NCBI accession No.: **cassava4.1_007971m|PACid:17991617**

Protein name: **Tubulin alpha-6 chain**

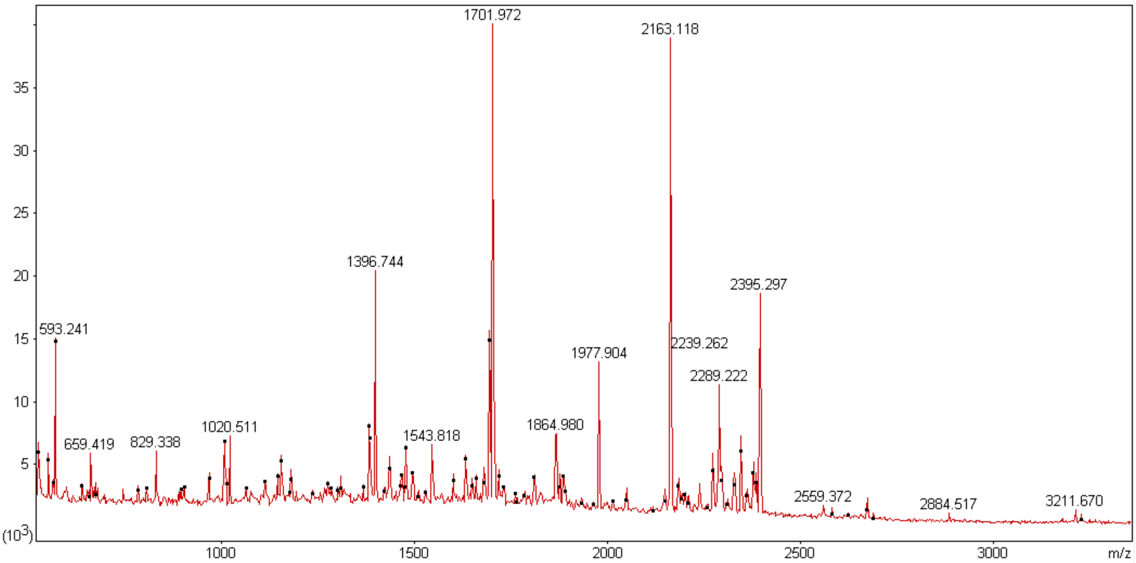
Plant species: ***Manihot esculenta*** Mascot score: **101**

Sequence coverage %: **51** p value: **5.8e-006**

Matched peptides No.: **15** Total peptides No.: **65**

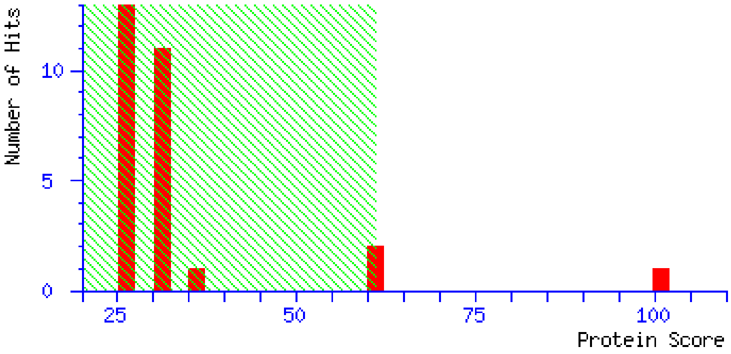
Calculated Mr: **48294** Calculated *p*I: **4.95**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **6**

NCBI accession No.: **cassava4.1_008310m|PACid:17966609**

Protein name：**26S protease regulatory subunit 6A homolog A**

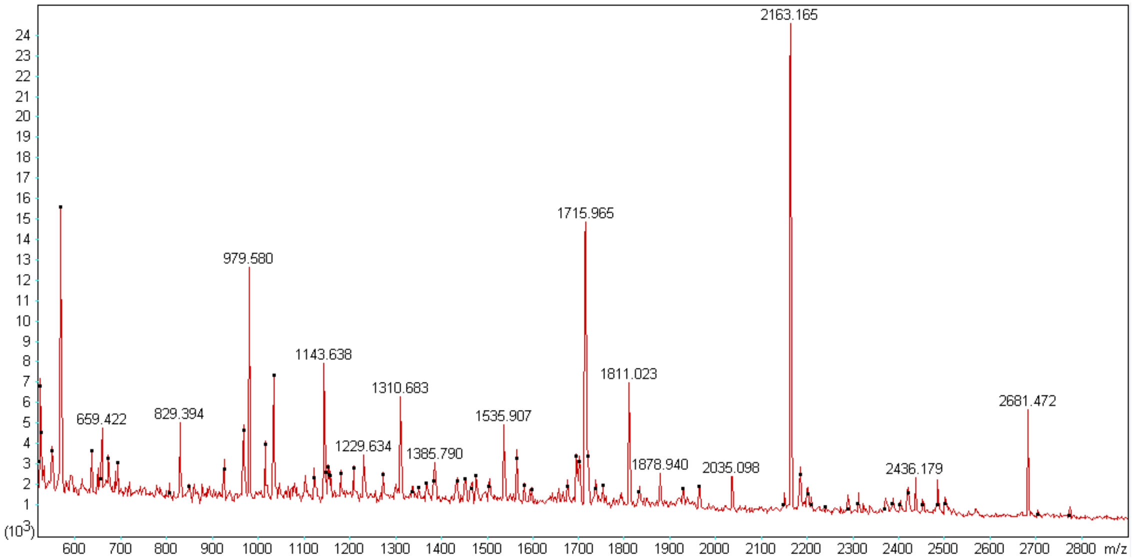
Plant species: ***Manihot esculenta*** Mascot score: **154**

Sequence coverage %: **59** p value: **2.9e-11**

Matched peptides No.: **29** Total peptides No.: **93**

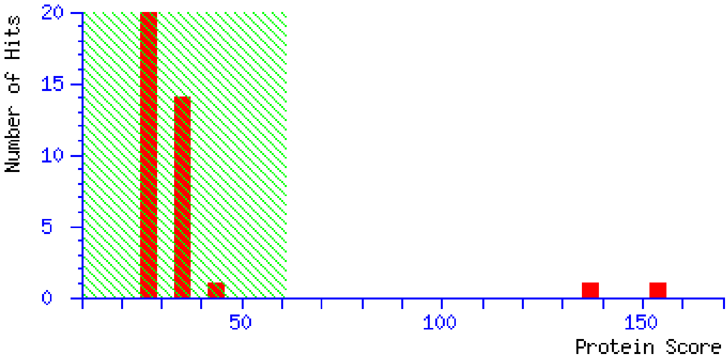
Calculated Mr: **47700** Calculated *p*I: **4.99**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **15**

NCBI accession No.: **cassava4.1_007971m|PACid:17991617**

Protein name：**Tubulin alpha-6 chain**

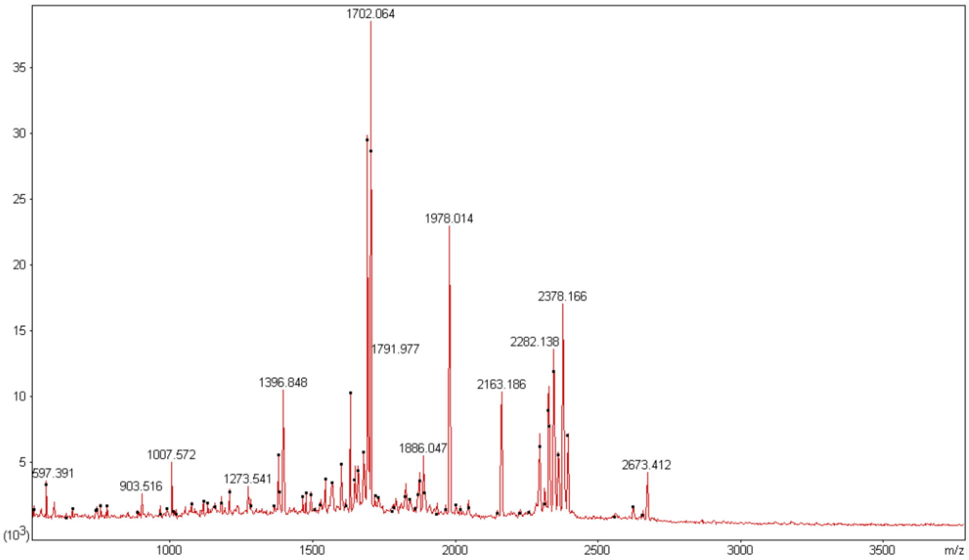
Plant species: ***Manihot esculenta*** Mascot score: **103**

Sequence coverage %: **48** p value: 3. 7e−006

Matched peptides No.: **18** Total peptides No.: **79**

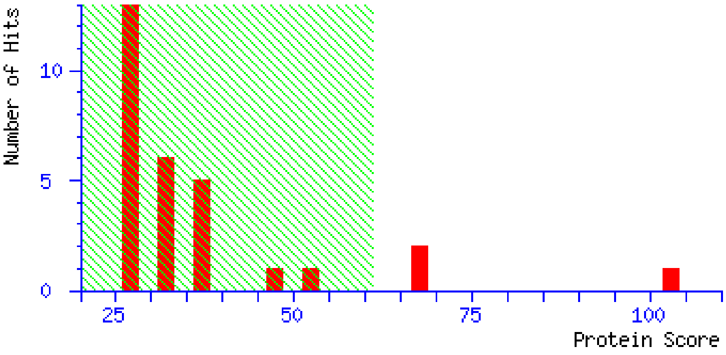
Calculated Mr: **48294** Calculated *p*I: **4.95**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **21**

NCBI accession No.: **cassava4.1_008086m|PACid:17989319**

Plant species: ***Manihot esculenta***

Protein name：**Glutamine synthetase cytosolic isozyme 1-1**

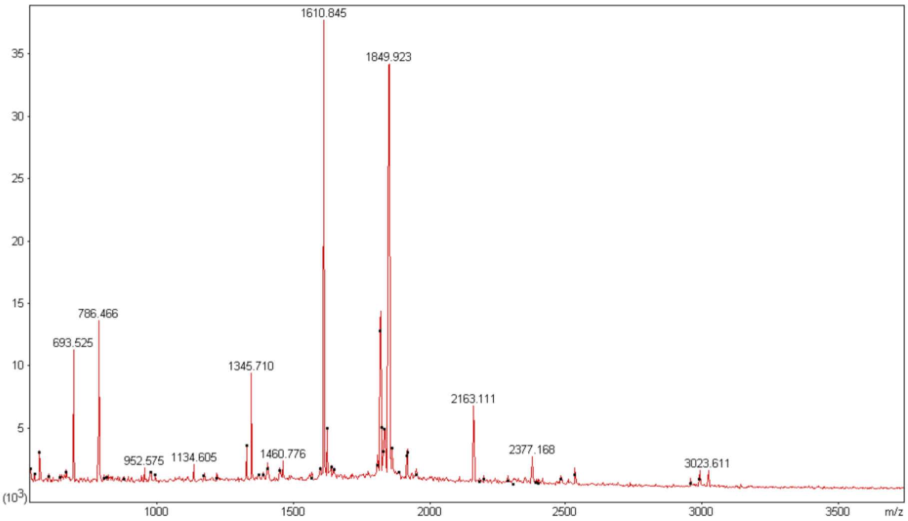
Mascot score: **101**

Sequence coverage %: **33** p value: **5.8e-006**

Matched peptides No.: **14** Total peptides No.: **54**

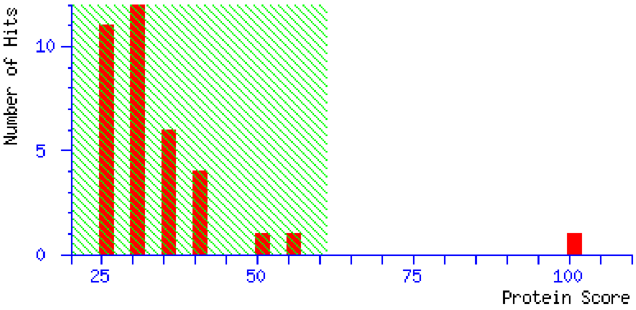
Calculated Mr: **47502** Calculated *p*I: **6.27**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **23**

NCBI accession No.: **cassava4.1_033108m|PACid:17973616**

Plant species: ***Manihot esculenta***

Protein name: **Actin-7**

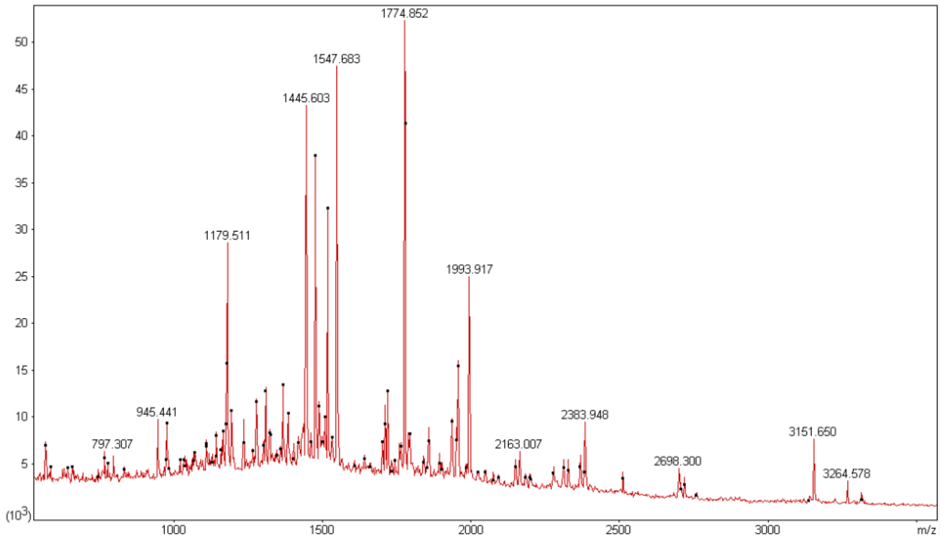
Mascot score: **93**

Sequence coverage %: **52** p value: **3.4e-005**

Matched peptides No.: **18** Total peptides No.: **87**

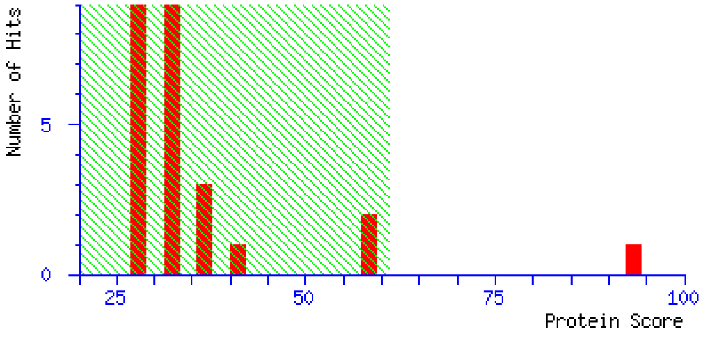
Calculated Mr: **41897** Calculated *p*I: **5.31**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **27**

NCBI accession No.: **cassava4.1_011177m|PACid:17972447**

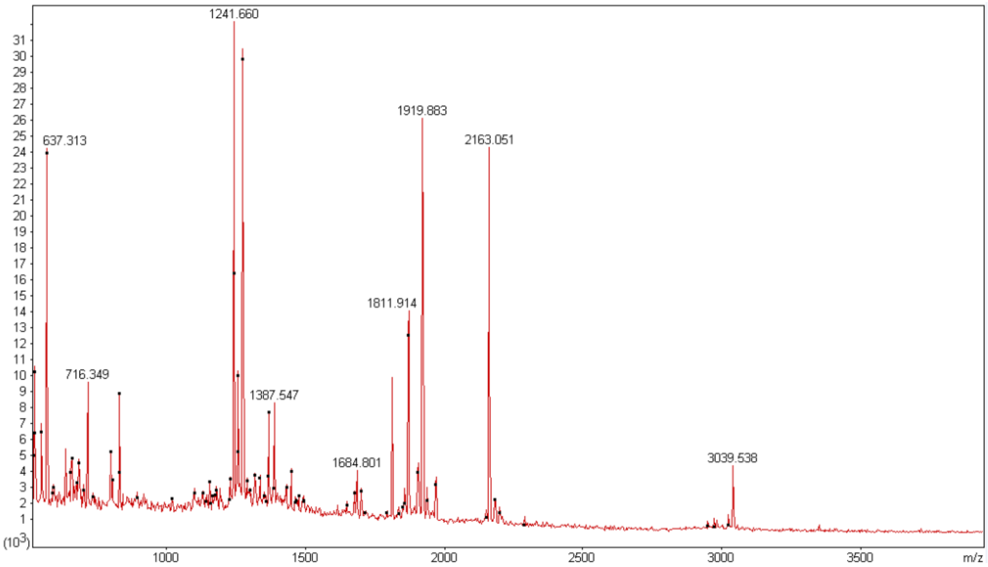
Protein name： **Adenosine kinase 1** Plant species: ***Manihot esculenta***

PFF Mascot score: [113] **Sequence coverage %:** [**7**]

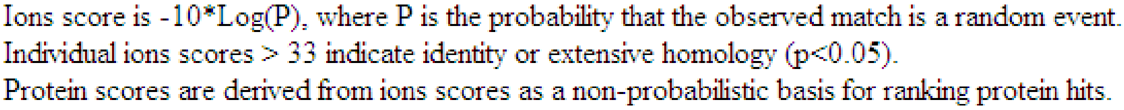
Matched peptides No.: [**2**] p value: 3.1e-006

Calculated Mr: **38107** Calculated *p*I: **5.38**

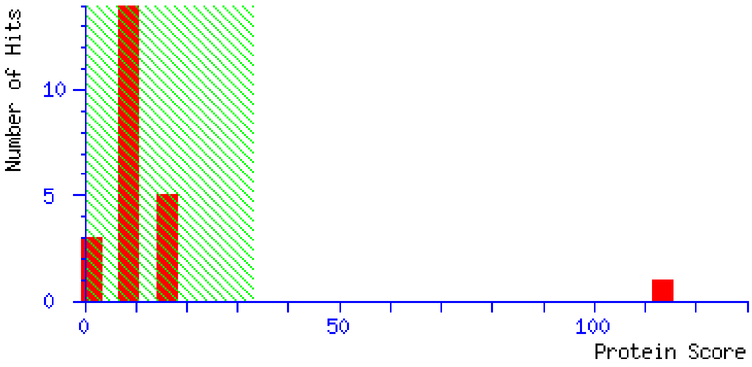
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **28**

NCBI accession No.: **cassava4.1_002747m|PACid:17960141**

Plant species: ***Manihot esculenta***

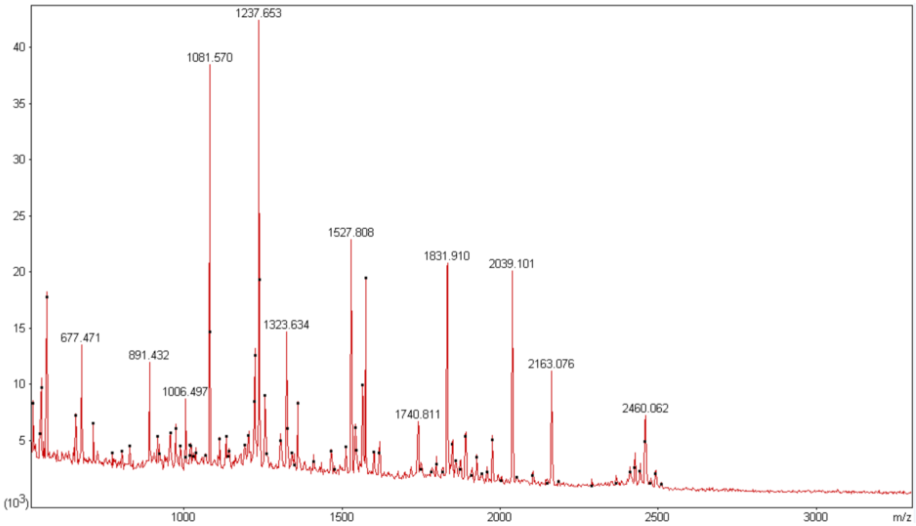
Protein name：**Heat shock protein 90-3** Mascot score: **127**

Sequence coverage %: **37** p value: **1.5e-008**

Matched peptides No.: **33** Total peptides No.: **77**

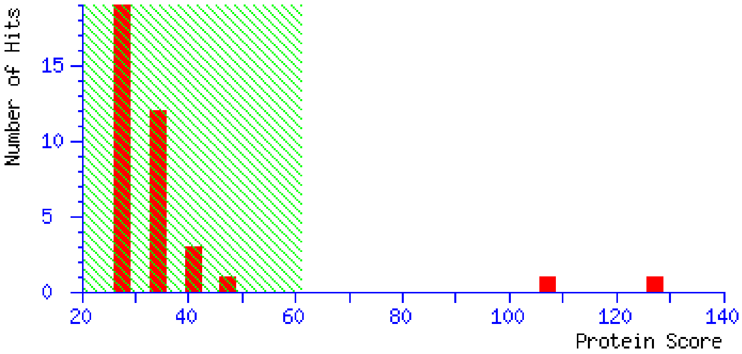
Calculated Mr: **80250** Calculated *p*I: **4.99**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **29**

NCBI accession No.: **cassava4.1_002466m|PACid:17978799**

Plant species: ***Manihot esculenta***

Protein name： **Alpha-glucan phosphorylase 1**

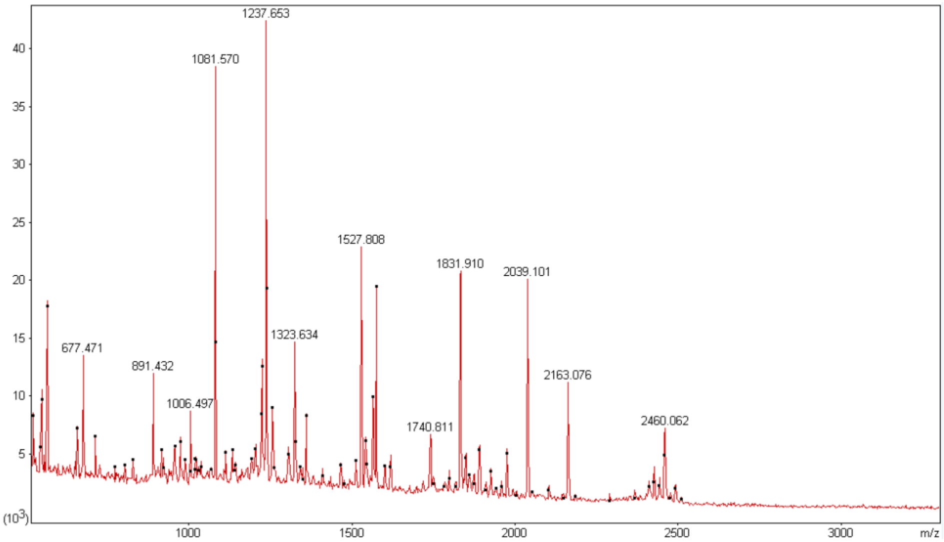
Mascot score: **81**

Sequence coverage %: **24**   p value: **0.00058**

Matched peptides No.: **24**   Total peptides No.: **95**

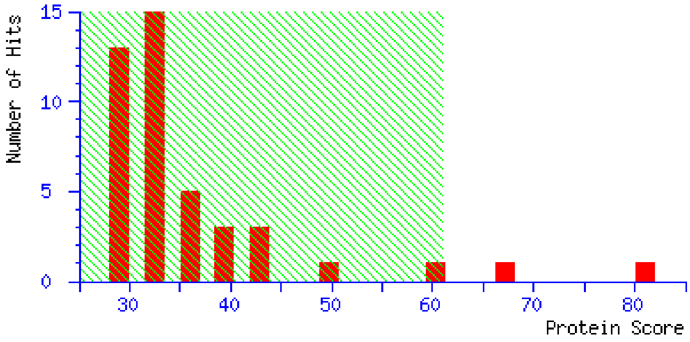
Calculated Mr: **81918**   Calculated *p*I: **8.50**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **30**

NCBI accession No.: **cassava4.1_002466m|PACid:17978799**

Plant species: **Manihot esculenta**

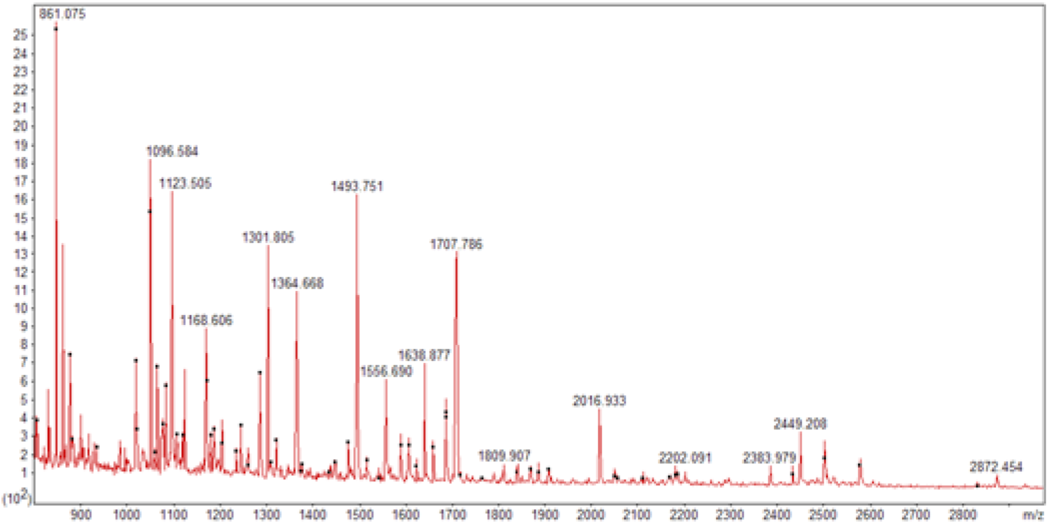
Protein name： **Alpha-glucan phosphorylase 1**

PFF **Mascot** score: **[387]**   Sequence coverage %: **[12]**

Matched peptides No.: **[7]**   p value: 3.5e-008

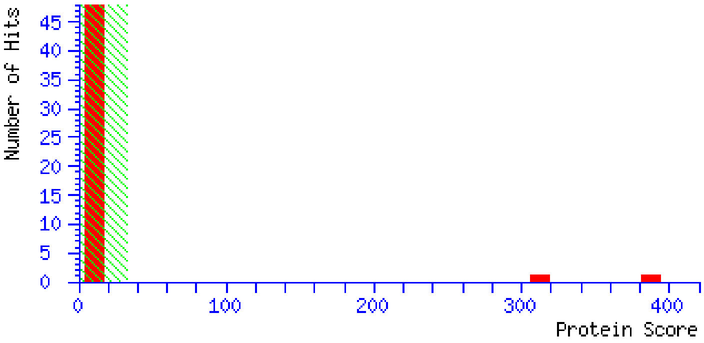
Calculated Mr: 81918   Calculated *p*I: **8.50**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **31**

NCBI accession No.: **cassava4.1_002614m|PACid:17978880**

Plant species: ***Manihot esculenta***

Protein name： **Alpha-glucan phosphorylase 1**

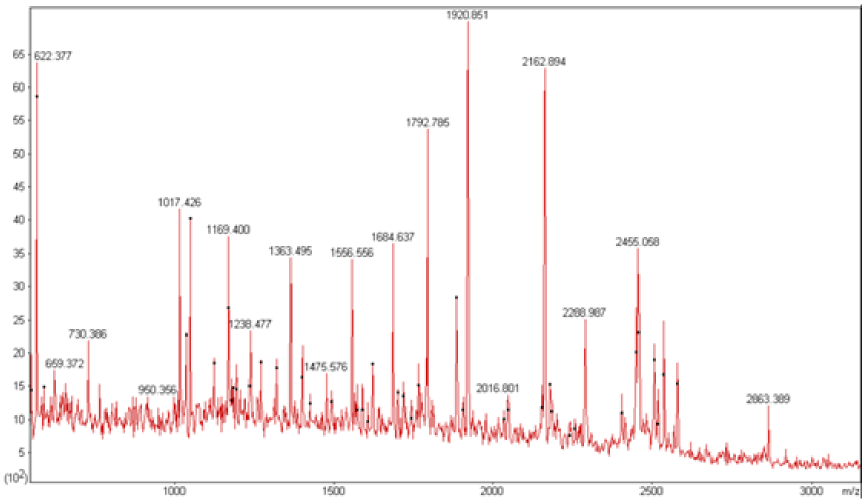
Mascot score: **76** p value: **0.019**

Sequence coverage %: **32**

Matched peptides No.: **16** Total peptides No.: **58**

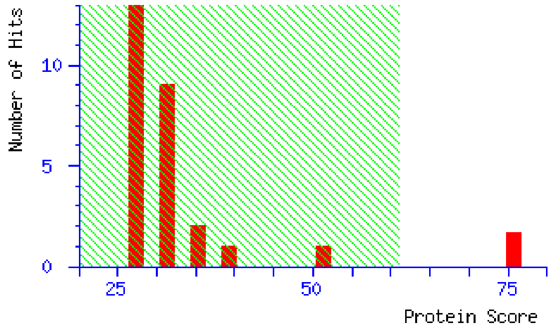
Calculated Mr: **80611** Calculated *p*I: **6.71**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **34**

NCBI accession No.: **cassava4.1_014251m|PACid:17989805**

Plant species: ***Manihot esculenta***   Mascot score: **115**

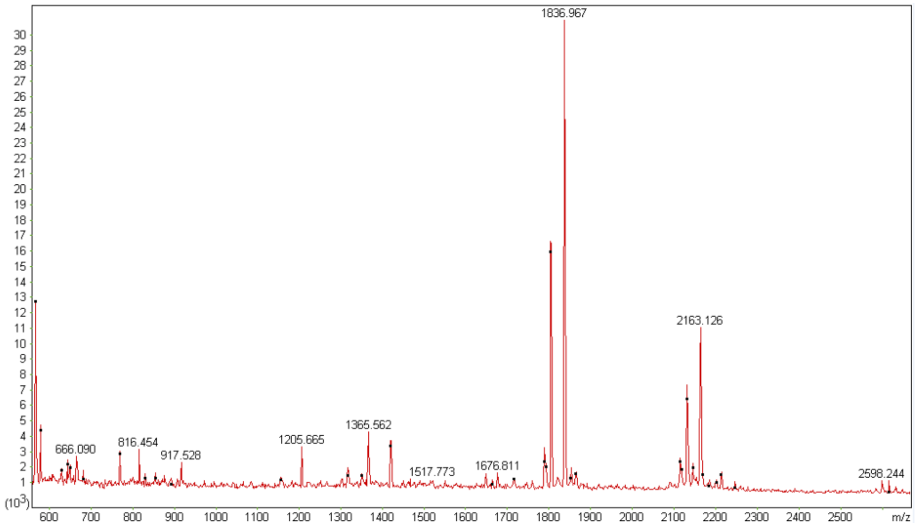
Protein name：**14-3-3-like protein GF14 omega**

Sequence coverage %: **44**   p value: **2.3e-007**

Matched peptides No.: **16**   Total peptides No.: **46**

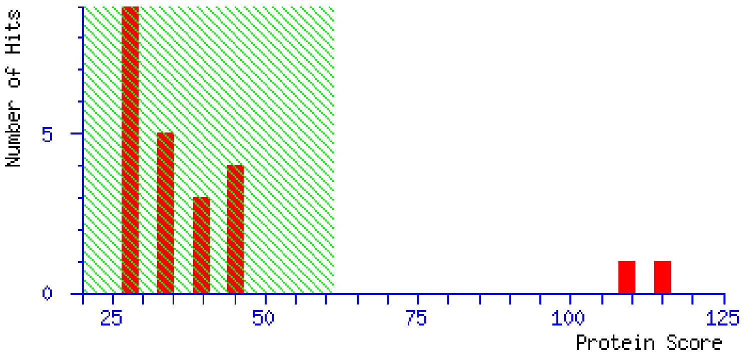
Calculated Mr: **29447**   Calculated *p*I: **4.77**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **35**

NCBI accession No.: **cassava4.1_014208m|PACid:17964823**

Plant species: *Manihot esculenta*

Protein name：**14-3-3-like protein GF14 omega**

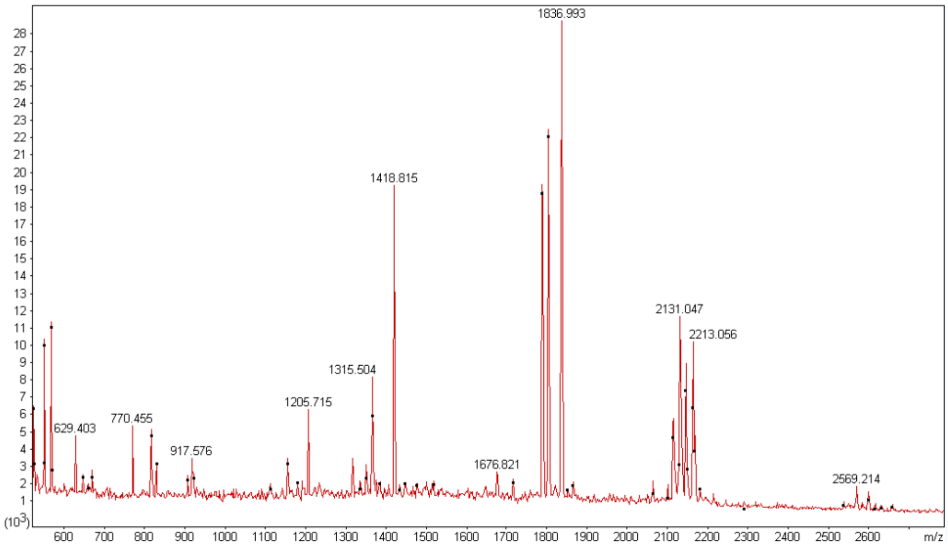
Mascot score: **159** p value: **9.2e-012**

Sequence coverage %: **54**

Matched peptides No.: **21** Total peptides No.: **56**

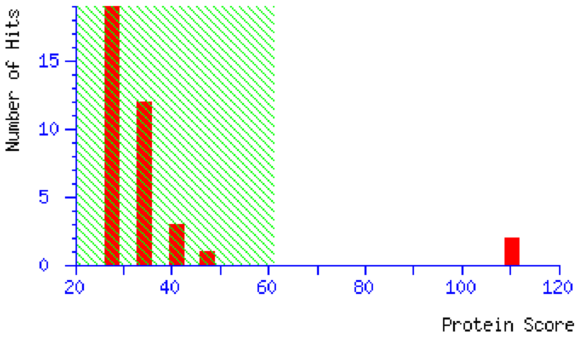
Calculated Mr: **29548** Calculated *p*I: **4.76**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **36**

NCBI accession No.: **cassava4.1_014065m|PACid:17989625**

Plant species: *Manihot esculenta*

Protein name： **14-3-3-like protein GF14 psi**

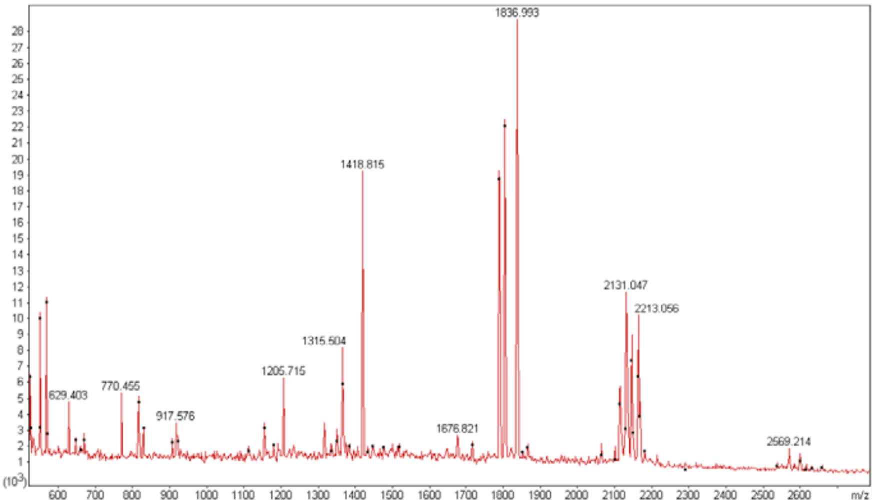
Mascot score: **111** p value: **0.00000058**

Sequence coverage %: **60**

Matched peptides No.: **16** Total peptides No.: **67**

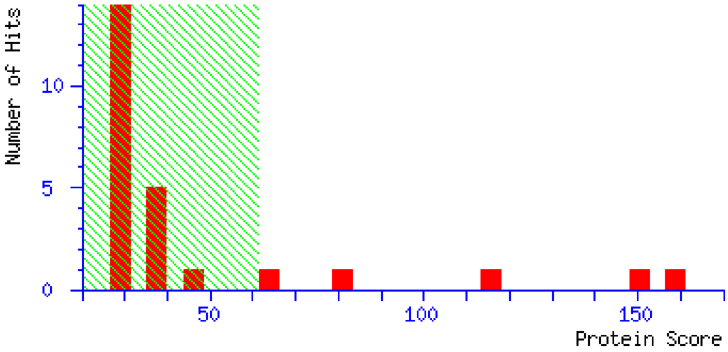
Calculated Mr: **29928** Calculated *p*I: **4.75**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **39**

NCBI accession No.: **cassava4.1_013158m|PACid:17968853** p value: **0.0017**

Plant species: ***Manihot esculenta*** Mascot score: **151**

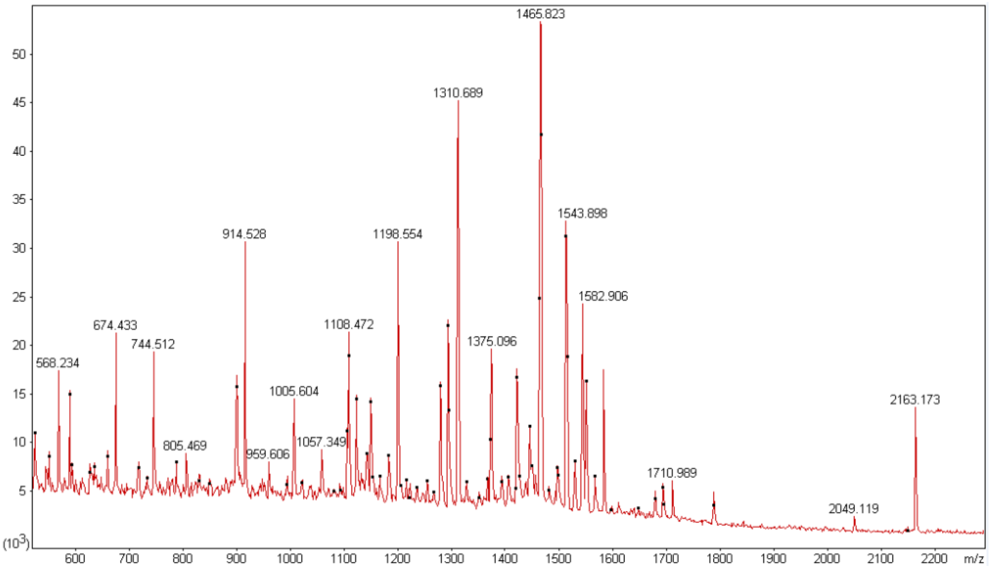
Protein name: **Probable lactoylglutathione lyase, chloroplast**

Sequence coverage %: **55** p value: **5.8e-011**

Matched peptides No.: **19** Total peptides No.: **77**

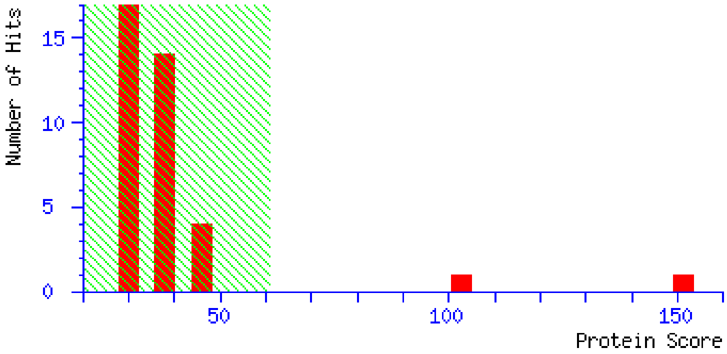
Calculated Mr: **32759** Calculated *p*I: **5.17**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **40**

NCBI accession No.: **cassava4.1_013158m|PACid:17968853**

Plant species: ***Manihot esculenta***

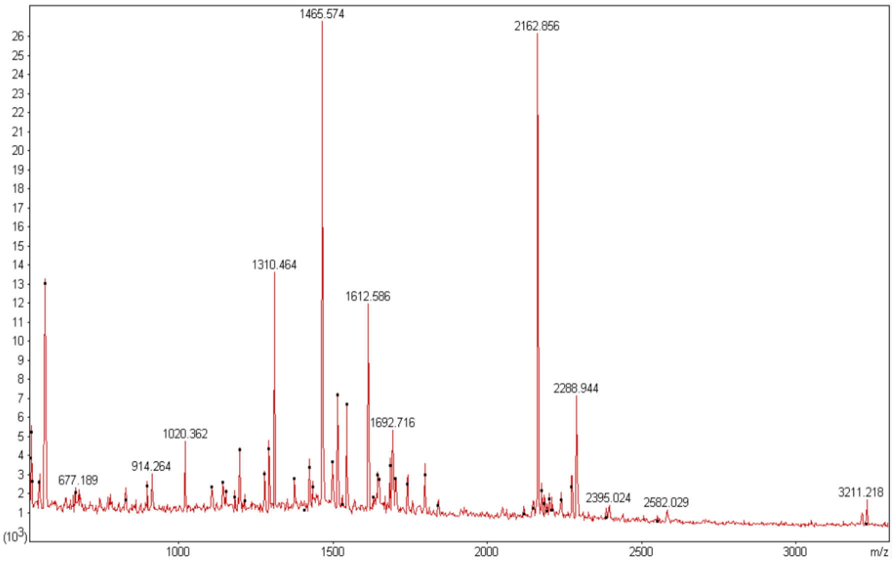
Protein name：**Probable lactoylglutathione lyase, chloroplast**

PFF Mascot score: **[73]** Sequence coverage %: **[7]**

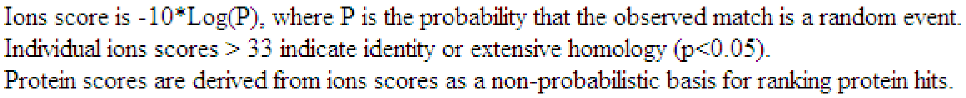
Matched peptides No.: **[2]** p value: 6.1e-006

Calculated Mr: **32759** Calculated *p*I: **5.17**

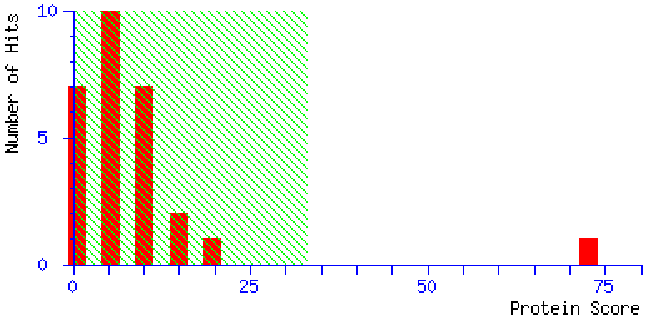
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **42**

NCBI accession No.: **cassava4.1_011578m|PACid:17975802**

Plant species: ***Manihot esculenta***

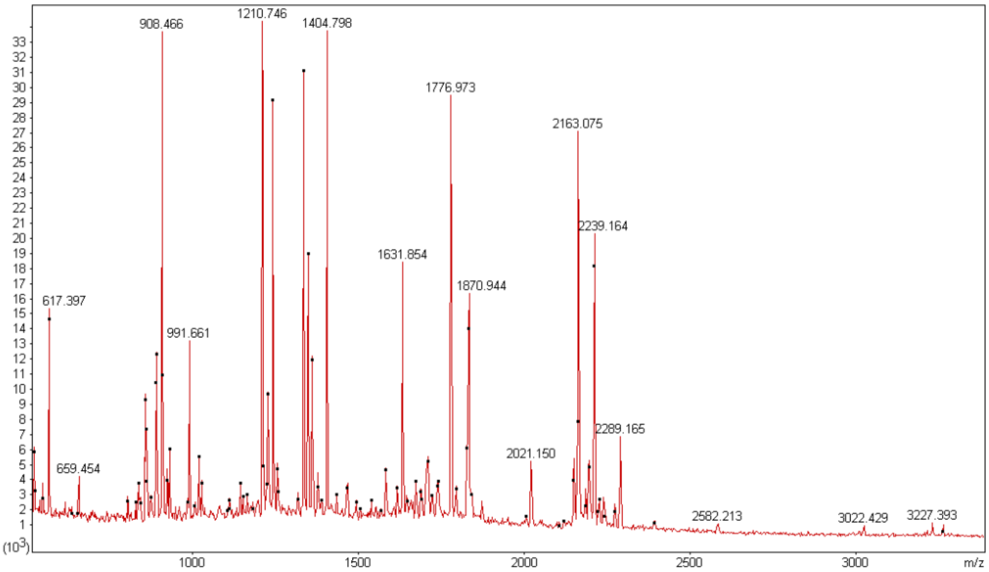
Protein name： **Probable fructokinase-1**

PFF Mascot score: **[146]** Sequence coverage %: **[11]**

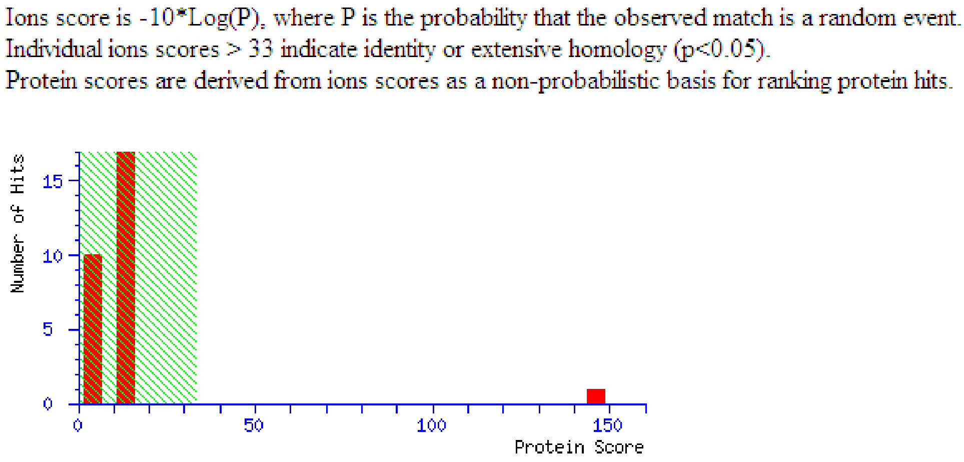
Matched peptides No.: **[3]** p value: **0.00019**

Calculated Mr: **35491** Calculated *p*I: **5.29**

Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Spot No.: **44**

NCBI accession No.: **cassava4.1_010863m|PACid:17977552**

Plant species: ***Manihot esculenta***

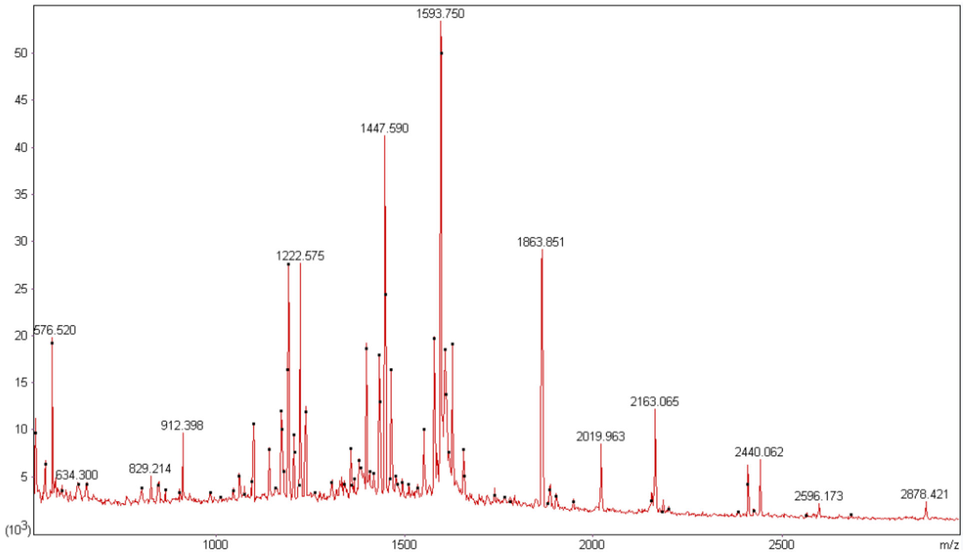
Protein name：**NADP-dependent alkenal double bond reductase**

PFF Mascot score: **[99]** Sequence coverage %: **[7]**

Matched peptides No.: **[2]** p value: **7.3e-008**

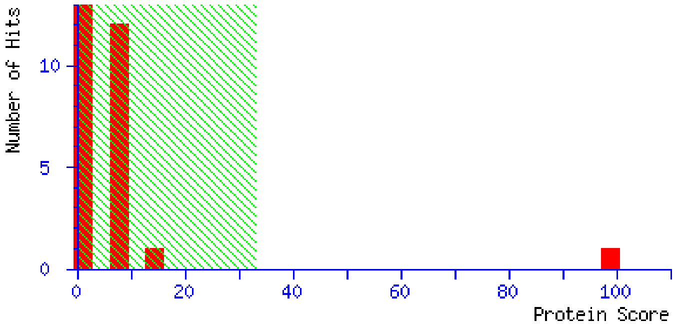
Calculated Mr: **38818** Calculated *p*I: **5.41**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **46**

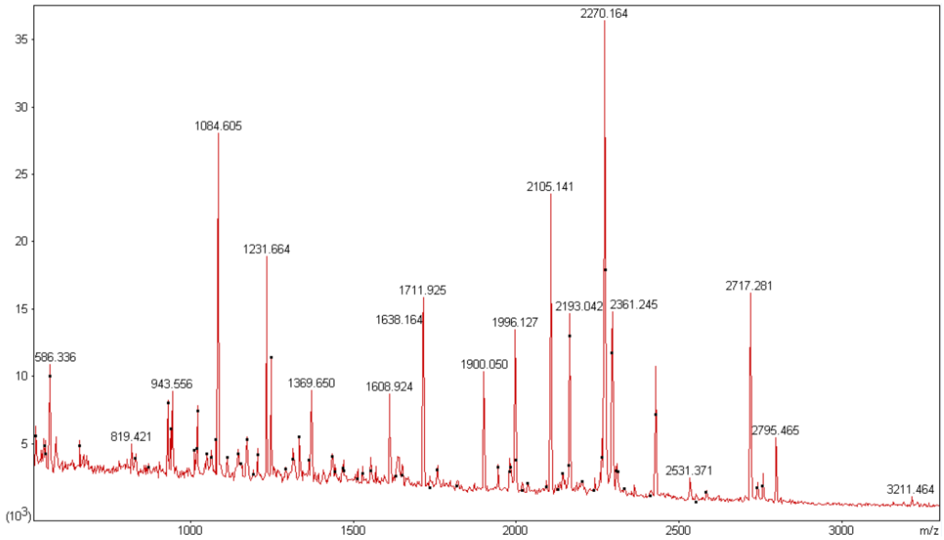
NCBI accession No.: **cassava4.1_012448m|PACid:17968446** Plant species: ***Manihot esculenta*** Protein name: **Putative NAD(P)H oxidoreductase, isoflavone reductase**

PFF Mascot score: **[254]** Sequence coverage %: **[15]**

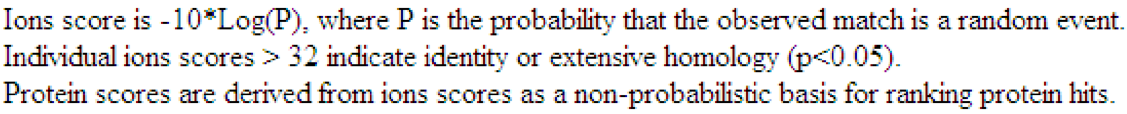
Matched peptides No.: **[3]** p value: **4.7e-012**

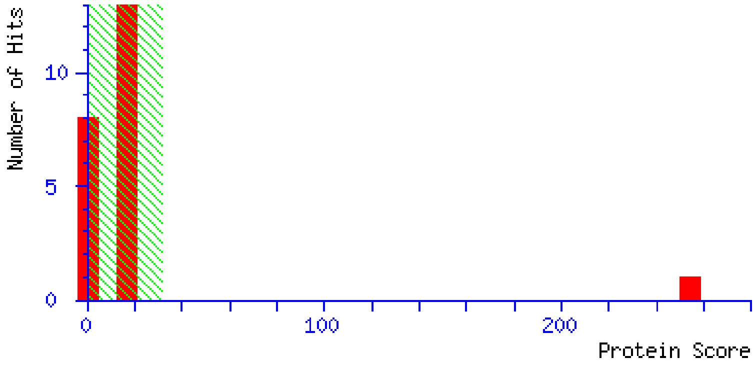
Calculated Mr: 33873 Calculated *p*I: **5.47**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 32 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **47**

NCBI accession No.: **cassava4.1_010620m|PACid:17987783**

Plant species: ***Manihot esculenta***

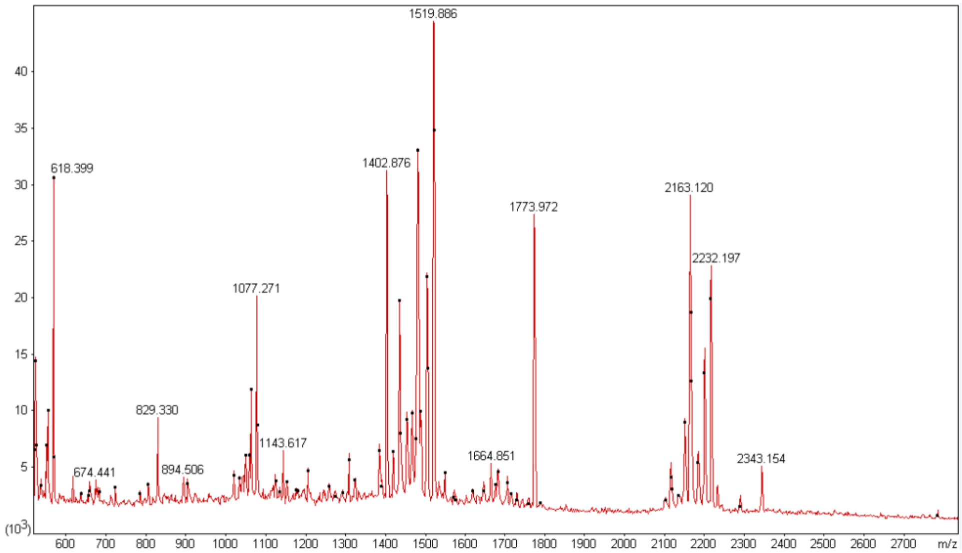
Protein name: **Thiamine thiazole synthase, chloroplastic**

PFF Mascot score: [133] **Sequence coverage %: [8]**

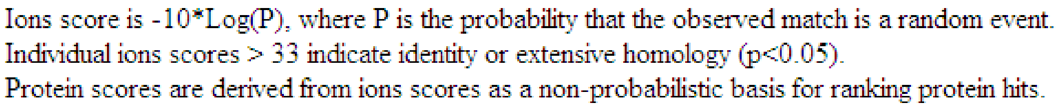
Matched peptides No.: **[2]** p value: **6.7e-006**

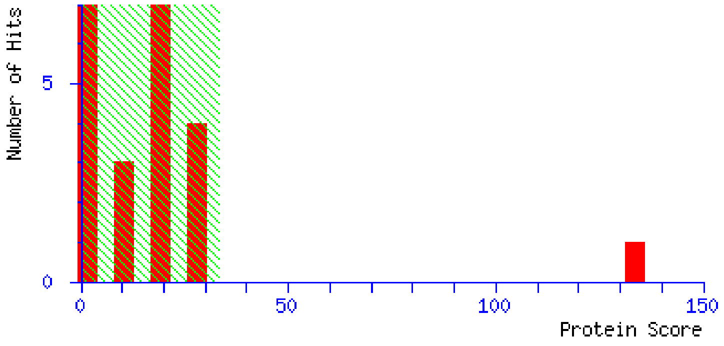
Calculated Mr: **37625** Calculated *p*I: **6.07**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **49**

NCBI accession No.: **cassava4.1_014185m|PACid:17964106**

Plant species: ***Manihot esculenta***

Protein name: **Ferritin-4, chloroplastic**

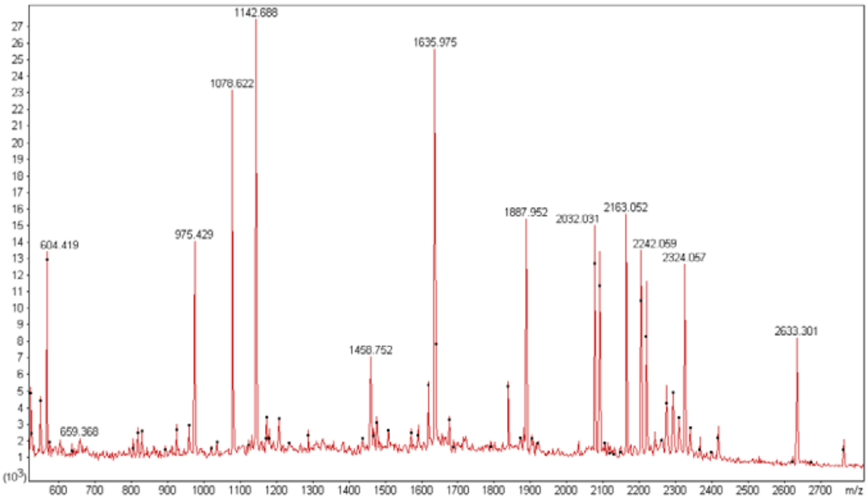
Mascot score: **125**

Sequence coverage %: **61** p value: **2.3e-008**

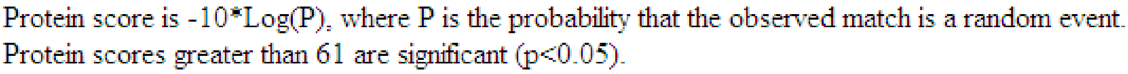
Matched peptides No.: **18** Total peptides No.: **68**

Calculated Mr: **29470** Calculated *p*I: **5.30**

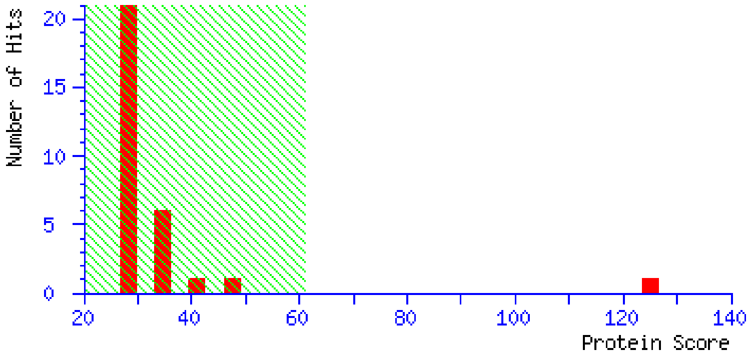
Annotated PMF **spectra:**



Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **50**

NCBI accession No.: **cassava4.1_014410m|PACid:17965277**

Plant species: ***Manihot esculenta***

Protein name： **20 kDa chaperonin, chloroplastic**

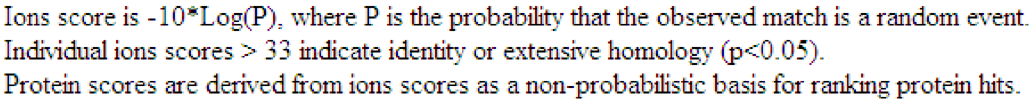
PFF Mascot score: **[172]** Sequence coverage %: **[21]**

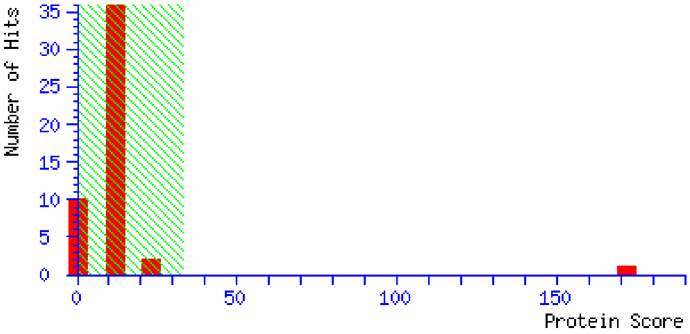
Matched peptides No.: **[3]** p value: **5e-005**

Calculated Mr: **26695** Calculated *p*I: **7.79**

Annotated PMF **spectra:**

PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **51**

NCBI accession No.: **cassava4.1_014643m|PACid:17991662**

Plant species: ***Manihot esculenta***

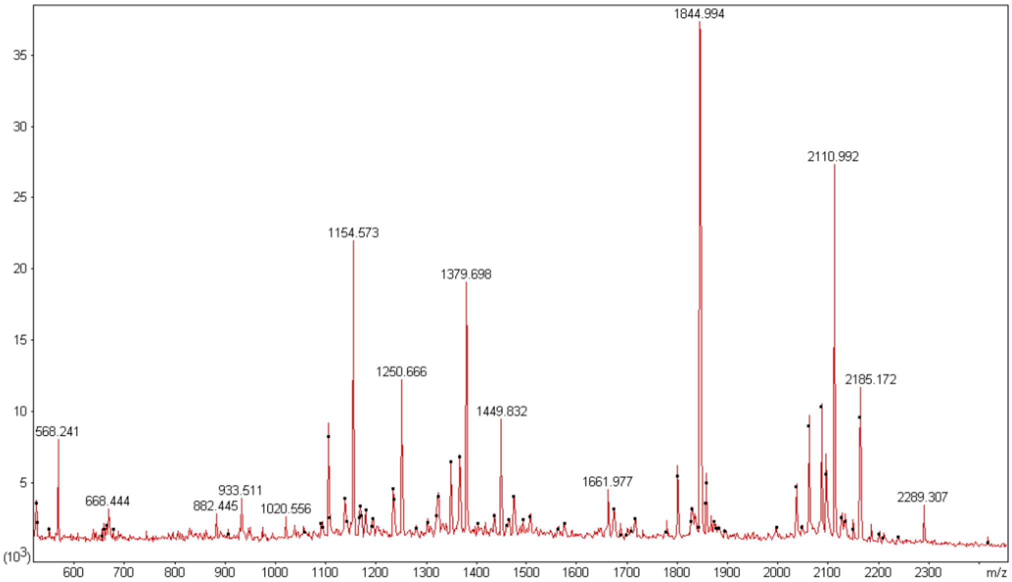
Protein name：**L-ascorbate peroxidase 1, cytosolic**

Mascot score: **82**　　　p value: **`0.00046`**

Sequence coverage %: **40**　　Matched peptides No.: **13**

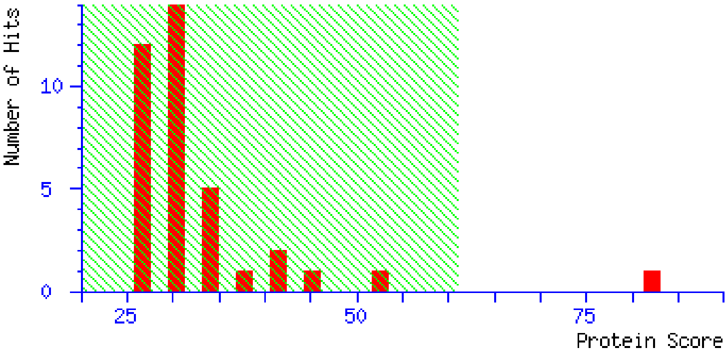
Calculated Mr: **27766**　　　　　Calculated *p*I: **5.31**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **53**

NCBI accession No.: **cassava4.1_009779m|PACid:17990964**

Plant species: ***Manihot esculenta***

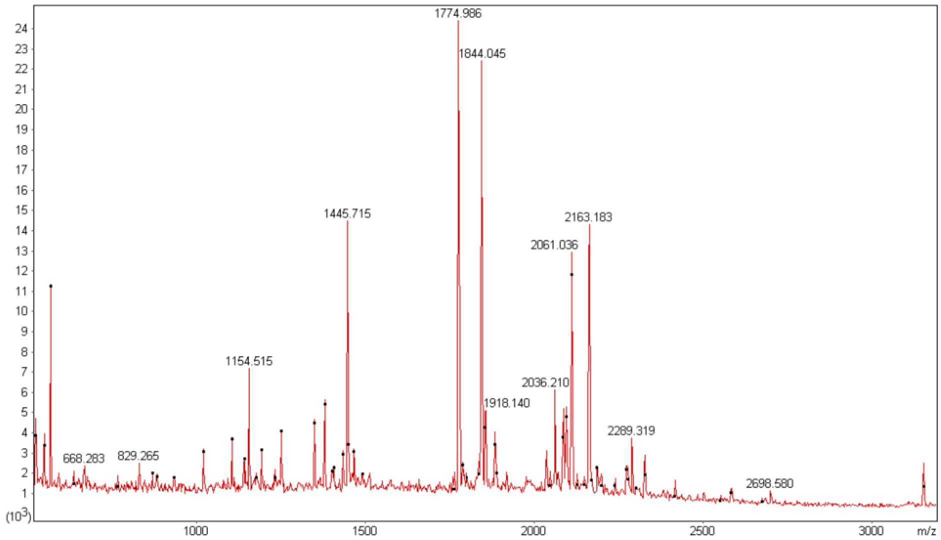
Protein name： **Actin-7**

PFF Mascot score: [96] **Sequence coverage %:** [7]

Matched peptides No.: [**2**] p value: **0.00065**

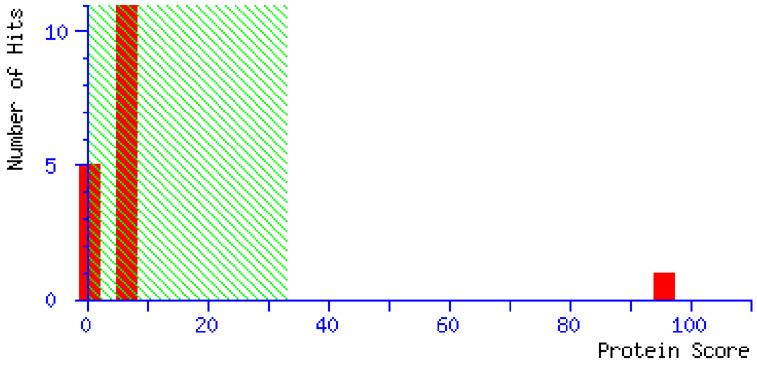
Calculated Mr: 41897 Calculated p*I*: **5.31**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **57**

NCBI accession No.: **cassava4.1_017832m|PACid:17961591**

Plant species: ***Manihot esculenta***

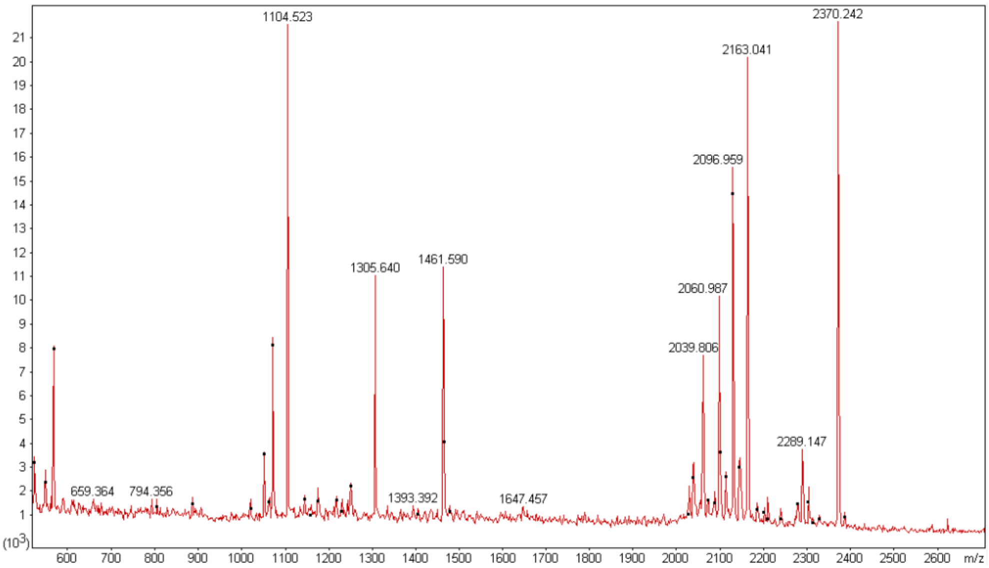
Protein name：**regulator of ribonuclease activity a**

PFF Mascot score: [133]   Sequence coverage %: [**16**]

Matched peptides No.: [**2**]   p value: **8.1e-007**

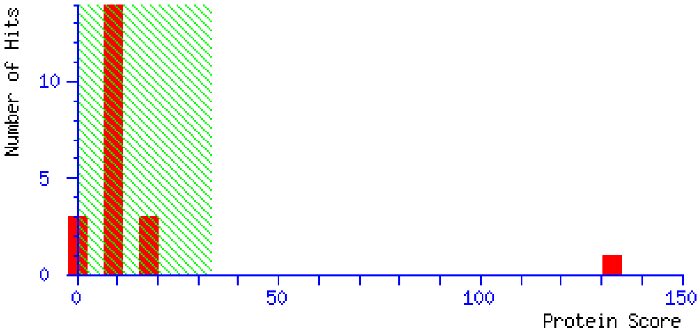
Calculated Mr: 18015   Calculated *p*I: **5.39**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **58**

NCBI accession No.: **cassava4.1_018059m|PACid:17963195**

Plant species: ***Manihot esculenta***

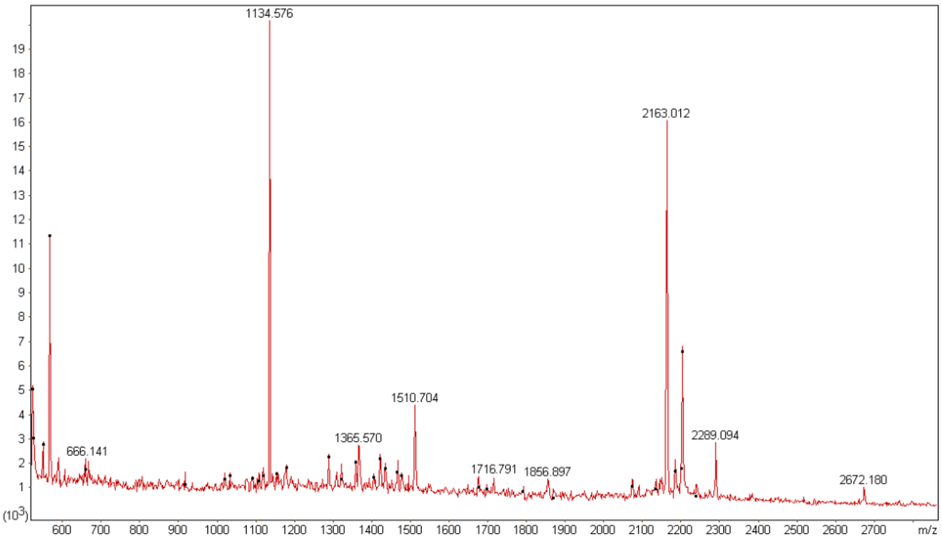
Protein name：**Eukaryotic translation initiation factor 5A-2**

PFF Mascot score: [66] **Sequence coverage %:** [**18]**

Matched peptides No.: [**2]** p value: **0.00026**

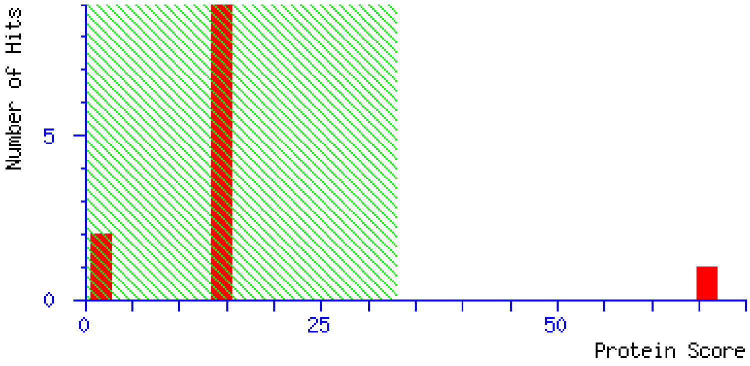
Calculated Mr: **17706** Calculated *p*I: **5.60**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **61**

NCBI accession No.: **cassava4.1_018737m|PACid:17986123**

Plant species: ***Manihot esculenta***

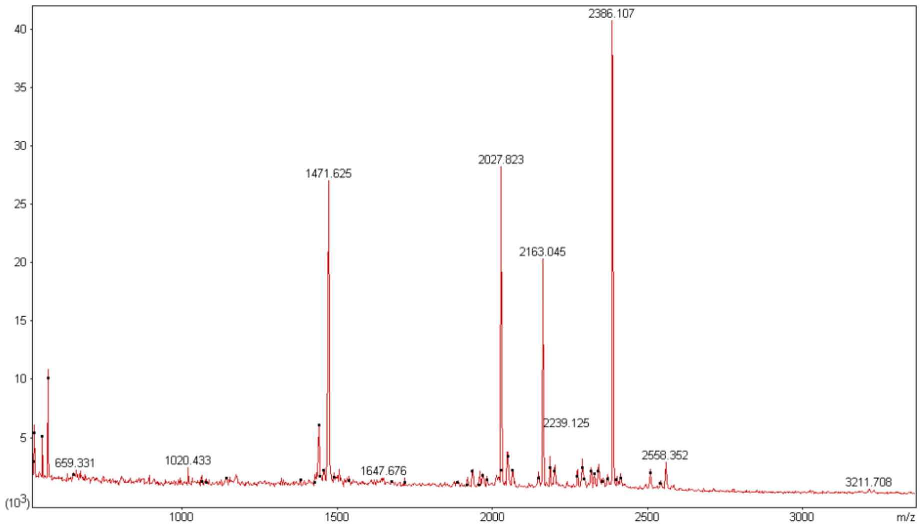
Protein name： **Actin-depolymerizing factor 3**

PFF Mascot score: [112] **Sequence coverage %: [11]**

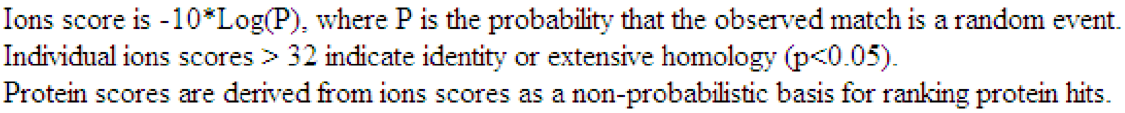
Matched peptides No.: **[2]** p value: **5.3e-010**

Calculated Mr: **16253** Calculated *p*I: **6.60**

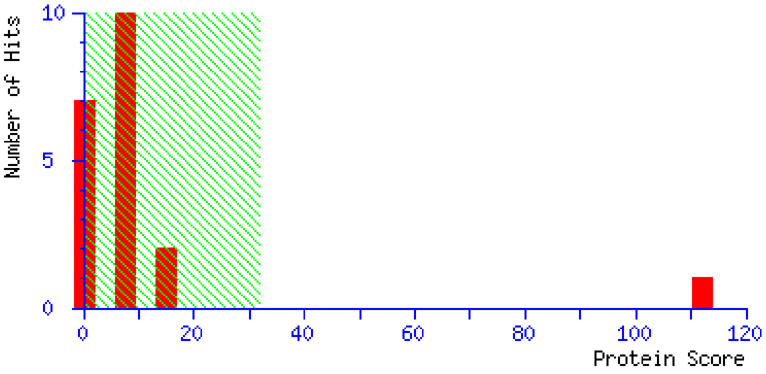
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 32 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **64**

NCBI accession No.: **cassava4.1_017973m|PACid:17985926**

Plant species: ***Manihot esculenta***

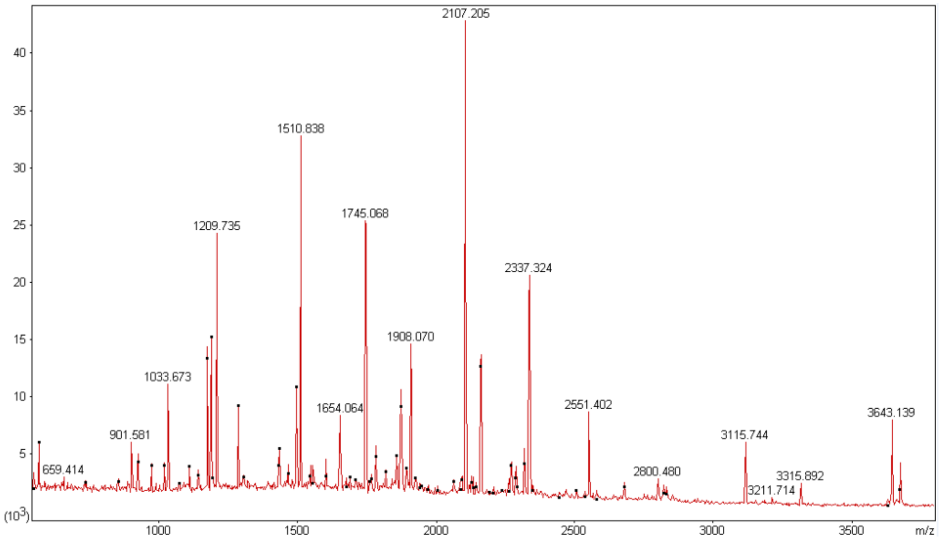
Protein name：**Peroxiredoxin-2B**

PFF Mascot score: [**180**] Sequence coverage %: **[22]**

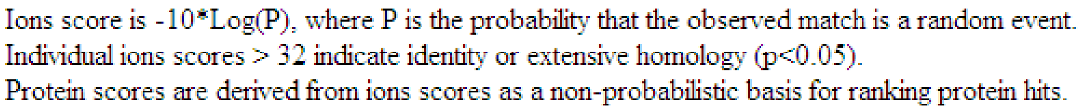
Matched peptides No.: [**10]** p value: 2e-013

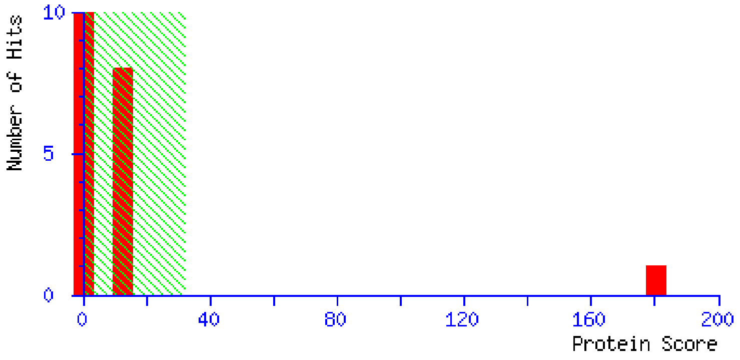
Calculated Mr: **17433** Calculated *p*I: **5.70**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 32 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **65**

NCBI accession No.: **cassava4.1_017871m|PACid:17980723**

Plant species: ***Manihot esculenta***

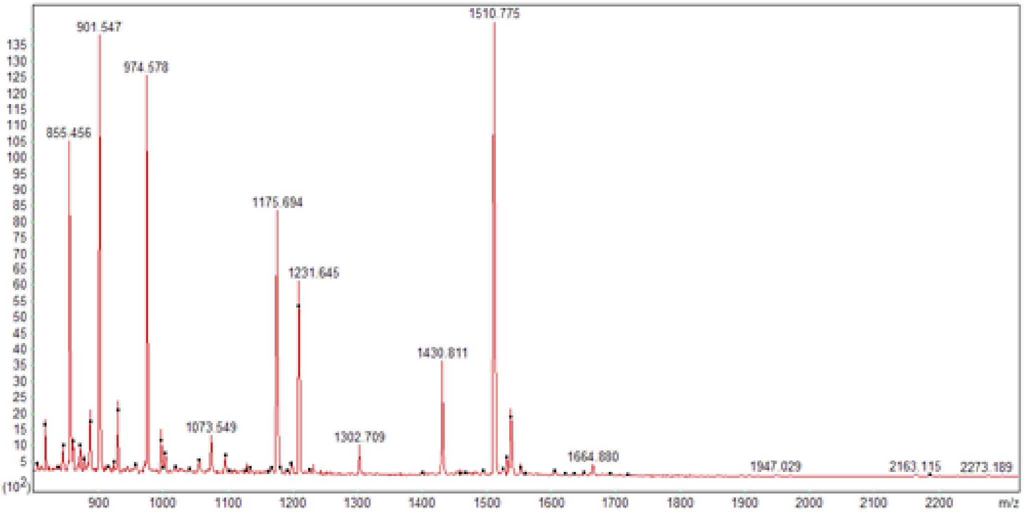
Protein name： **18.1 kDa class I heat shock protein**

PFF Mascot score: **[164]** Sequence coverage %: **[25]**

Matched peptides No.: **[5]** p value: **0.00017**

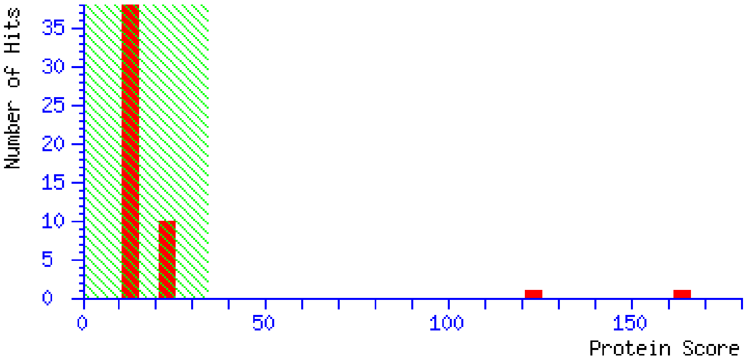
Calculated Mr: **18750** Calculated *p*I: **7.93**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **68**

NCBI accession No.: **cassava4.1_018338m|PACid:17992346**

Plant species: ***Manihot esculenta***

Protein name: **Ubiquitin-conjugating enzyme E2 variant 1C**

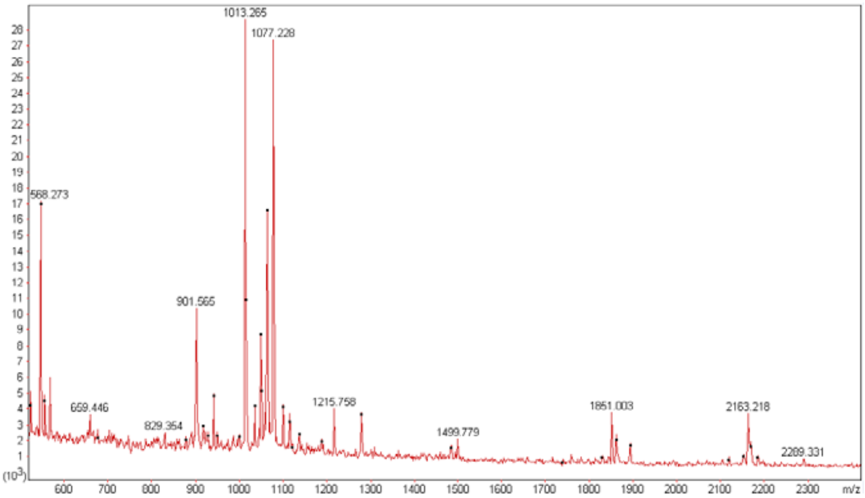
Mascot score: **119**

Sequence coverage %: **72** p value: **9.2e-008**

Matched peptides No.: **12** Total peptides No.: **37**

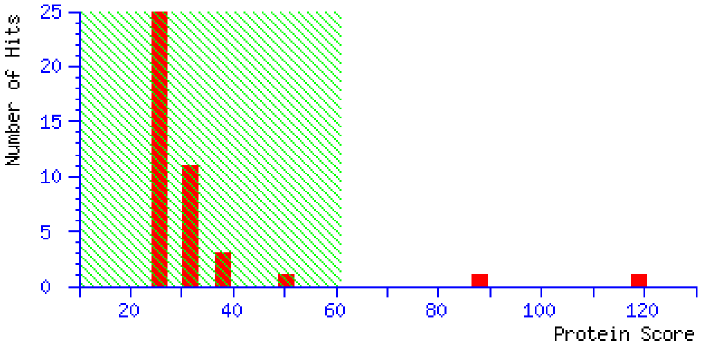
Calculated Mr: **17236** Calculated *p*I: **5.73**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **69**

NCBI accession No.: **cassava4.1_018010m|PACid:17970081**

Plant species: ***Manihot esculenta***

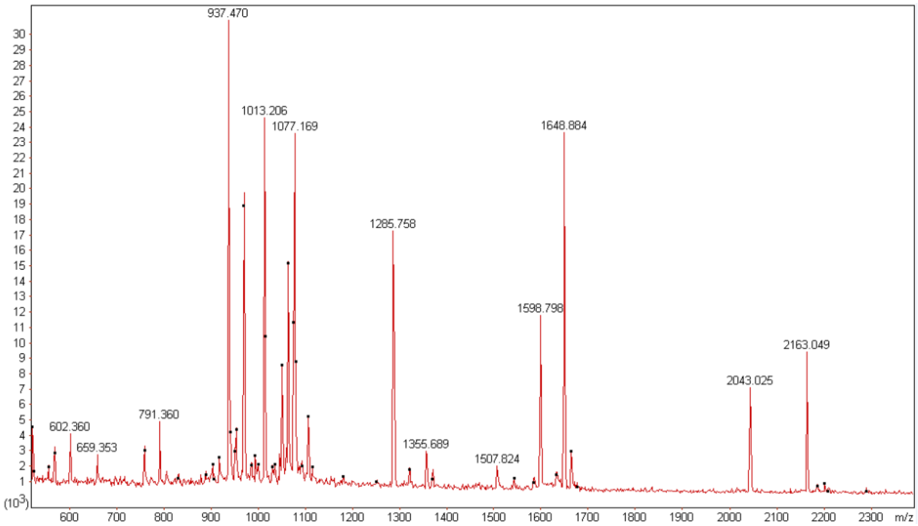
Protein name：**AT3g53990/F5K20_290**

PFF Mascot score: [195] **Sequence coverage %: [21]**

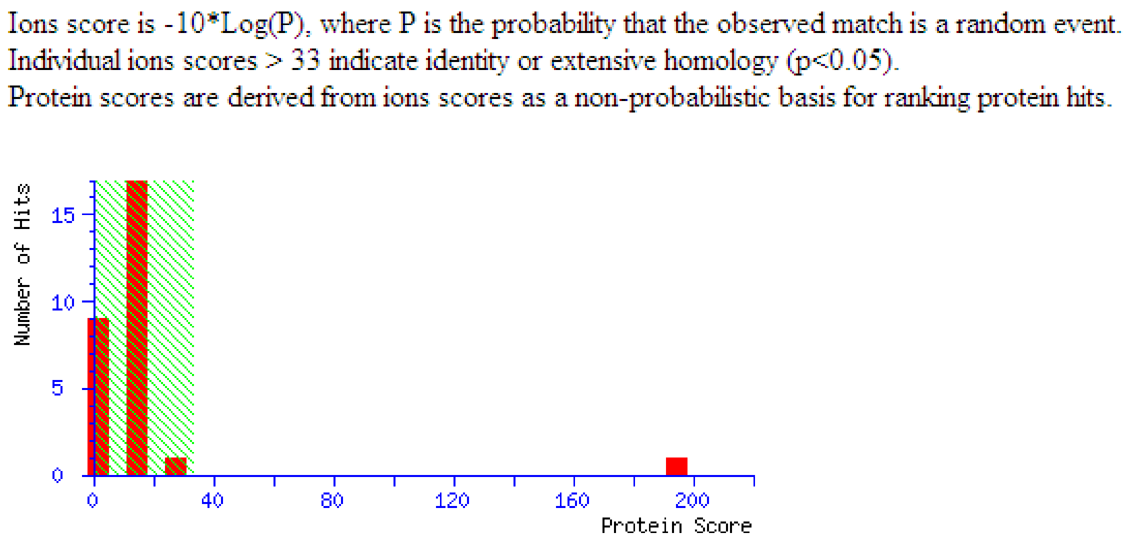
Matched peptides No.: **[3]** p value: **5.2e-006**

Calculated Mr: **18044** Calculated *p*I: **6.14**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Spot No.: 71

NCBI accession No.: cassava4.1_013840m|PACid:17968262

Plant species: ***Manihot esculenta***

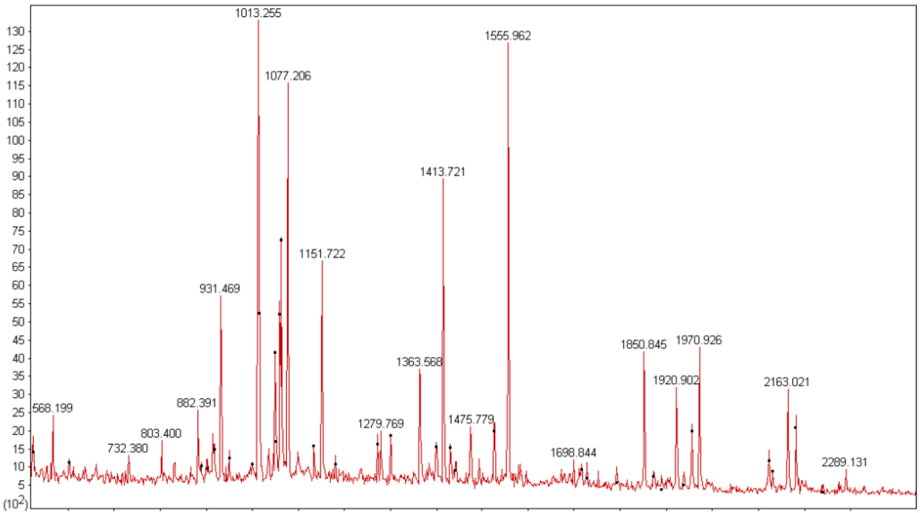
Protein name：**Proteasome subunit alpha type-2-A**

PFF Mascot score: [99] **Sequence coverage %: [8]**

Matched peptides No.: **[2]** p value: **0.0001**

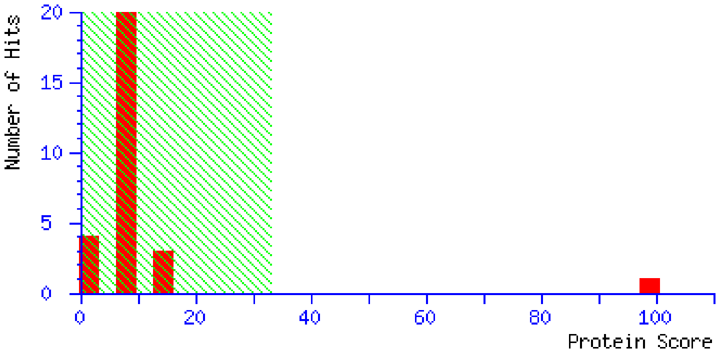
Calculated Mr: **29845** Calculated *p*I: **6.13**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **77**

NCBI accession No.: **cassava4.1_010971m|PACid:17987784**

Plant species: ***Manihot esculenta***

Protein name：**Thiamine thiazole synthase, chloroplastic**

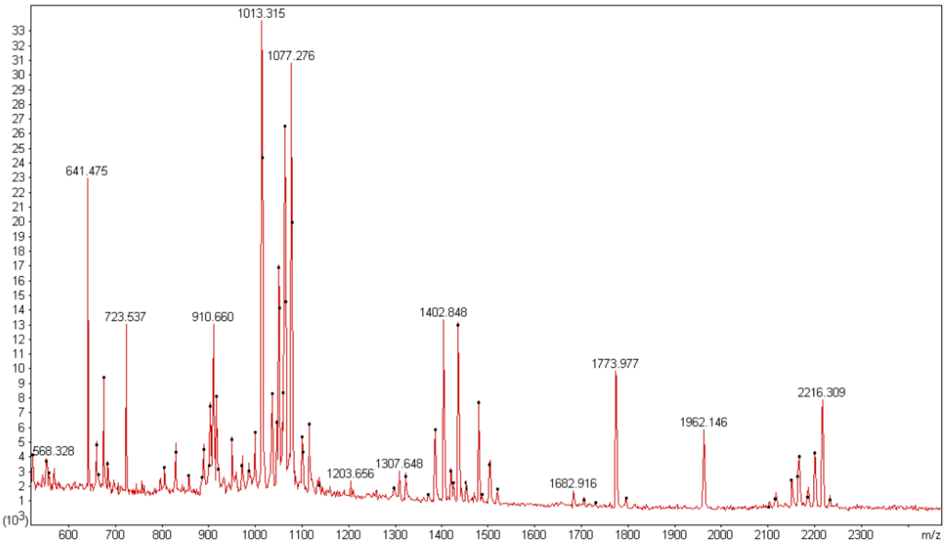
Mascot score: **88**

Sequence coverage %: **38**   p value: **`0.00011`**

Matched peptides No.: **17**   Total peptides No.: **70**

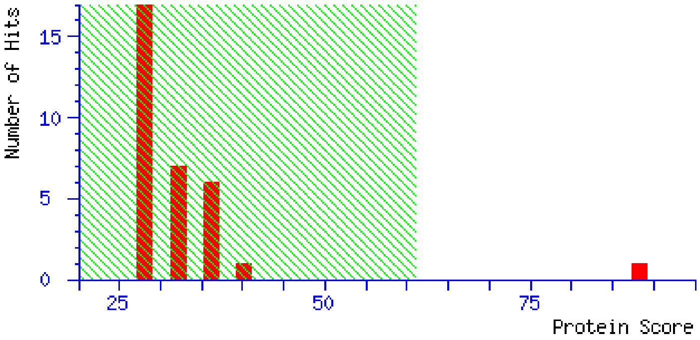
Calculated Mr: **36908**   Calculated *p*I: **7.10**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **78**

NCBI accession No.: **cassava4.1_009245m|PACid:17963775**

Plant species: ***Manihot esculenta***

Protein name：**S-adenosylmethionine synthase 1**

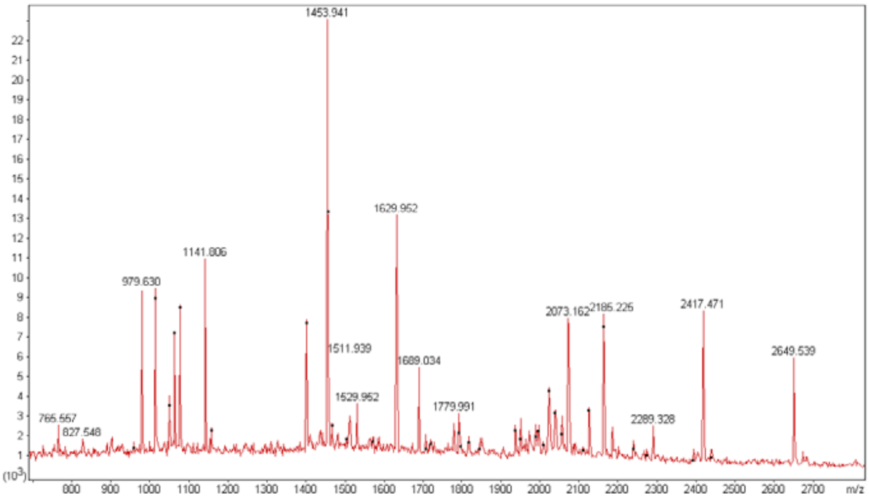
Mascot score: **119**

Sequence coverage %: **55** p value: **9.2e-008**

Matched peptides No.: **16** Total peptides No.: **54**

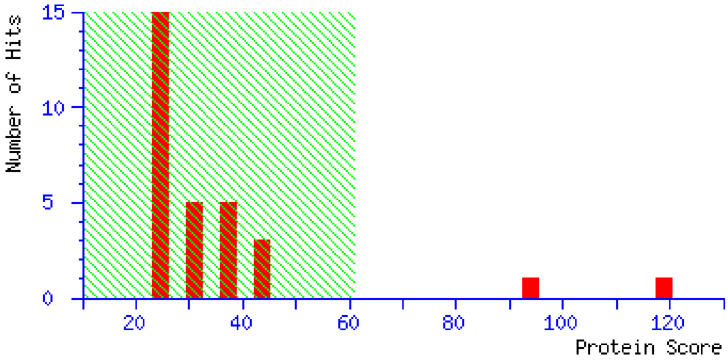
Calculated Mr: **43709** Calculated *p*I: **5.68**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **79**

NCBI accession No.: **cassava4.1_011550m|PACid:17993466**

Plant species: ***Manihot esculenta***

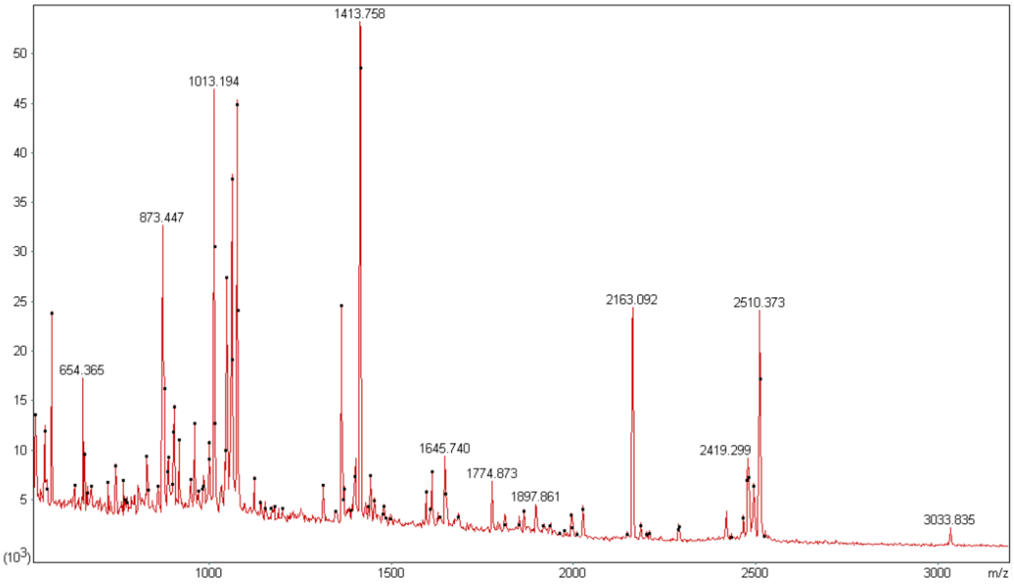
Protein name： **predicted protein** Mascot score: **108**

Sequence coverage %: **50** p value: **`1.2e-006`**

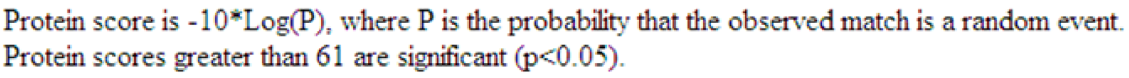
Matched peptides No.: **17** Total peptides No.: **67**

Calculated Mr: **36178** Calculated *p*I: **6.09**

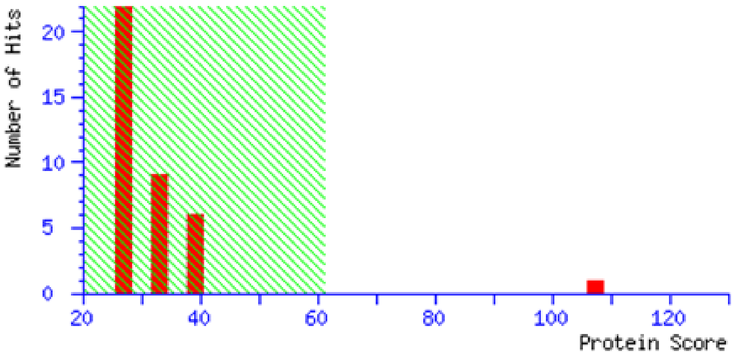
Annotated PMF **spectra:**



Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **86**

NCBI accession No.: **cassava4.1_004164m|PACid:17985770**

Plant species: ***Manihot esculenta***

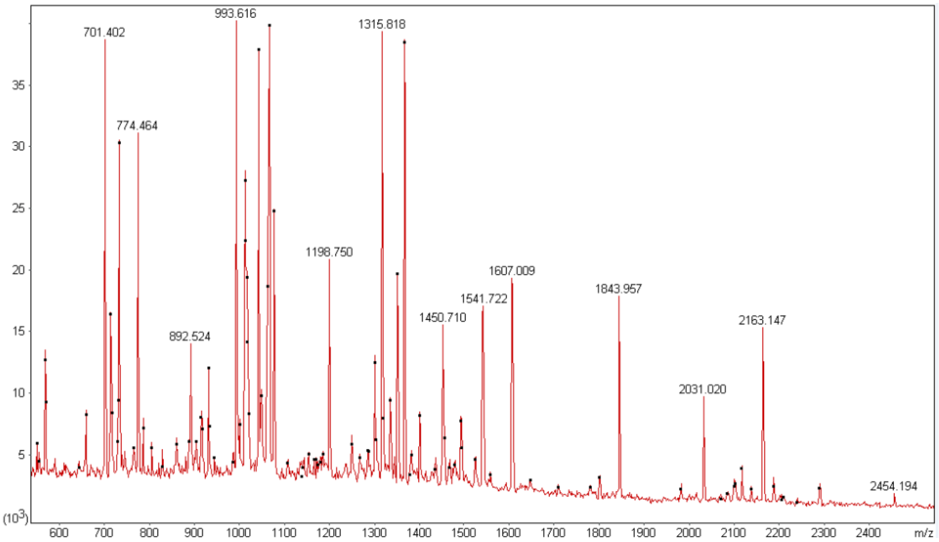
Protein name：**malic enzyme, putative** Mascot score: **177**

Sequence coverage %: **47** p value: **1.5e-013**

Matched peptides No.: **33** Total peptides No.: **90**

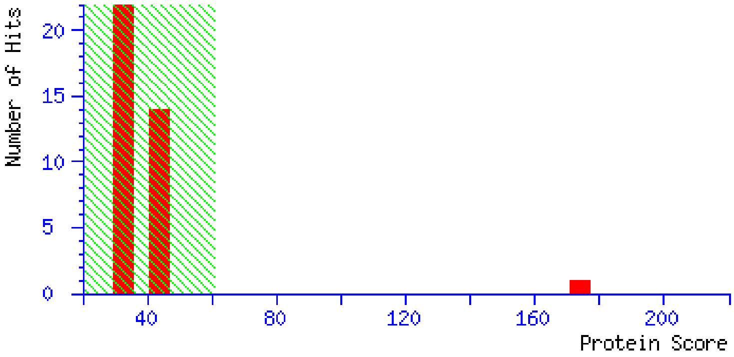
Calculated Mr: **65246** Calculated *p*I: **6.03**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **88**

NCBI accession No.: **cassava4.1_007678m|PACid:17961094**

Plant species: ***Manihot esculenta*** Mascot score: **160**

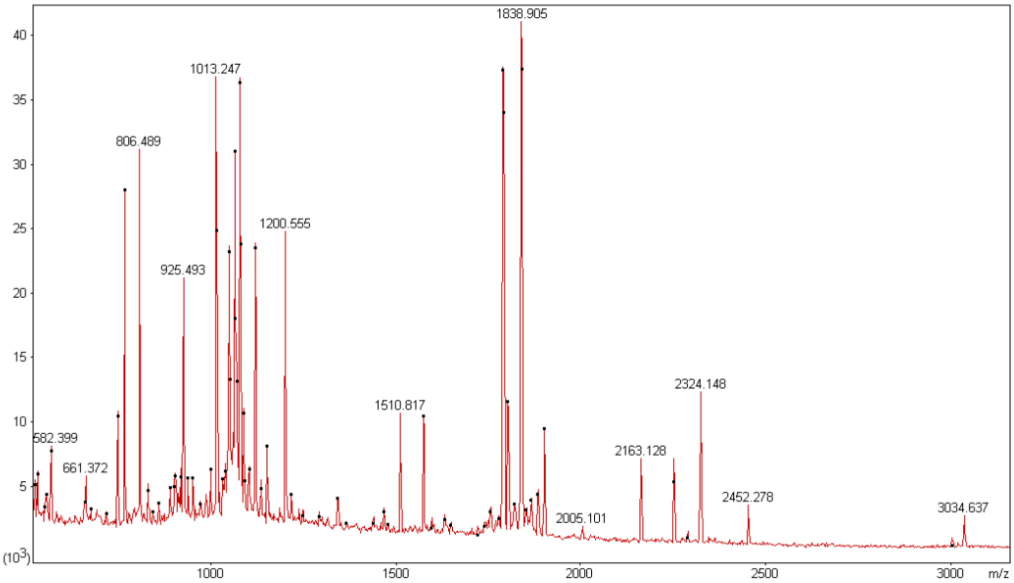
Protein name: **Bifunctional enolase 2/transcriptional activator**

Sequence coverage %: **62** p value: **7.3e-012**

Matched peptides No.: **25** Total peptides No.: **78**

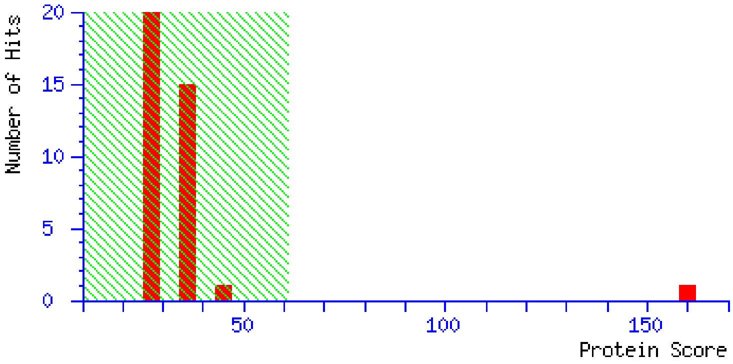
Calculated Mr: **47854** Calculated *p*I: **5.86**

Annotated PMF **spectra:**



Probability Based Mowse Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event. Protein scores greater than 61 are significant (p<0.05).



Spot No.: **89**

NCBI accession No.: **cassava4.1_003677m|PACid:17968299**

Plant species: ***Manihot esculenta*** Mascot score: **234**

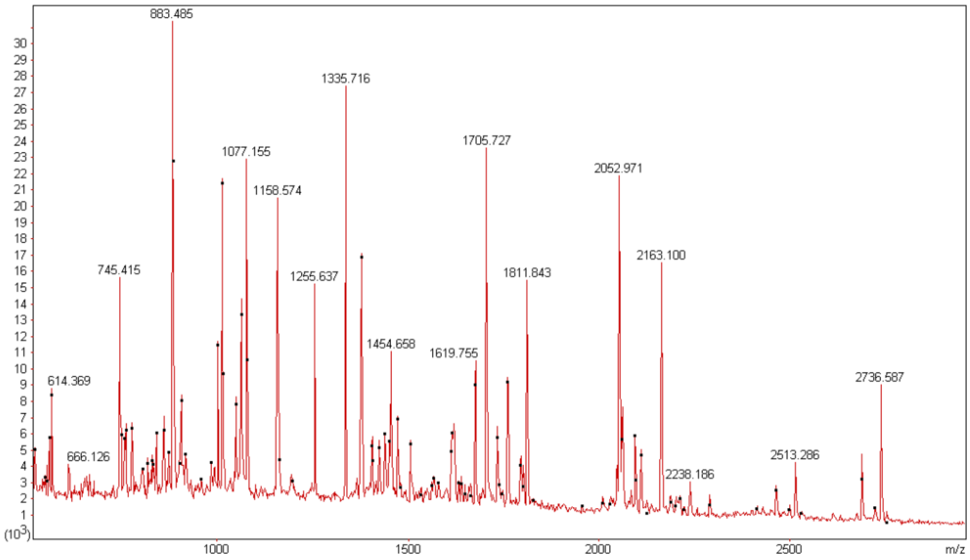
Protein name：**V-type proton ATPase catalytic subunit A**

Sequence coverage %: **61** p value: **2.9e-019**

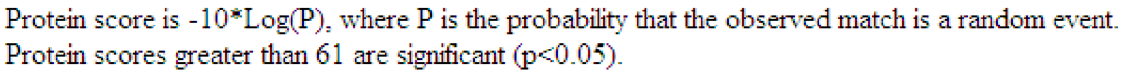
Matched peptides No.: **41** Total peptides No.: **95**

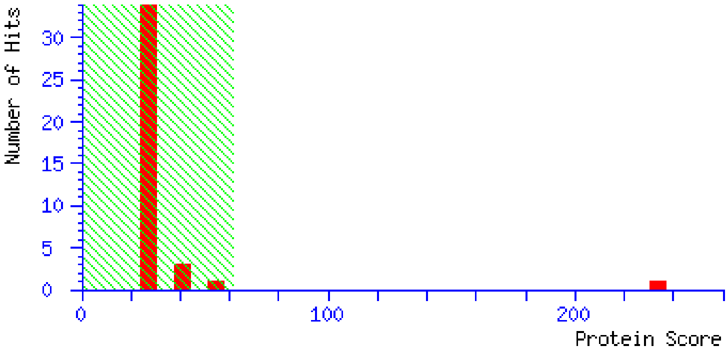
Calculated Mr: **68989** Calculated *p*I: **5.29**

Annotated PMF **spectra:**



Probability Based Mowse Score:


Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).



Spot No.: **92**

NCBI accession No.: **cassava4.1_004164m|PACid:17985770**

Plant species: ***Manihot esculenta***

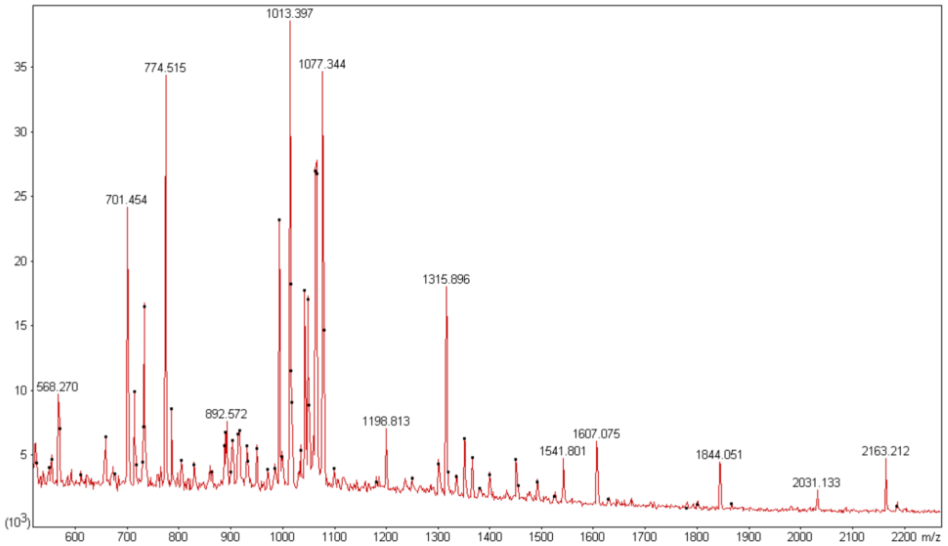
Protein name: **malic enzyme, putative** Mascot score: **154**

Sequence coverage %: **35** p value: **2.9e-11**

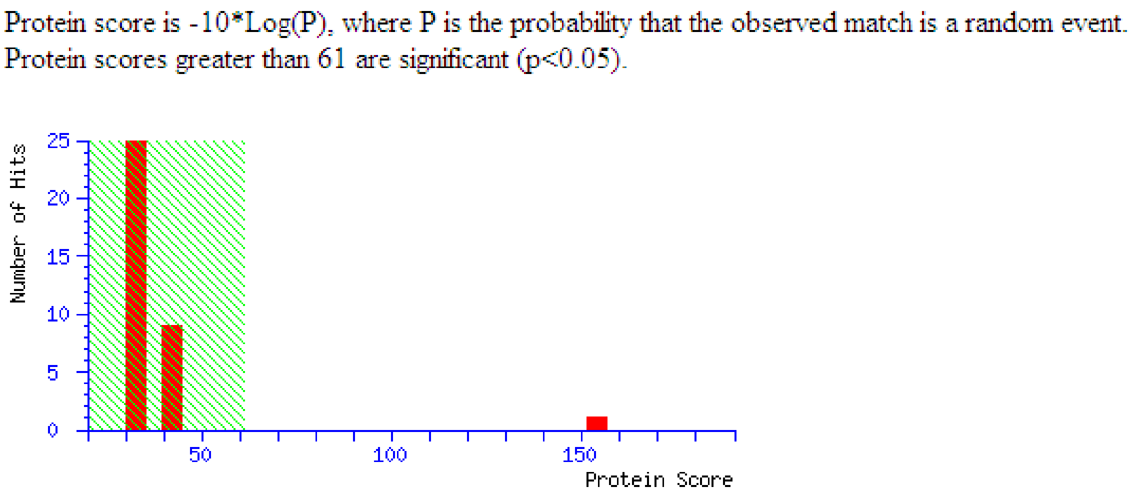
Matched peptides No.: **26** Total peptides No.: **66**

Calculated Mr: **65246** Calculated *p*I: **6.03**

Annotated PMF **spectra:**



Probability Based Mowse Score:



Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant (p<0.05).

Spot No.: **94**

NCBI accession No.: **cassava4.1_002466m|PACid:17978799**

Plant species: ***Manihot esculenta***

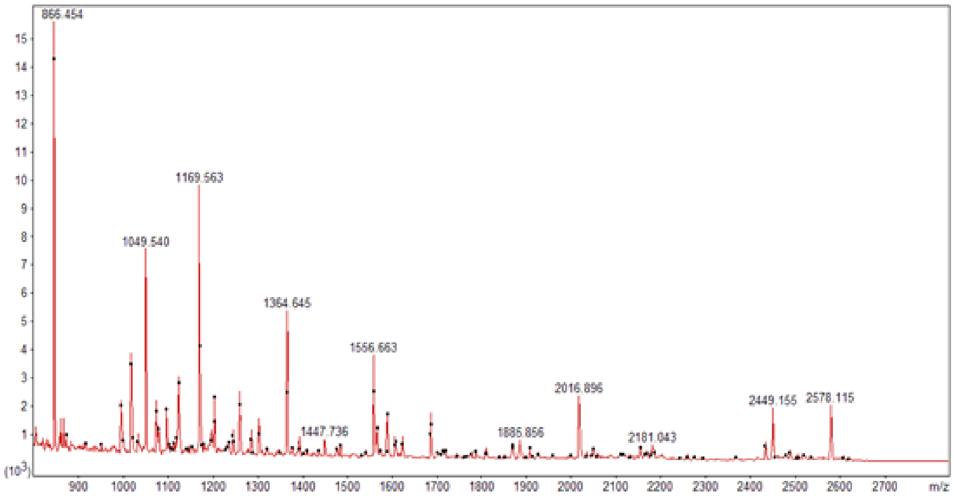
Protein name：**Alpha-glucan phosphorylase 1**

PFF Mascot score: **[278]** Sequence coverage %: **[12]**

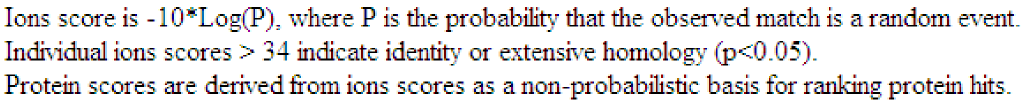
Matched peptides No.: **[7]** p value: **1.1e-007**

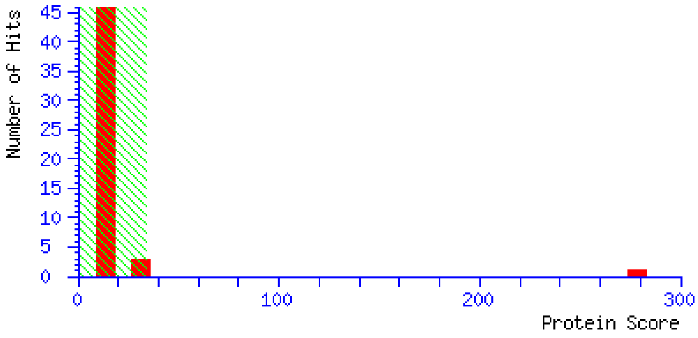
Calculated Mr: 81918 Calculated *p*I: **8.50**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **97**

NCBI accession No.: **cassava4.1_011729m|PACid:17989246**

Plant species: ***Manihot esculenta***

Protein name：**nitrile-specifier protein 5-like**

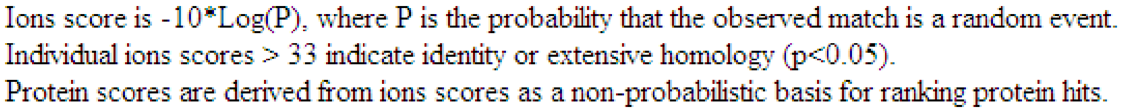
PFF Mascot score: **[165]**　　　Sequence coverage %: **[24]**

Matched peptides No.: **[7]**　　　p value: **0.00081**

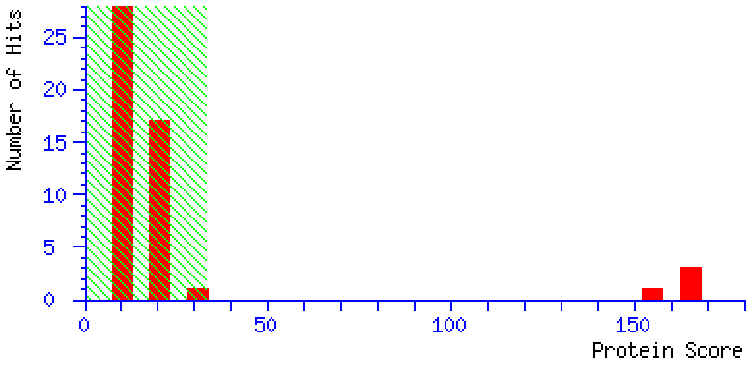
Calculated Mr: 35840　　　Calculated *p*I: **5.49**

Annotated PMF **spectra:**

PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology ($p<0.05$).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **105**

NCBI accession No.: **cassava4.1_017871m|PACid:17980723**

Plant species: ***Manihot esculenta***

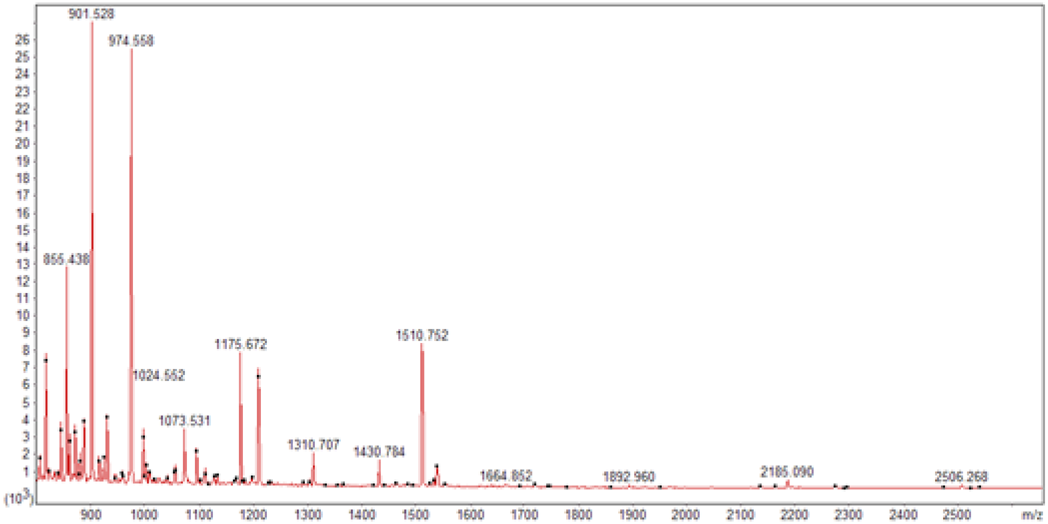
Protein name：**18.1 kDa class I heat shock protein**

PFF Mascot score: **[142]** Sequence coverage %: **[23]**

Matched peptides No.: **[5]** p value: **0.00014**

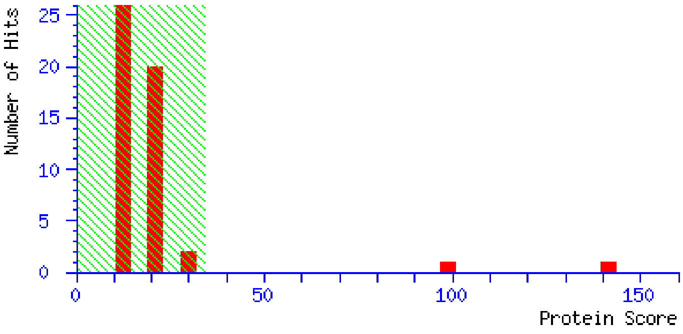
Calculated Mr: 18750 Calculated *p*I: **7.93**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **113**

NCBI accession No.: **cassava4.1_009779m|PACid:17990964**

Plant species: ***Manihot esculenta***

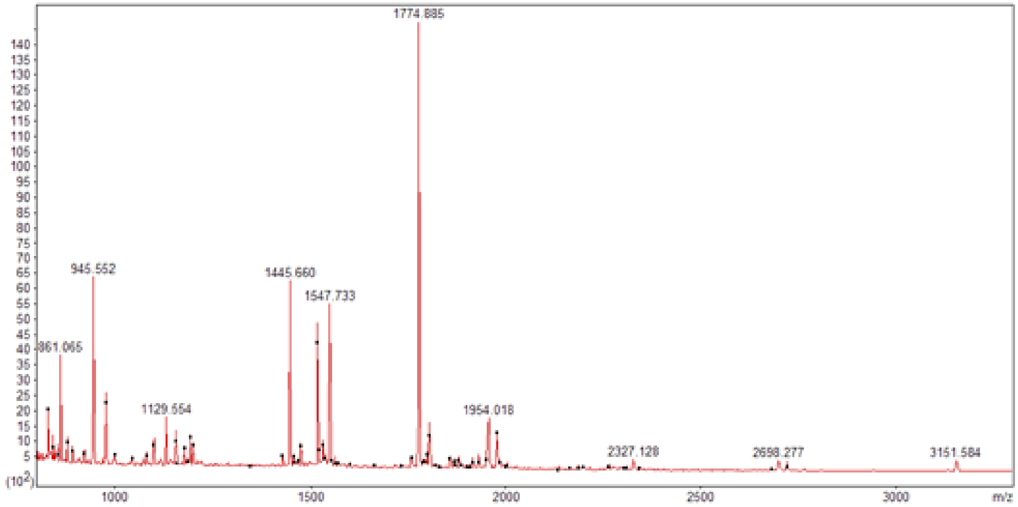
Protein name： **Actin-7**

PFF Mascot score: **[440]** Sequence coverage %: **[36]**

Matched peptides No.: **[9]** p value: **2.9e-012**

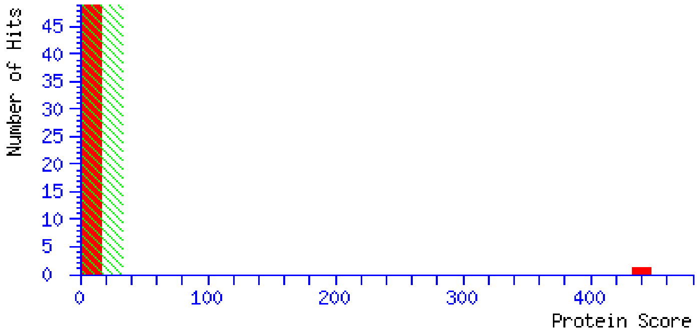
Calculated Mr: 41897 Calculated *p*I: **5.31**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **118**

NCBI accession No.: **cassava4.1_005314m|PACid:17981128**

Plant species: ***Manihot esculenta***

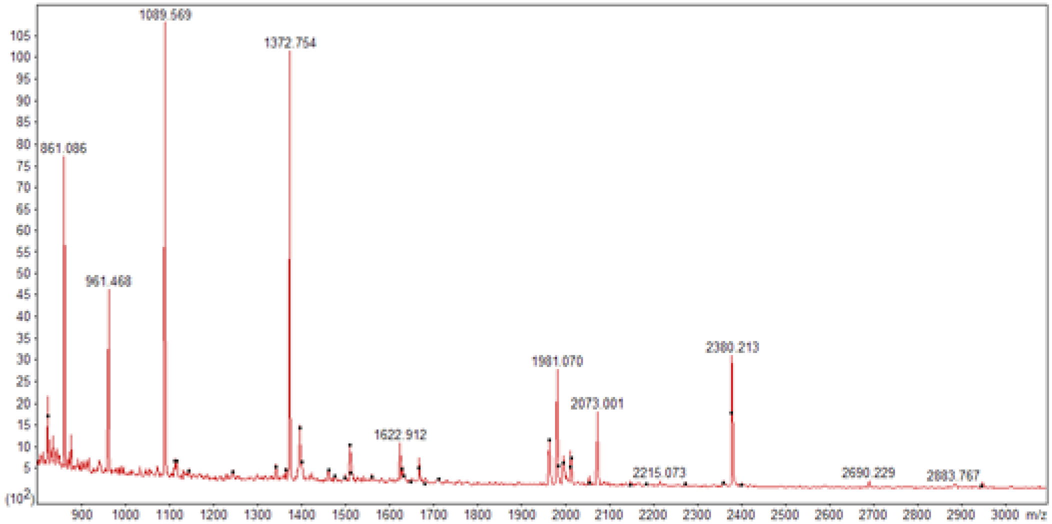
Protein name：**Ketol-acid reductoisomerase, chloroplastic**

PFF Mascot score: **[214]** Sequence coverage %: **[9]**

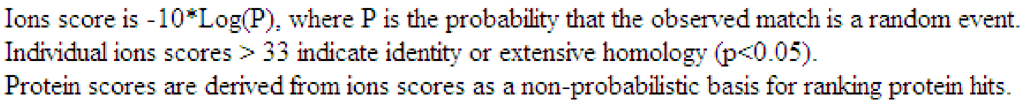
Matched peptides No.: **[4]** p value: **9.6e-005**

Calculated Mr: **58515** Calculated *p*I: **5.50**

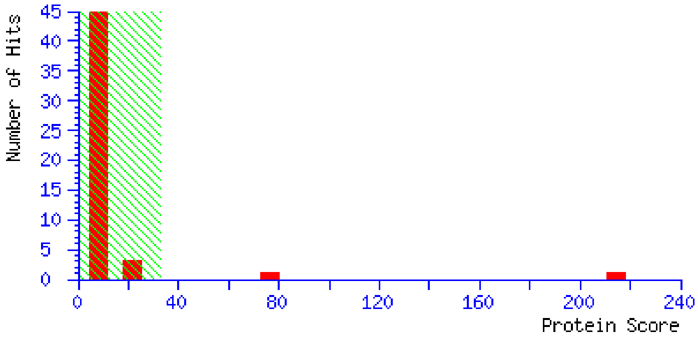
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **130**

NCBI accession No.: **cassava4.1_001644m|PACid:17971276**

Plant species: ***Manihot esculenta***

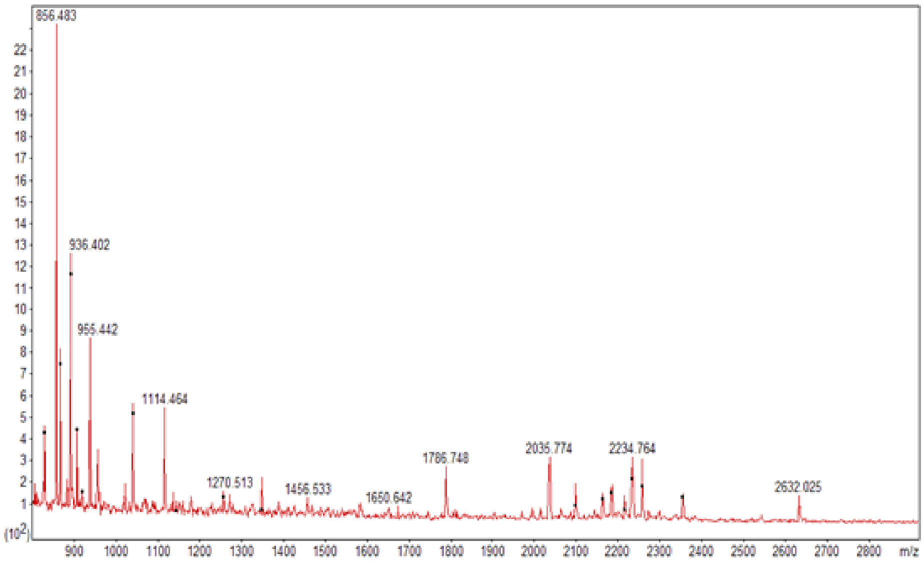
Protein name： **At1g56070/T6H22_13**

PFF Mascot score: **[184]** Sequence coverage %: **[10]**

Matched peptides No.: **[7]** p value: **`2.5e-005`**

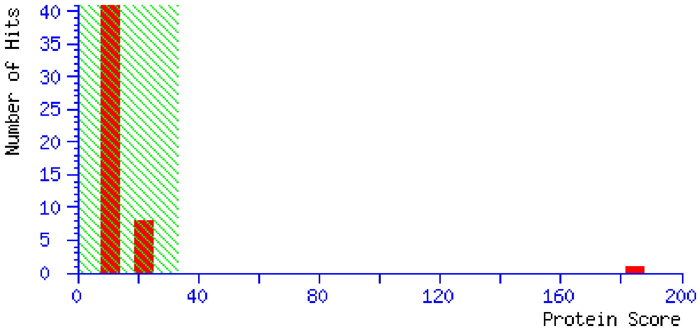
Calculated Mr: **95045** Calculated *p*I: **5.86**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **131**

NCBI accession No.: **cassava4.1_002747m|PACid:17960141**

Plant species: ***Manihot esculenta***

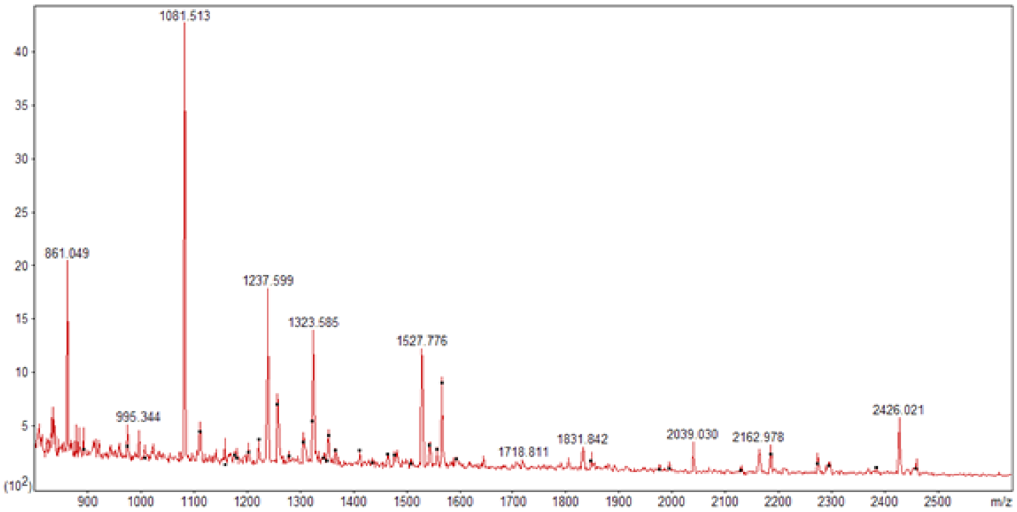
Protein name：**Heat shock protein 90-3**

PFF Mascot score: **[181]** Sequence coverage %: **[7]**

Matched peptides No.: **[4]** p value: **0.00052**

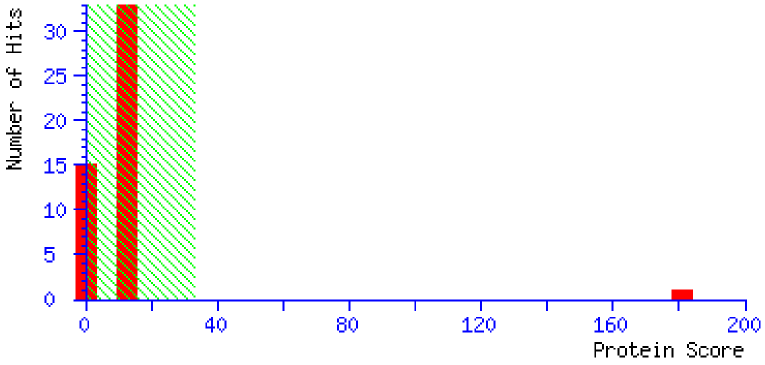
Calculated Mr: **80250** Calculated *p*I: **4.99**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **132**

NCBI accession No.: **cassava4.1_002716m|PACid:17962449**

Plant species: ***Manihot esculenta***

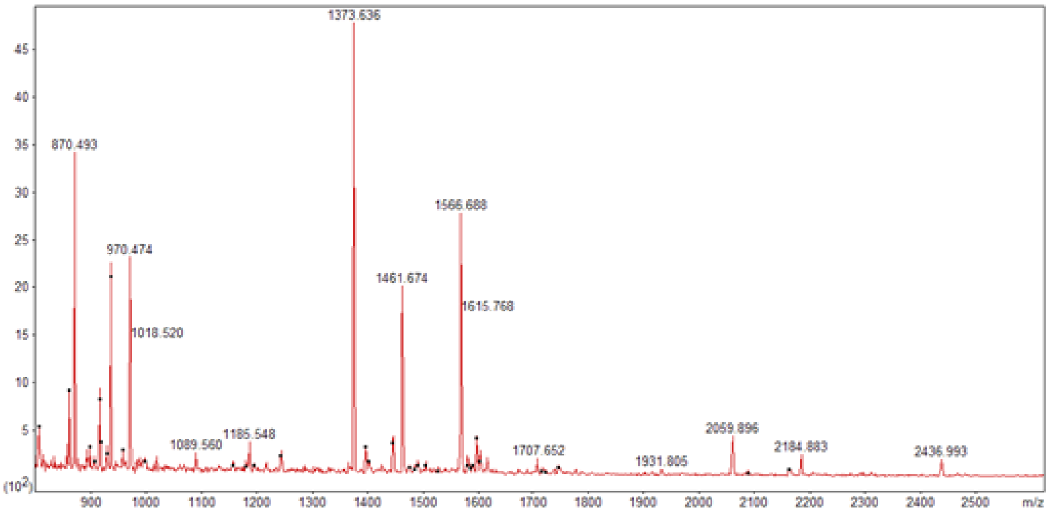
Protein name： **Heat shock 70 kDa protein 7, chloroplastic**

PFF Mascot score: **[516]**   Sequence coverage %: **[16]**

Matched peptides No.: **[9]**   p value: **1.7e-012**

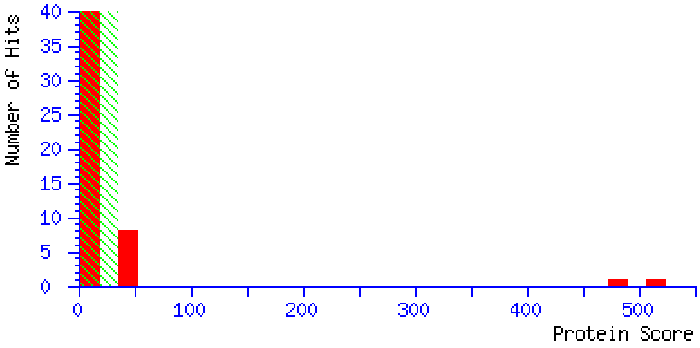
Calculated Mr: **75341**   Calculated *p*I: **5.20**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **133**

NCBI accession No.: **cassava4.1_002706m|PACid:17974818**

Plant species: ***Manihot esculenta***

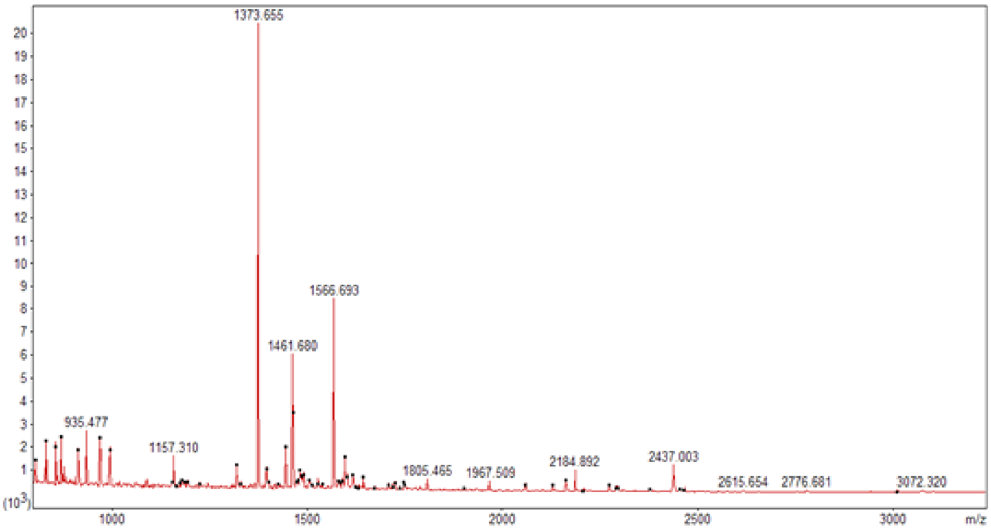
Protein name: **Heat shock 70 kDa protein 7, chloroplastic**

PFF Mascot score: **[386]** Sequence coverage %: **[12]**

Matched peptides No.: **[7]** p value: **6.6e-011**

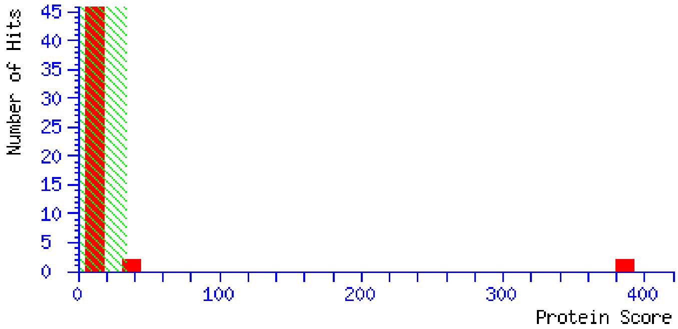
Calculated Mr: **75452** Calculated *p*I: **5.24**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **134**

NCBI accession No.: **cassava4.1_005468m|PACid:17987918**

Plant species: ***Manihot esculenta***

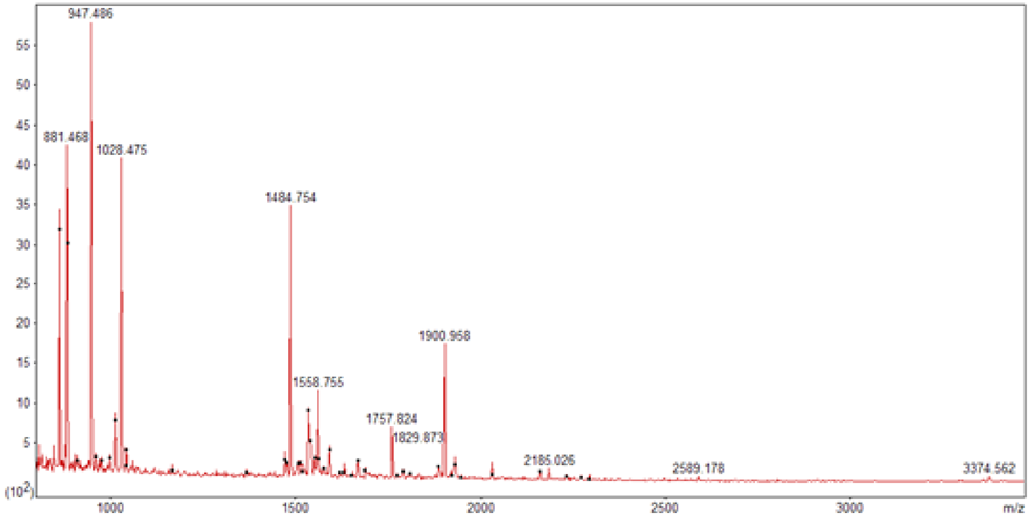
Protein name：**Putative S9 Tyrosyl aminopeptidase**

PFF Mascot score: **[305]**　　Sequence coverage %: **[14]**

Matched peptides No.: **[6]**　　p value: **1.6e-007**

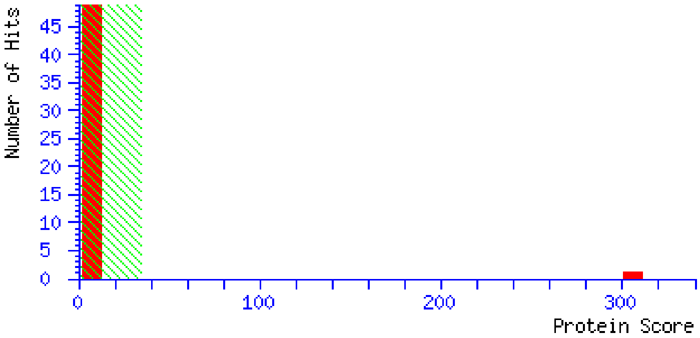
Calculated Mr: **59341**　　Calculated *p*I: **4.99**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **135**

NCBI accession No.: **cassava4.1_002307m|PACid:17988755**

Plant species: ***Manihot esculenta***

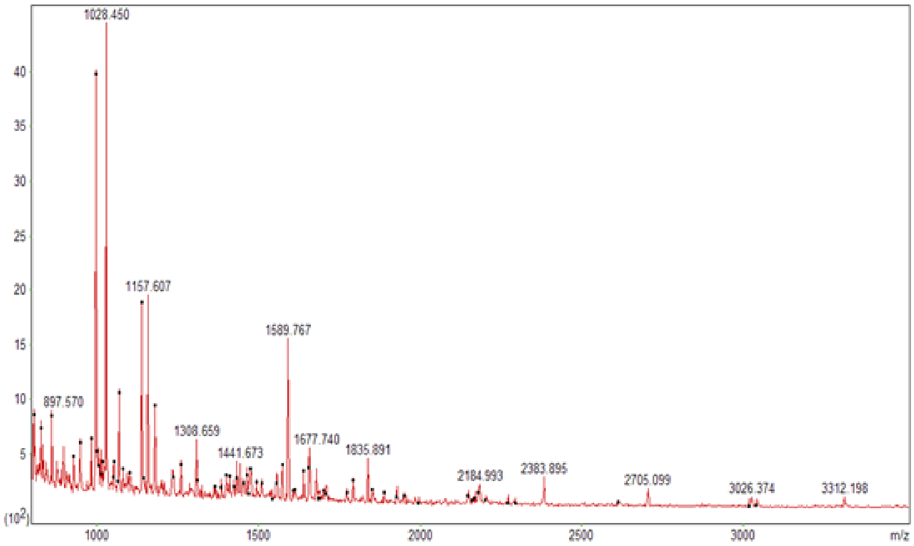
Protein name：**Transketolase-2, chloroplastic**

PFF score: **78** Sequence coverage %: **[7]**

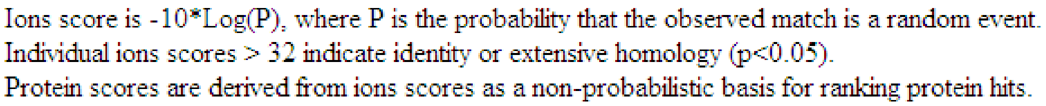
Matched peptides No.: **[2]** p value: **0.0001**

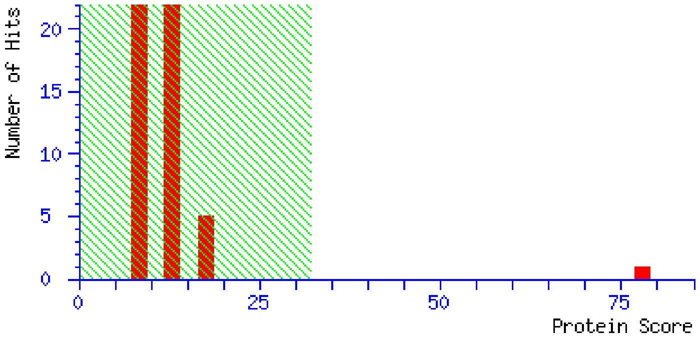
Calculated Mr: **80925** Calculated *p*I: **6.31**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 32 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **136**

NCBI accession No.: **cassava4.1_006409m|PACid:17968834**

Plant species: ***Manihot esculenta***

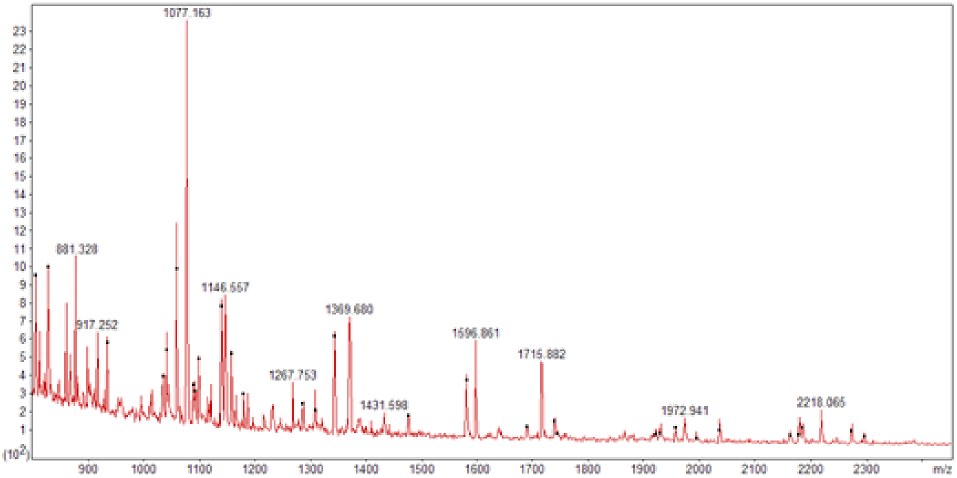
Protein name： **V-type proton ATPase subunit B3**

PFF Mascot score: **[78]** Sequence coverage %: **[8]**

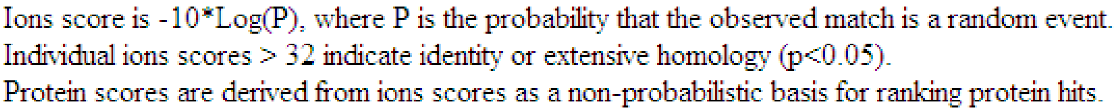
Matched peptides No.: **[2]** p value: **0.0009**

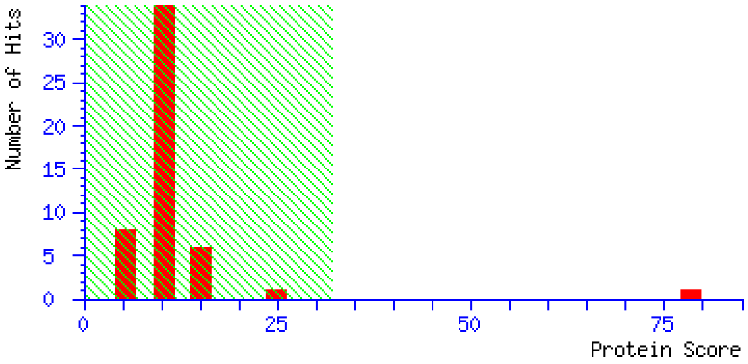
Calculated Mr: **54514** Calculated *p*I: **4.91**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 32 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **137**

NCBI accession No.: **cassava4.1_007650m|PACid:17967223**

Plant species: ***Manihot esculenta***

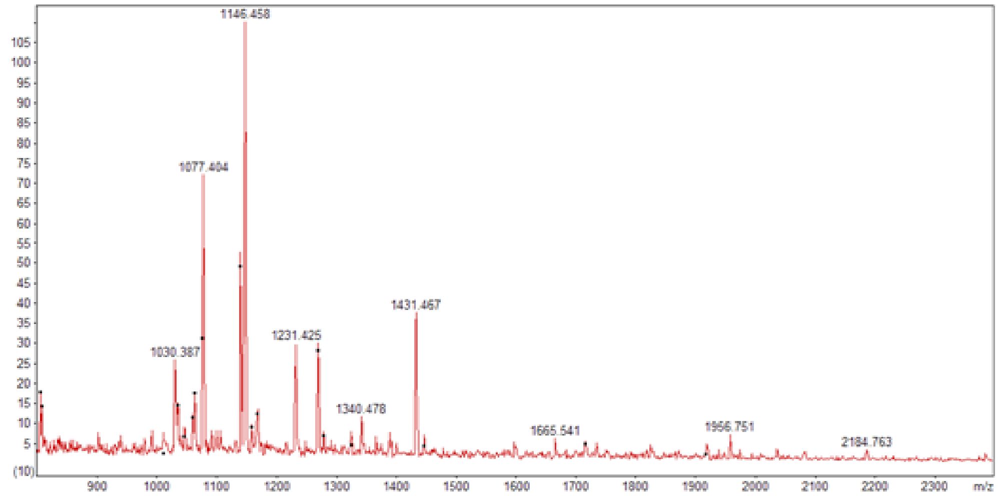
Protein name：**Tubulin beta-6 chain**

PFF Mascot score: **[193]** Sequence coverage %: **[11]**

Matched peptides No.: **[5]** p value: **0.00015**

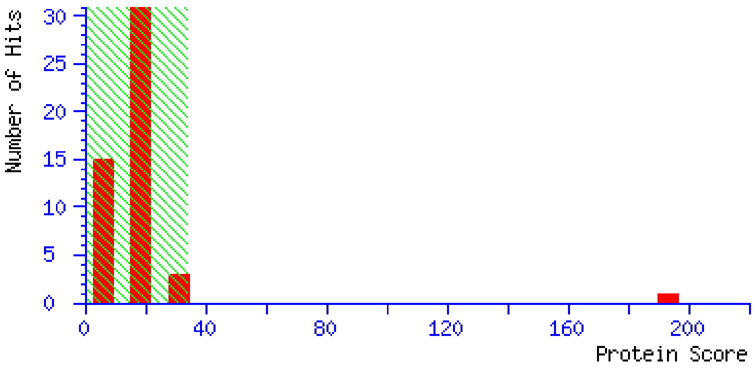
Calculated Mr: **50741** Calculated *p*I: **4.77**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **138**

NCBI accession No.: **cassava4.1_005250m|PACid:17973850**

Plant species: ***Manihot esculenta***

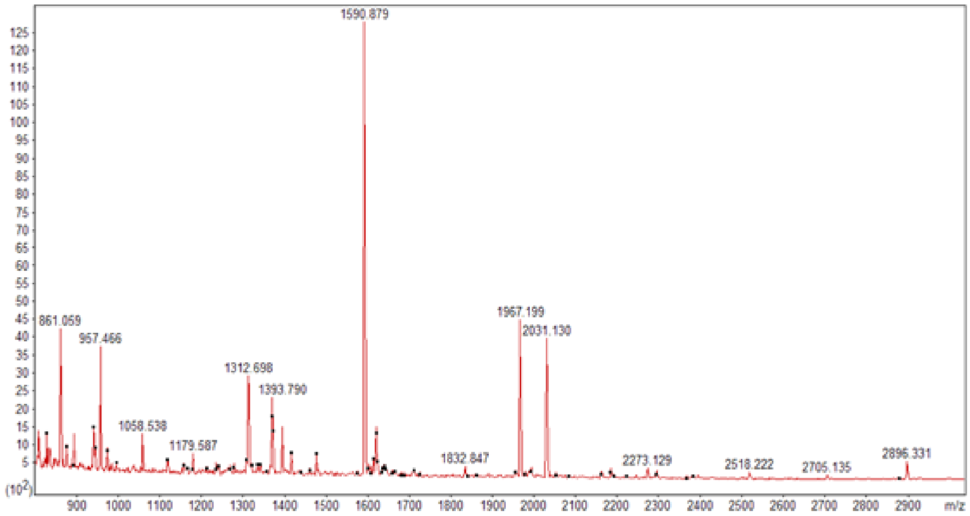
Protein name：**Importin subunit alpha-1**

PFF Mascot score: **[195]** Sequence coverage %: **[13]**

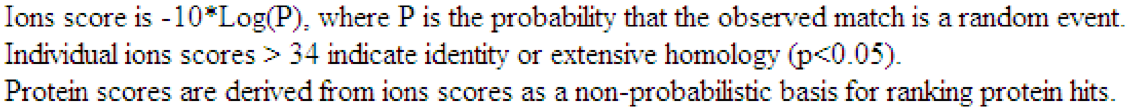
Matched peptides No.: **[4]** p value: **1.6e-009**

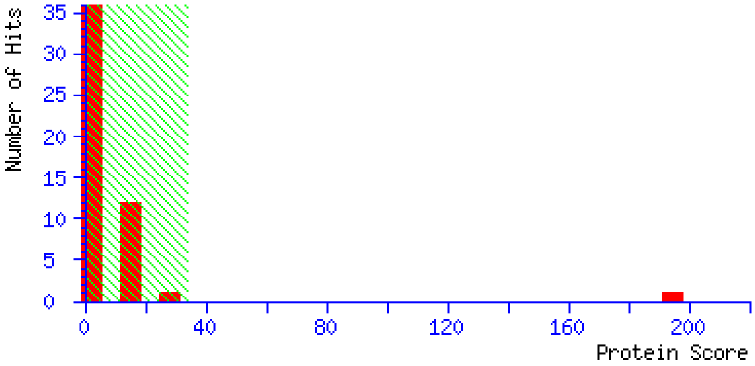
Calculated Mr: **59677** Calculated *p*I: **5.30**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **139**

NCBI accession No.: **cassava4.1_007640m|PACid:17979054**

Plant species: ***Manihot esculenta***

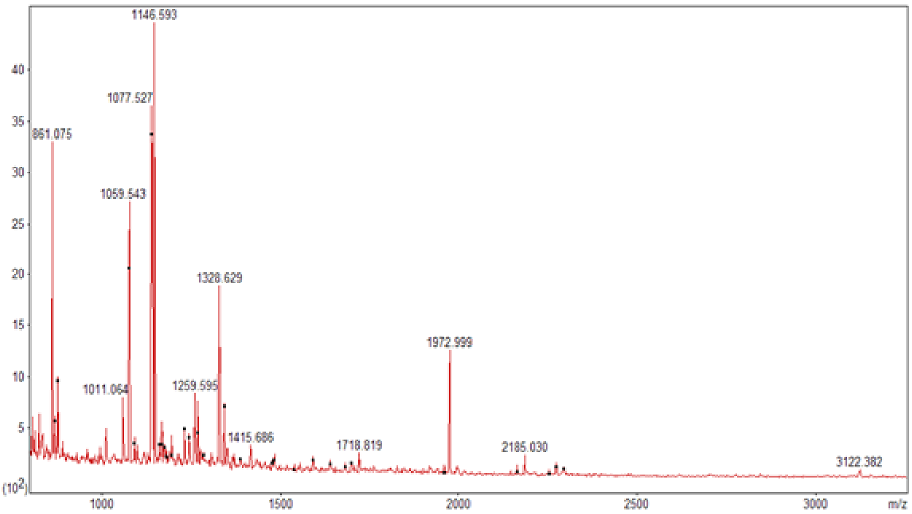
Protein name：**Tubulin beta-6 chain**

PFF Mascot score: **[170]** Sequence coverage %: **[10]**

Matched peptides No.: **[4]** p value: **1.1e-008**

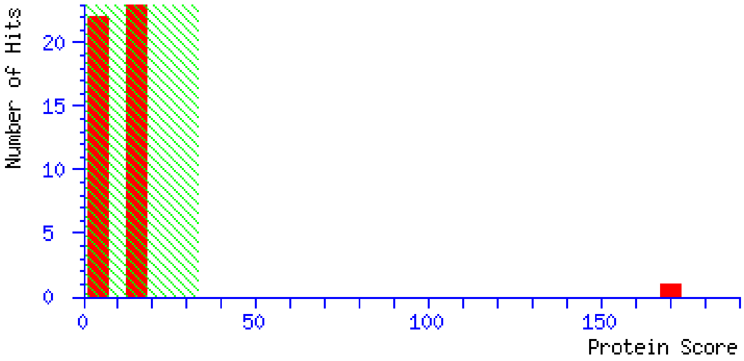
Calculated Mr: **50722** Calculated *p*I: **4.68**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **140**

NCBI accession No.: **cassava4.1_006508m|PACid:17967572**

Plant species：Manihot esculenta

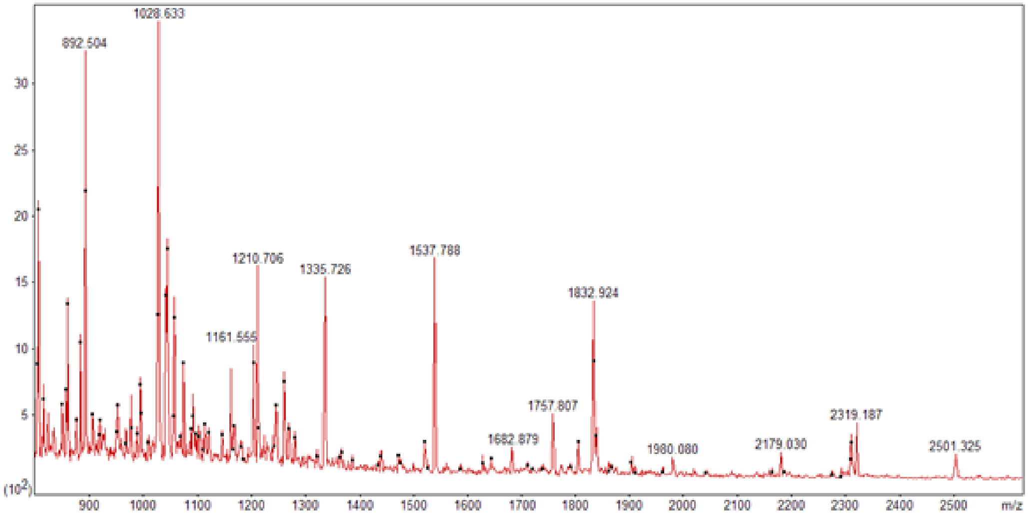
Protein name：**Adenosylhomocysteinase 1**

PFF Mascot score: **[65]**   Sequence coverage %: **[10]**

Matched peptides No.: **[4]**   p value: **0.0011**

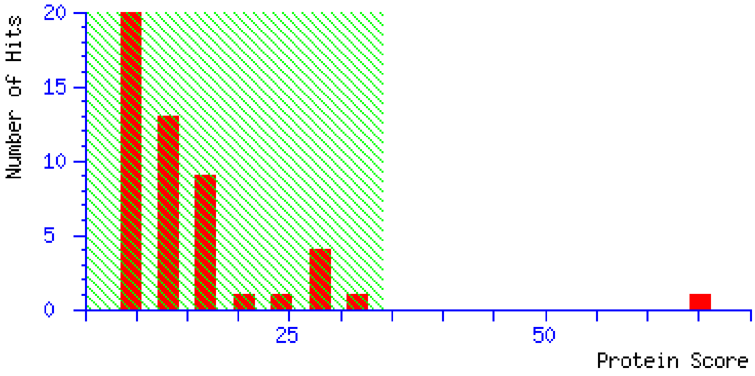
Calculated Mr: **53894**   Calculated *p*I: **5.86**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **141**

NCBI accession No.: cassava4.1_020254m|PACid:17972349

Plant species: ***Manihot esculenta***

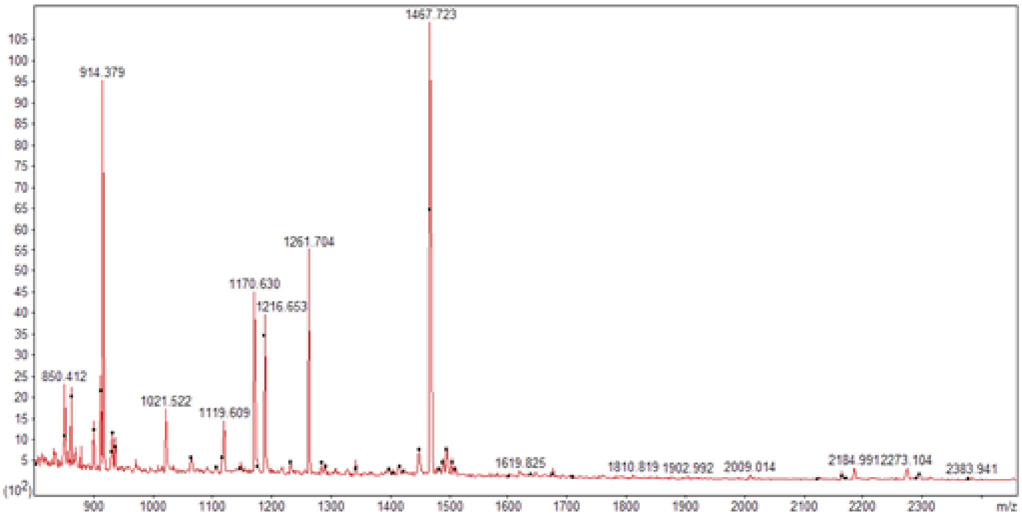
Protein name： **ribulose 1,5 bisphosphate carboxylase-oxygenase**

PFF Mascot score: **[153]** Sequence coverage %: **[7]**

Matched peptides No.: **[3]** p value: **0.00069**

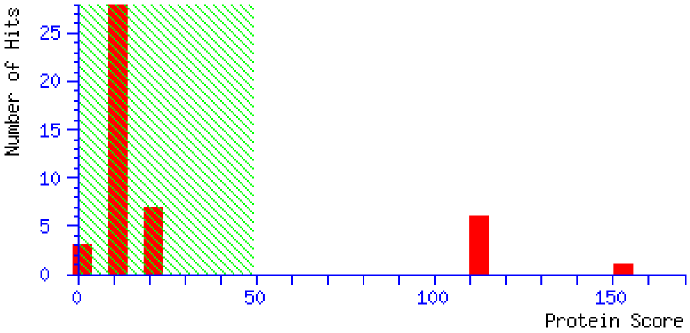
Calculated Mr: **51876** Calculated *p*I: **5.70**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 49 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **142**

NCBI accession No.: **cassava4.1_007756m|PACid:17993326**

Plant species: ***Manihot esculenta***

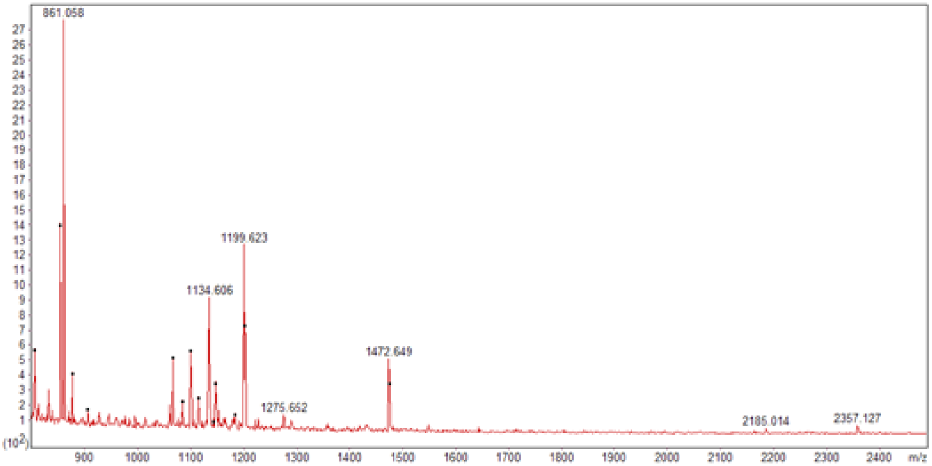
Protein name：**Aldolase-type TIM barrel family protein**

PFF Mascot score: **[94]** Sequence coverage %: **[10]**

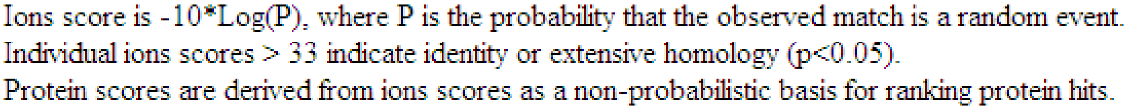
Matched peptides No.: **[4]** p value: **0.00026**

Calculated Mr: **48525** Calculated *p*I: **6.19**

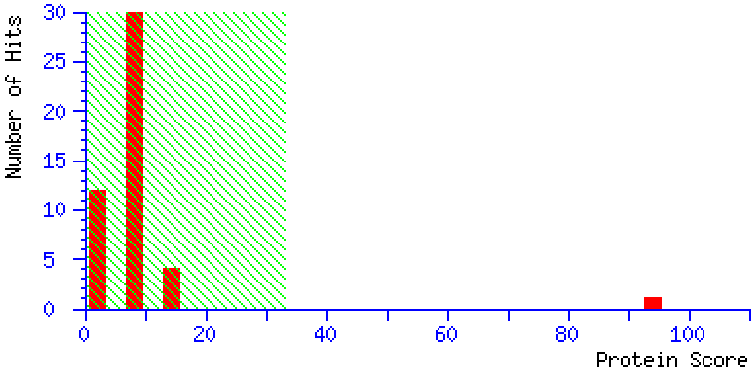
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **143**

NCBI accession No.: **cassava4.1_026035m|PACid:17968666**

Plant species: ***Manihot esculenta***

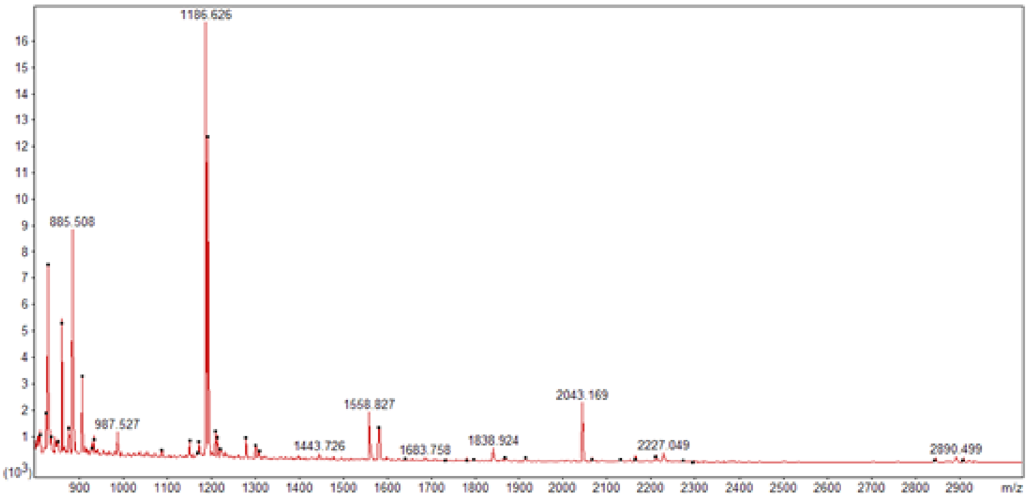
Protein name： **Alcohol dehydrogenase class-P**

PFF Mascot score: **[152]** Sequence coverage %: **[20]**

Matched peptides No.: **[5]** p value: **0.00014**

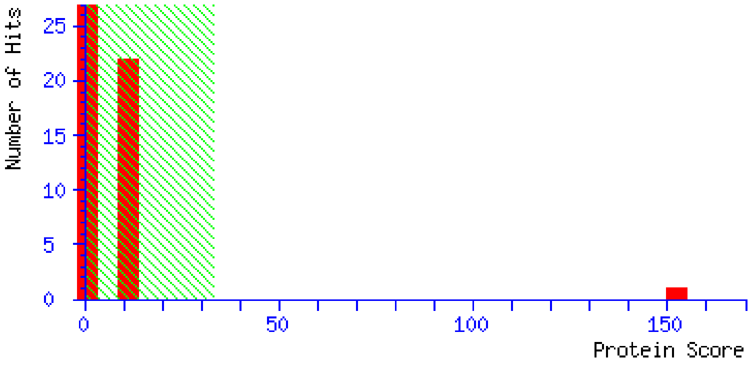
Calculated Mr: **38296** Calculated *p*I: **6.02**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **144**

NCBI accession No.: **cassava4.1_014881m|PACid:17982856**

Plant species: ***Manihot esculenta***

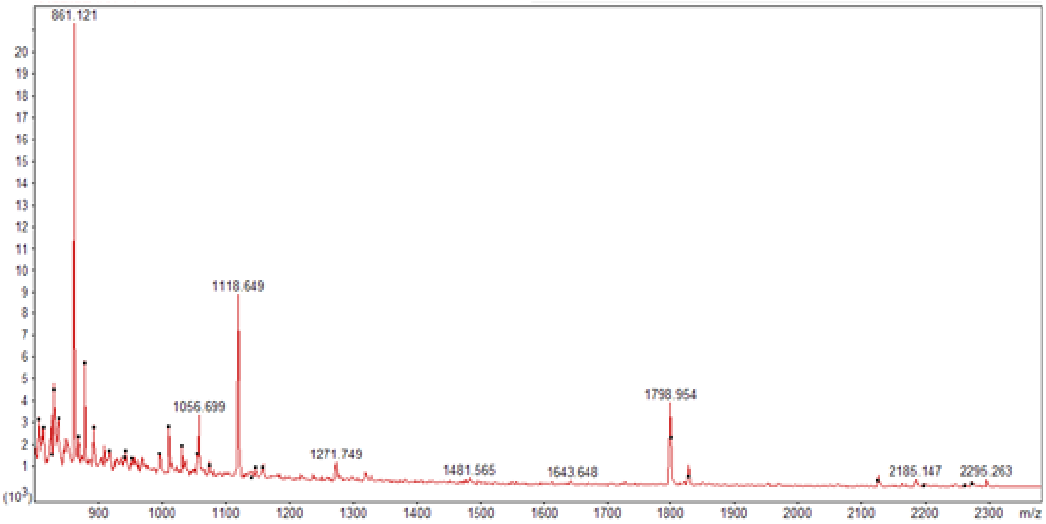
Protein name： **acetylornithine deacetylase-like**

PFF Mascot score: **[61]** Sequence coverage %: **[6]**

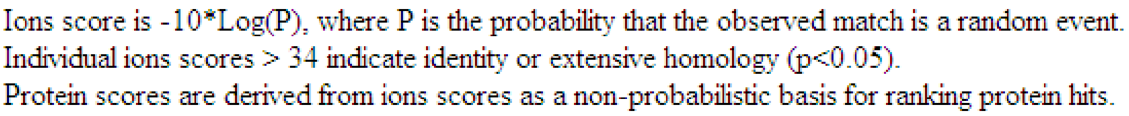
Matched peptides No.: **[2]** p value: **7.1e-005**

Calculated Mr: **26425** Calculated *p*I: **5.50**

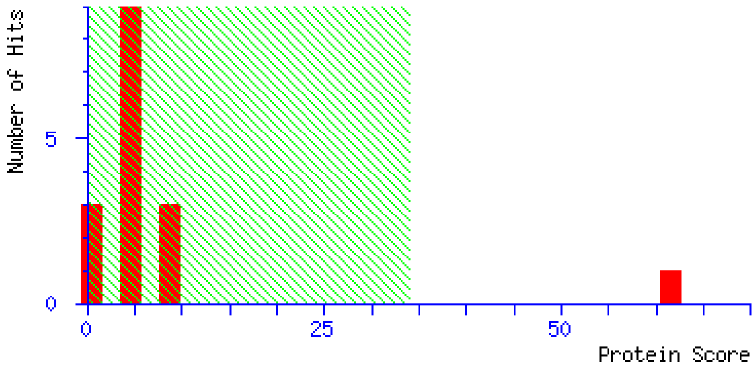
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **145**

NCBI accession No.: **cassava4.1_009780m|PACid:17993116**

Plant species: ***Manihot esculenta***

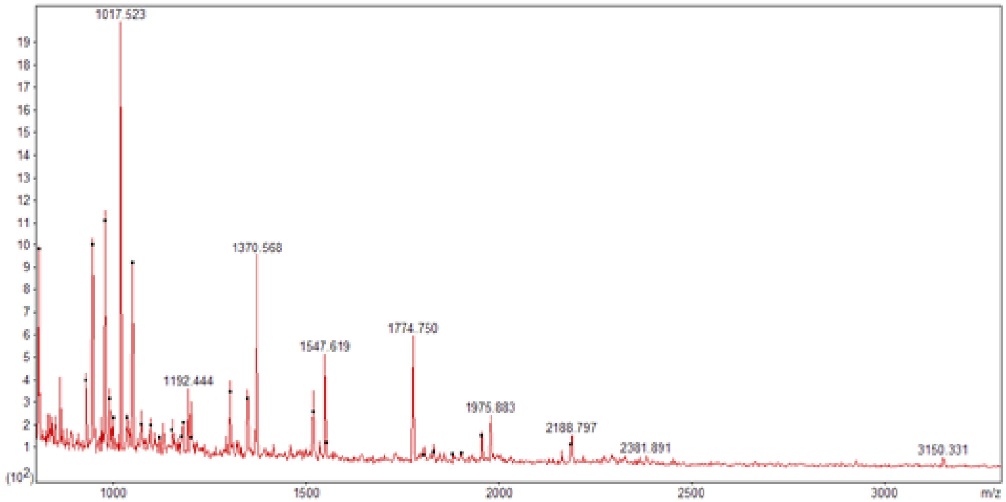
Protein name： **Actin-7**

PFF Mascot score: **[115]** Sequence coverage %: **[6]**

Matched peptides No.: **[2]** p value: **2.6e-06**

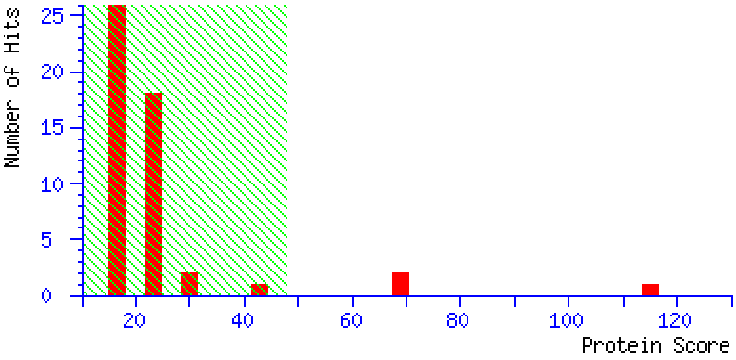
Calculated Mr: **42246** Calculated *p*I: **5.64**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **146**

NCBI accession No.: **cassava4.1_010334m|PACid:17962764**

Plant species: ***Manihot esculenta***

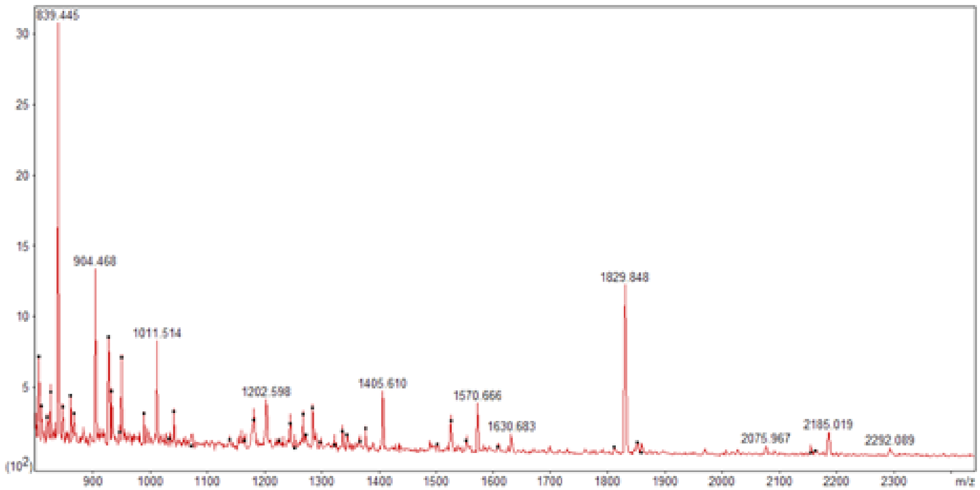
Protein name：**UDP-arabinopyranose mutase 3**

PFF Mascot score: **[73]**　　Sequence coverage %: **[8]**

Matched peptides No.: **[2]**　　p value: **4.4e-006**

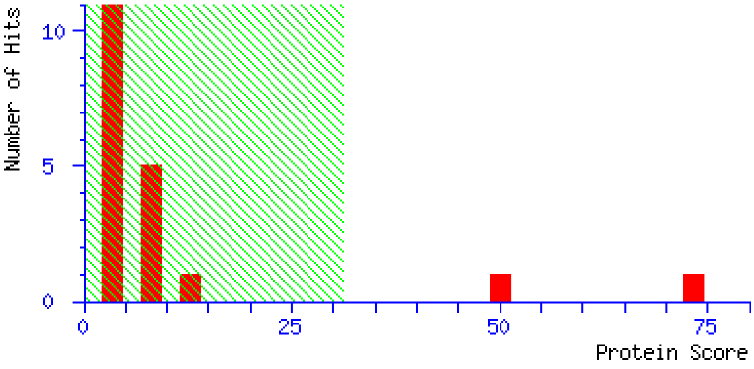
Calculated Mr: **41616**　　Calculated *p*I: **5.82**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 31 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **147**

NCBI accession No.: **cassava4.1_006605m|PACid:17968275**

Plant species: ***Arabidopsis thaliana***

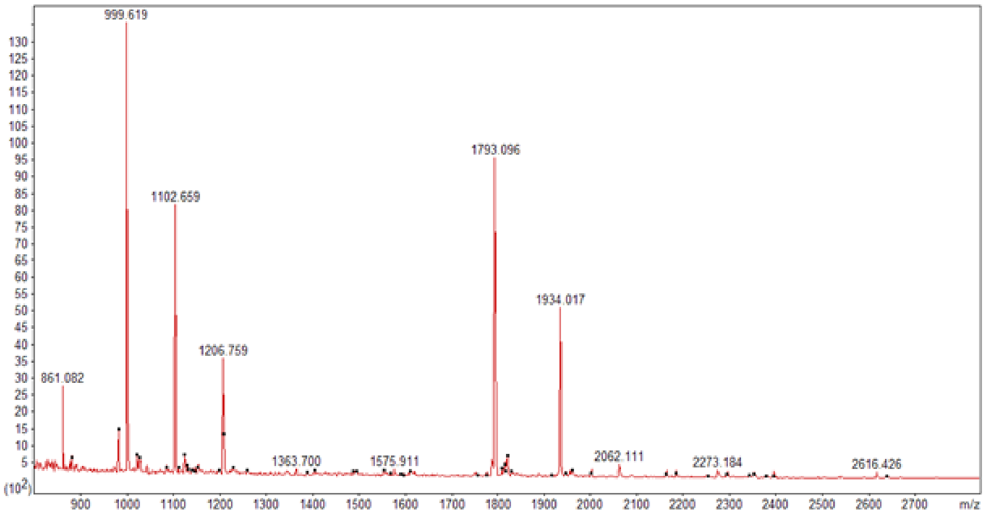
Protein name： **Phosphoglycerate kinase 1, chloroplastic**

PFF Mascot score: **[103]** Sequence coverage %: **[9]**

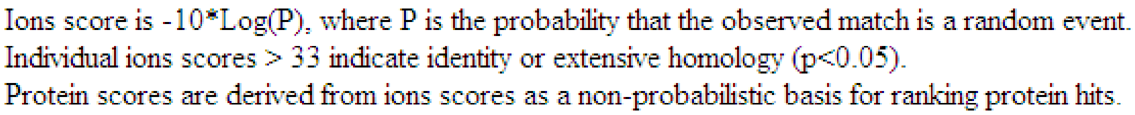
Matched peptides No.: **[4]** p value: **0.00031**

Calculated Mr: **50372** Calculated *p*I: **8.26**

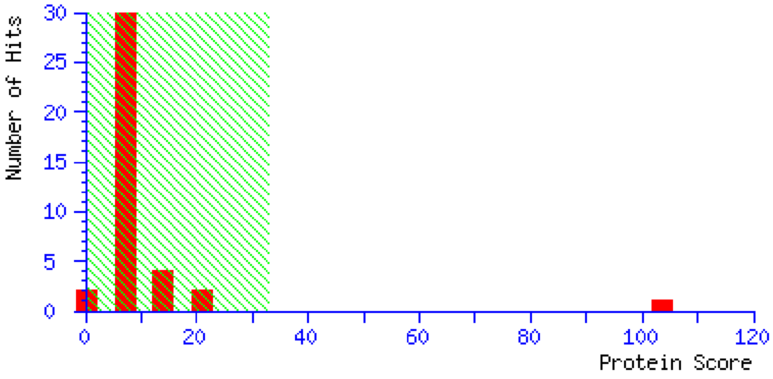
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **148**

NCBI accession No.: **cassava4.1_009233m|PACid:17991143**

Plant species: ***Manihot esculenta***

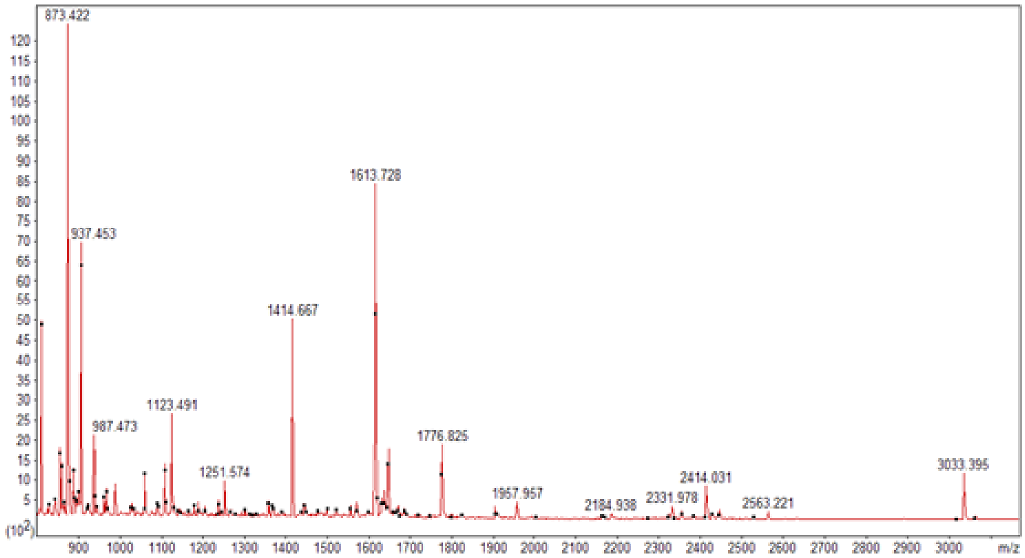
Protein name：**Probable fructose-bisphosphate aldolase 3**

PFF Mascot score: **[380]**   Sequence coverage %: **[20]**

Matched peptides No.: **[7]**   p value: **1.5e-010**

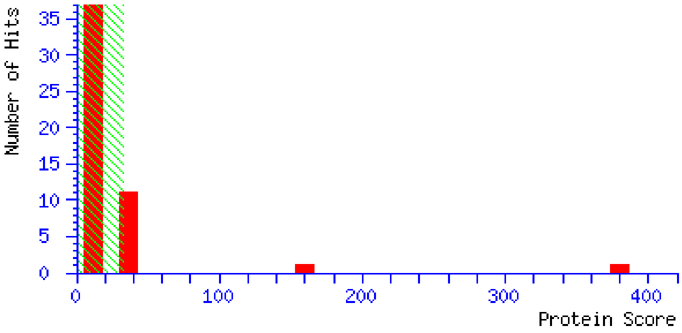
Calculated Mr: **43050**   Calculated *p*I: **8.63**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **149**

NCBI accession No.: **cassava4.1_009217m|PACid:17976496**

Plant species: ***Manihot esculenta***

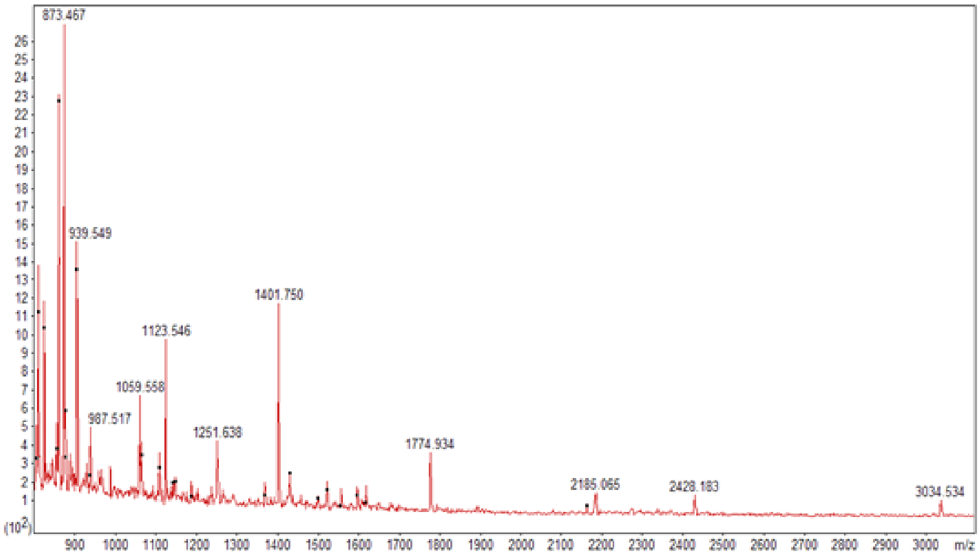
Protein name：**fructose-bisphosphate aldolase, putative**

PFF Mascot score: **[118]** Sequence coverage %: **[15]**

Matched peptides No.: **[4]** p value: **0.00029**

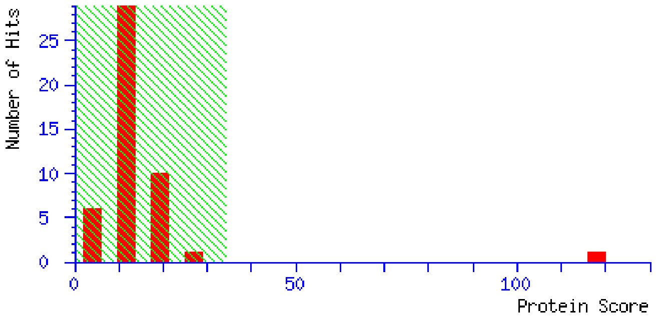
Calculated Mr: **24559** Calculated *p*I: **8.93**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **150**

NCBI accession No.: **cassava4.1_022763m|PACid:17989911**

Plant species: ***Manihot esculenta***

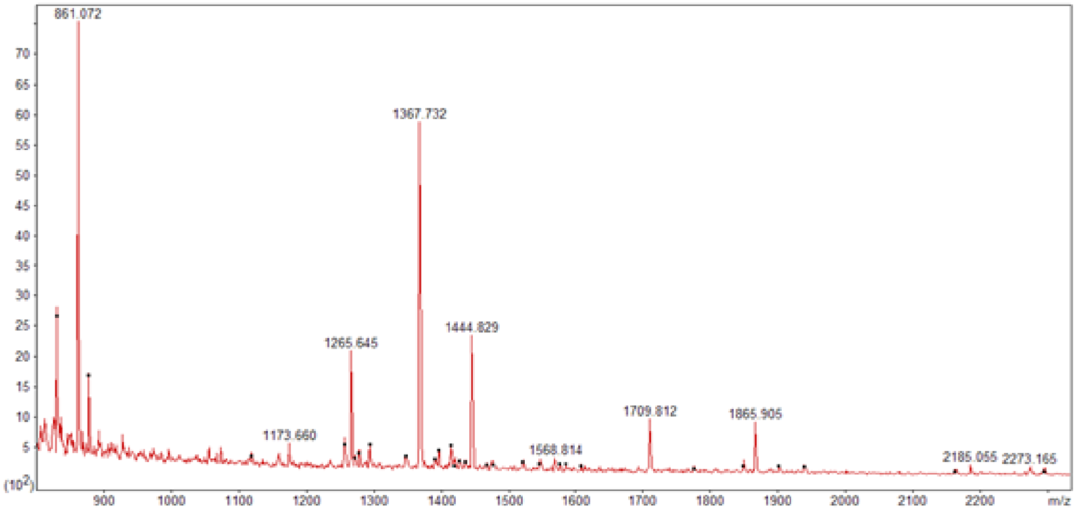
Protein name： **aldo/keto reductase AKR**

PFF Mascot score: **[69]** Sequence coverage %: **[10]**

Matched peptides No.: **[2]** p value: **9.7e-005**

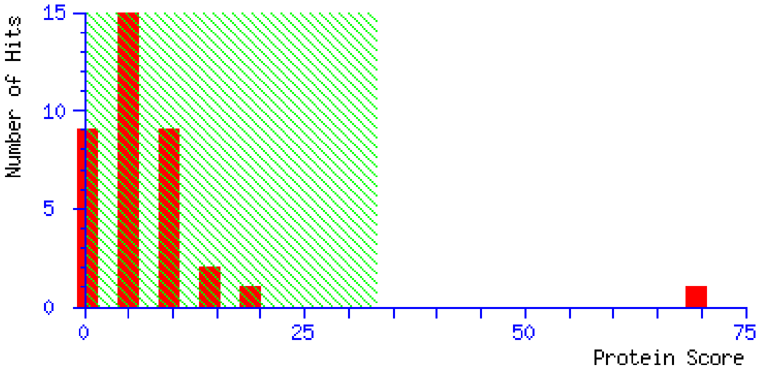
Calculated Mr: **15199** Calculated *p*I: **7.72**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **151**

NCBI accession No.: **cassava4.1_011584m|PACid:17982732**

Plant species: ***Manihot esculenta***

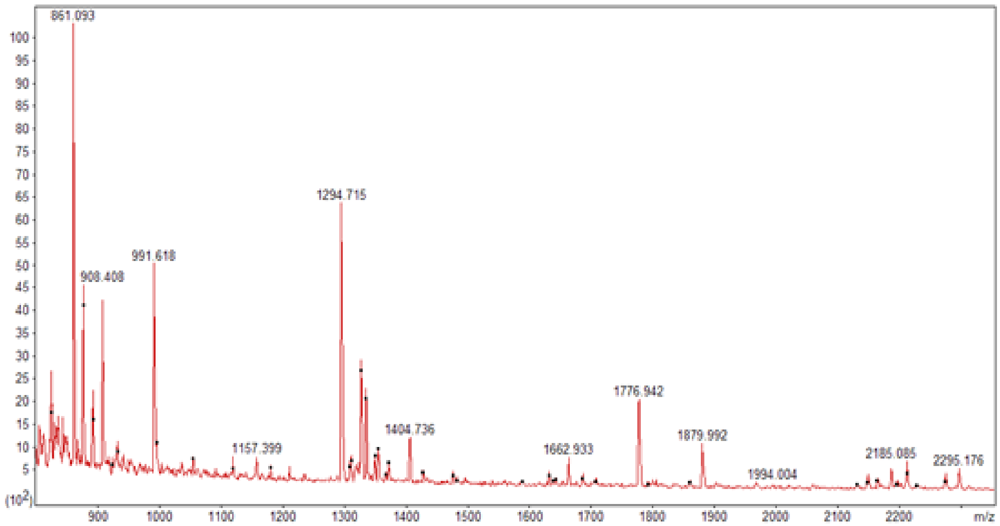
Protein name：**Probable fructokinase-1**

PFF Mascot score: **[110]** Sequence coverage %: **[16]**

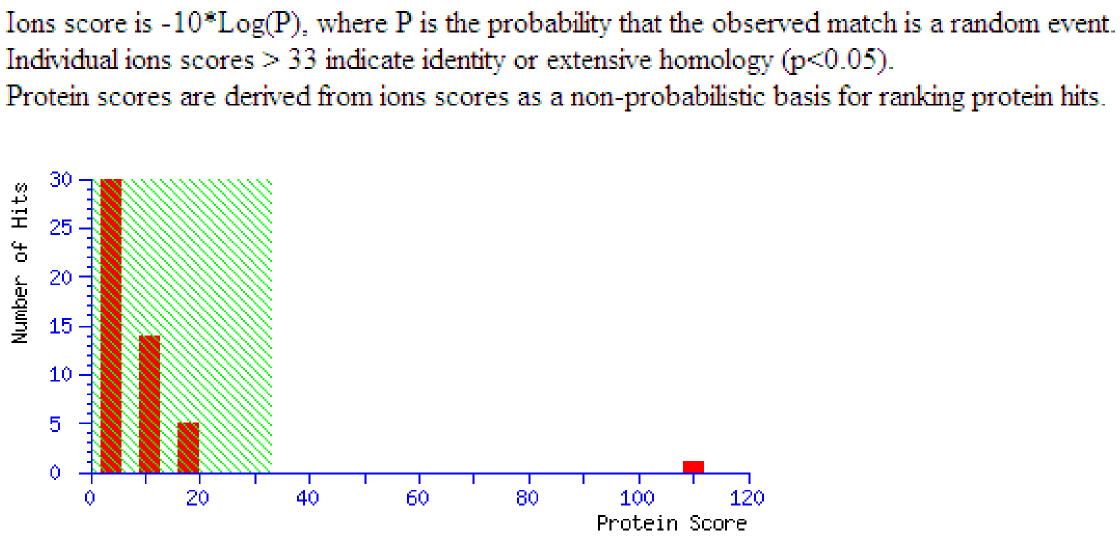
Matched peptides No.: **[4]** p value: **0.00064**

Calculated Mr: **35621** Calculated *p*I: **5.12**

Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Spot No.: **152**

NCBI accession No.: **cassava4.1_025676m|PACid:17984832**

Plant species: ***Manihot esculenta***

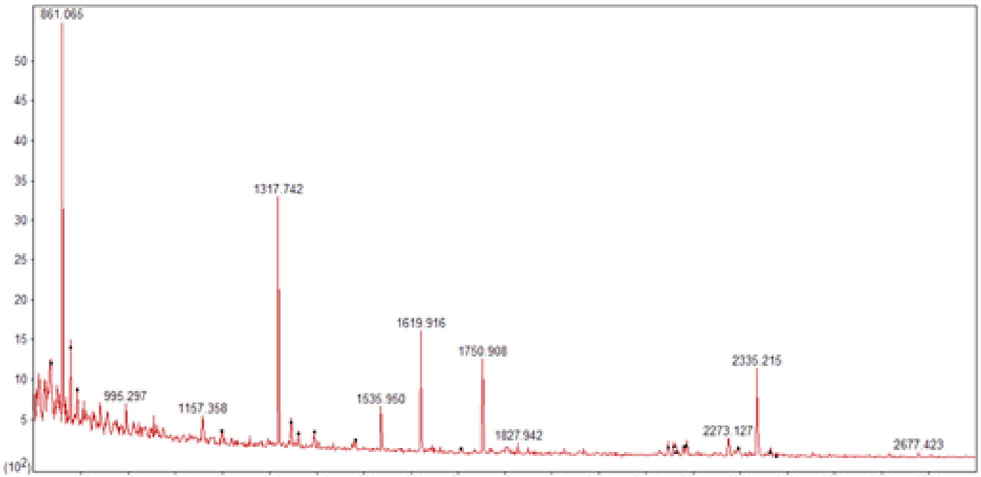
Protein name：**Similar to late embryogenesis abundant proteins**

PFF Mascot score: **[125]** Sequence coverage %: **[14]**

Matched peptides No.: **[3]** p value: **7.1e-006**

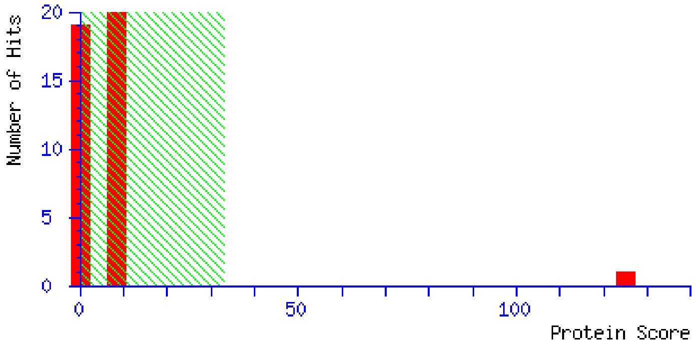
Calculated Mr: **34906** Calculated *p*I: **4.75**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **153**

NCBI accession No.: **cassava4.1_009779m|PACid:17990964**

Plant species: ***Manihot esculenta***

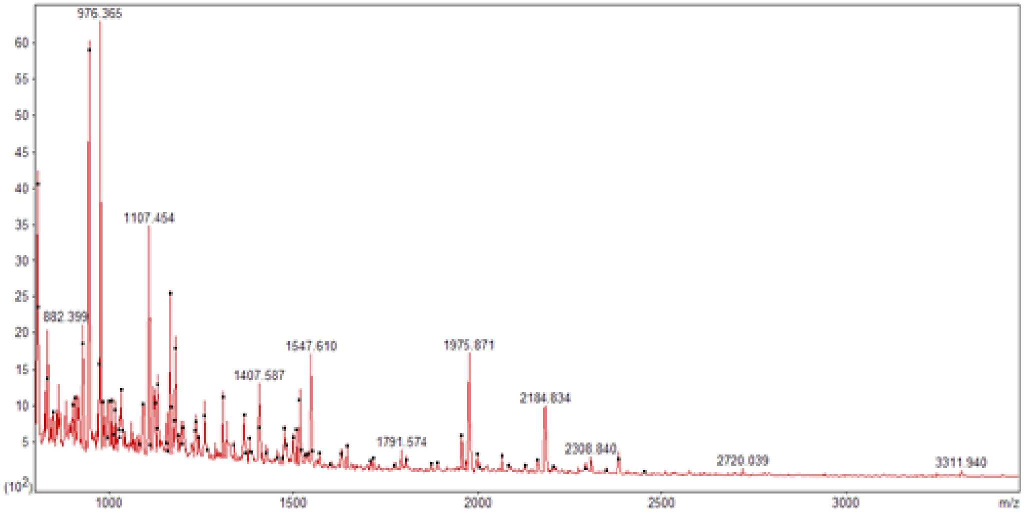
Protein name: **Actin-7**

PFF Mascot score: **[62]** Sequence coverage %: **[7]**

Matched peptides No.: **[3]** p value: **0.0079**

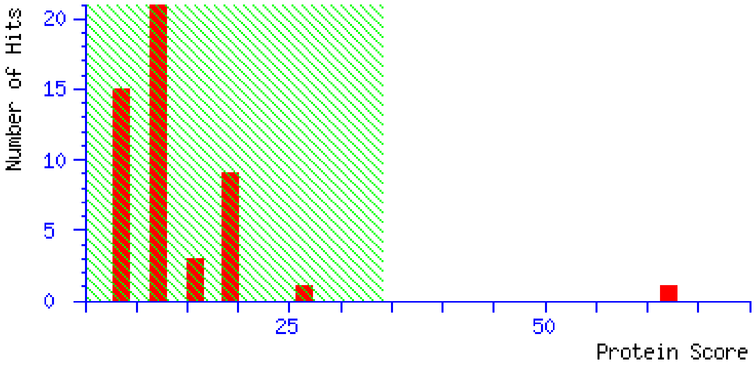
Calculated Mr: **41897** Calculated *p*I: **5.31**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **154**

NCBI accession No.: **cassava4.1_013984m|PACid:17980530**

Plant species: ***Manihot esculenta***

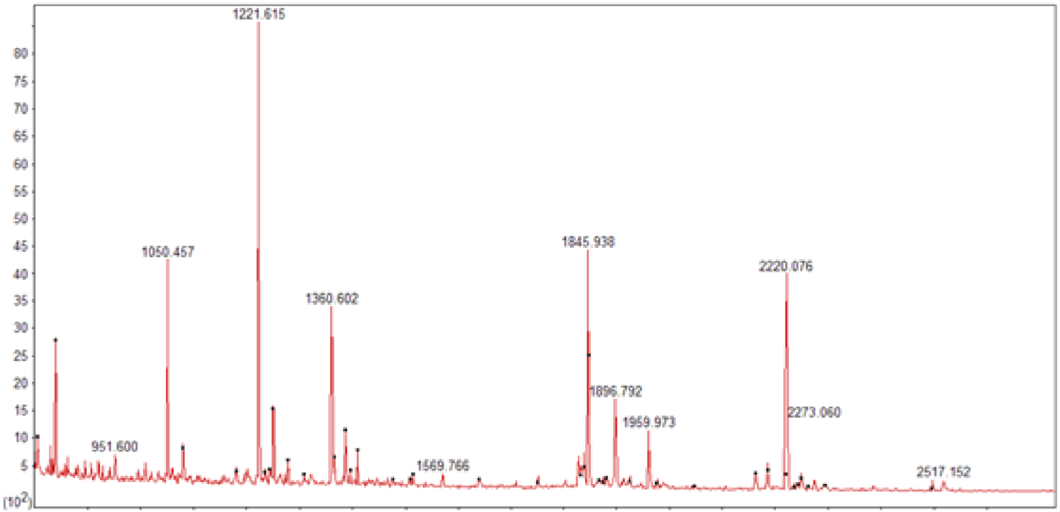
Protein name: **26S proteasome non-ATPase regulatory subunit 8 homolog A**

PFF Mascot score: **[343]** Sequence coverage %: **[37]**

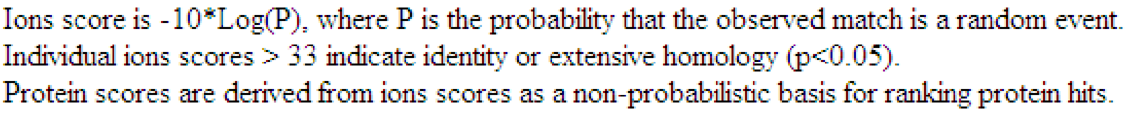
Matched peptides No.: **[7]** p value: **0.00000000028**

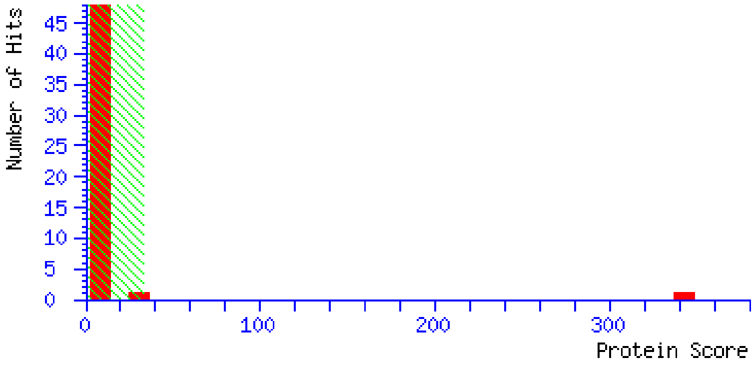
Calculated Mr: 30915 Calculated *p*I: 4.93

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **155**

NCBI accession No.: **cassava4.1_014432m|PACid:17967798**

Plant species: ***Manihot esculenta***

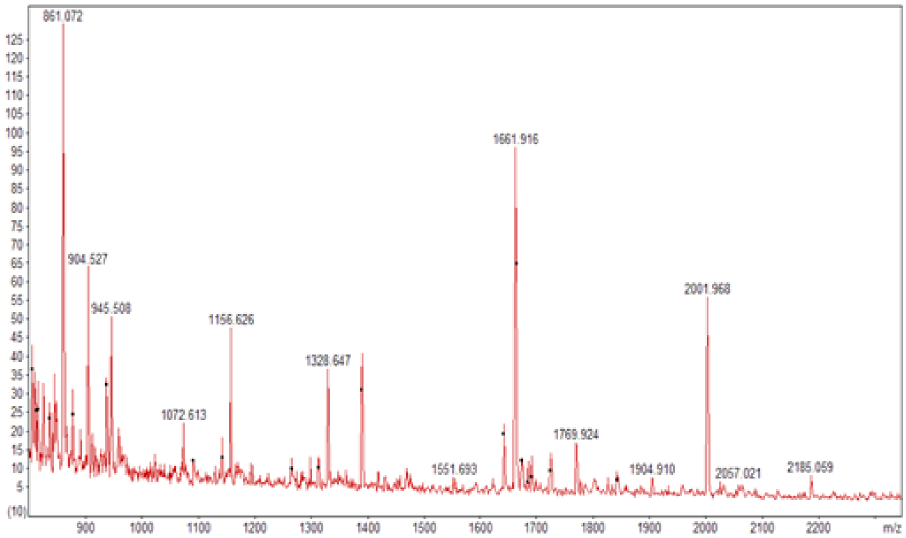
Protein name：**Triosephosphate isomerase, cytosolic**

PFF Mascot score: **[107]** Sequence coverage %: **[10]**

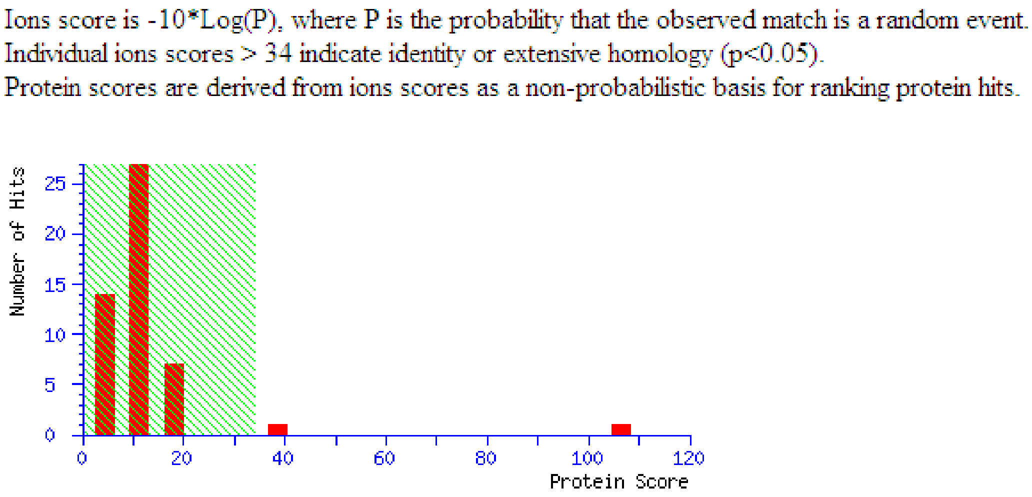
Matched peptides No.: **[2]** p value: **3.9e-007**

Calculated Mr: **27729** Calculated *p*I: **5.77**

Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.

Spot No.: **156**

NCBI accession No.: **cassava4.1_015127m|PACid:17970169**

Plant species: ***Manihot esculenta***

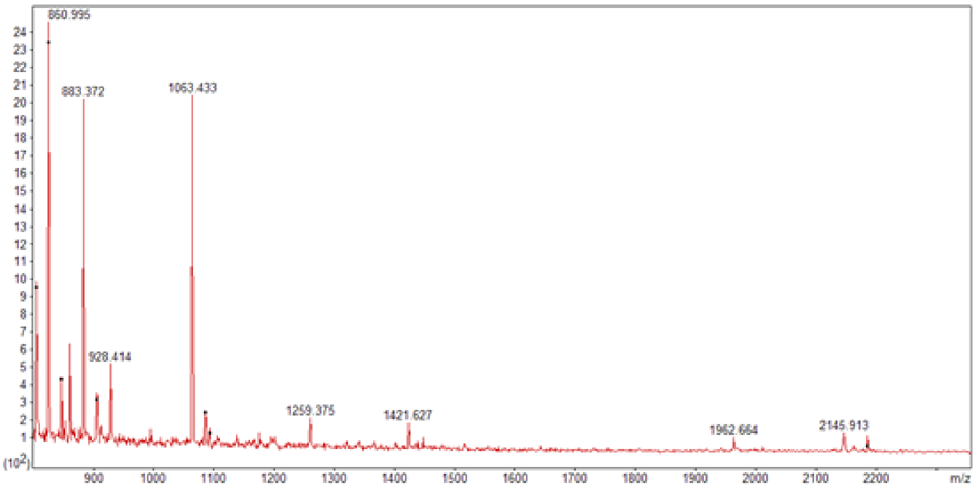
Protein name：**Proteasome subunit alpha type-5-A**

PFF Mascot score: **[123]**　　Sequence coverage %: **[10]**

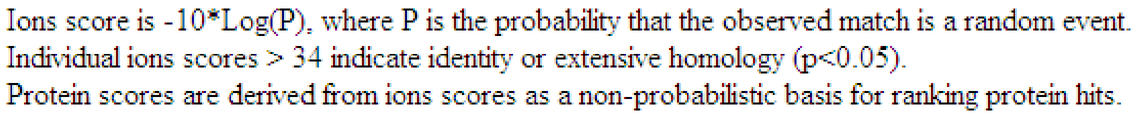
Matched peptides No.: **[3]**　　p value: **9.4e-005**

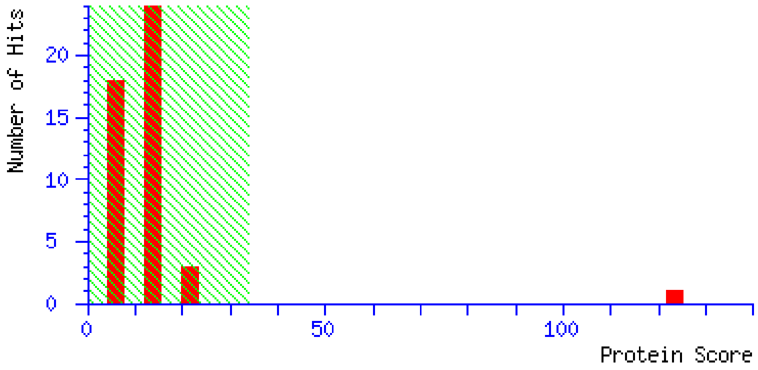
Calculated Mr: **26165**　　Calculated *p*I: **4.70**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **157**

NCBI accession No.: **cassava4.1_015667m|PACid:17963200**

Plant species: ***Manihot esculenta***

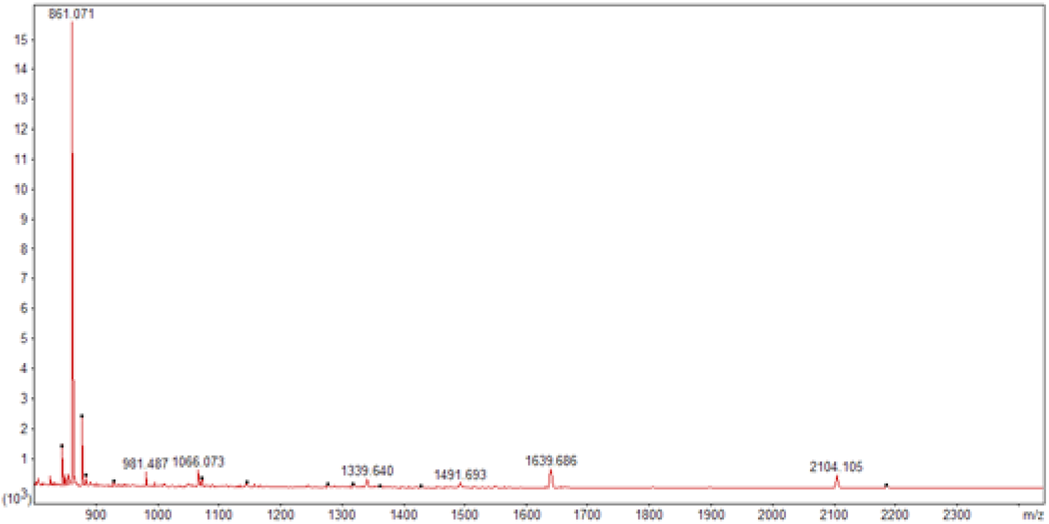
Protein name： **Proteasome subunit beta type-1**

PFF Mascot score: **[61]** Sequence coverage %: **[8]**

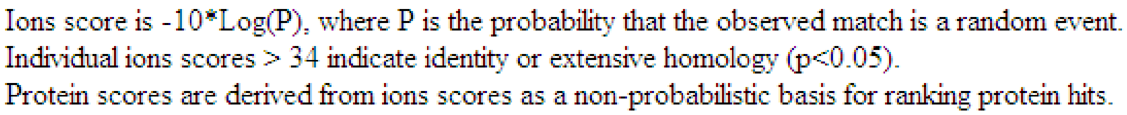
Matched peptides No.: **[2]** p value: **7.2e-005**

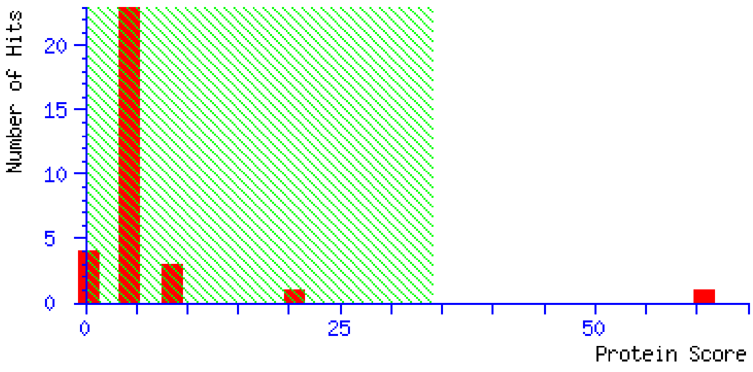
Calculated Mr: **24884** Calculated *p*I: **6.42**

Annotated PMF **spectra:**



PFF Searched Score:


Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **158**

NCBI accession No.: **cassava4.1_014674m|PACid:17976440**

Plant species: ***Manihot esculenta***

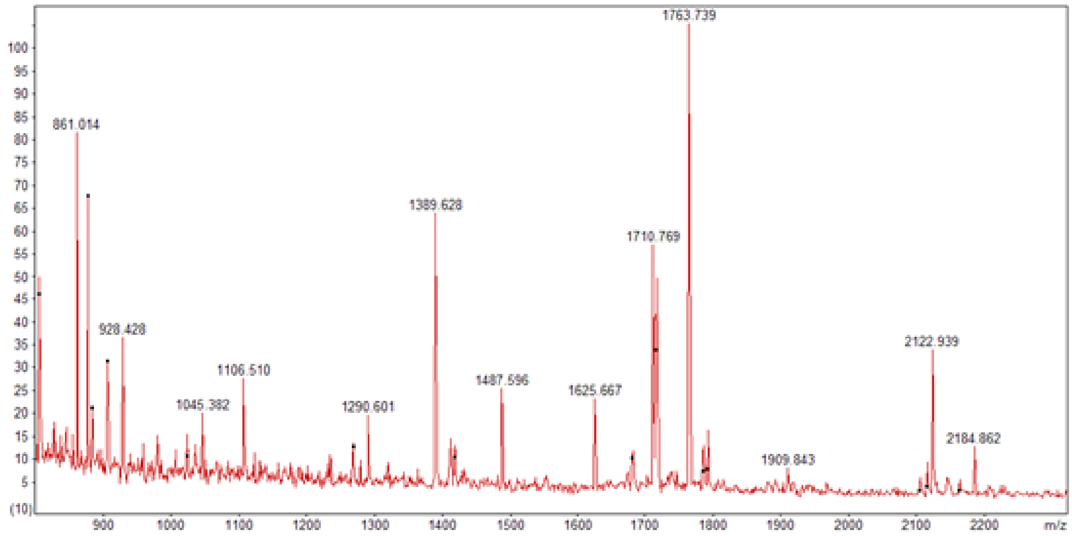
Protein name：**3-isopropylmalate dehydratase small subunit 3**

PFF Mascot score: **[292]** Sequence coverage %: **[26]**

Matched peptides No.: **[4]** p value: **9.3e-007**

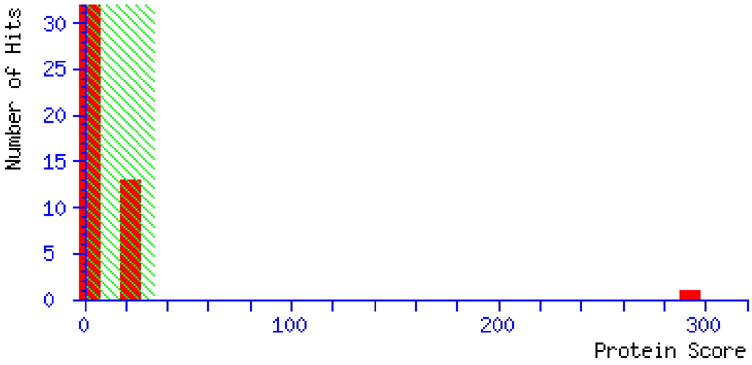
Calculated Mr: **26948** Calculated *p*I: **6.52**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **159**

NCBI accession No.: **cassava4.1_016068m|PACid:17988757**

Plant species: ***Manihot esculenta***

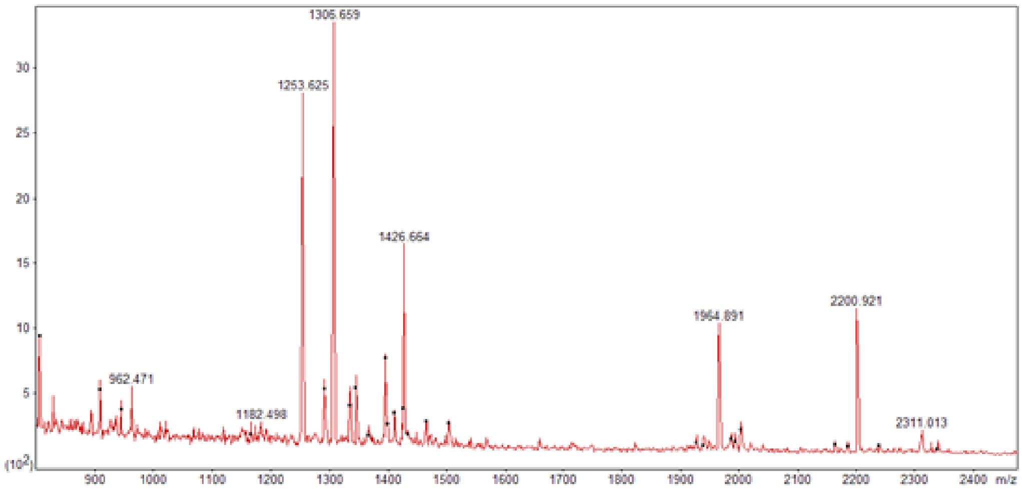
Protein name： **glutathione-s-transferase theta, gst,**

PFF Mascot score: **[192]** Sequence coverage %: **[24]**

Matched peptides No.: **[4]** p value: **1.7e-005**

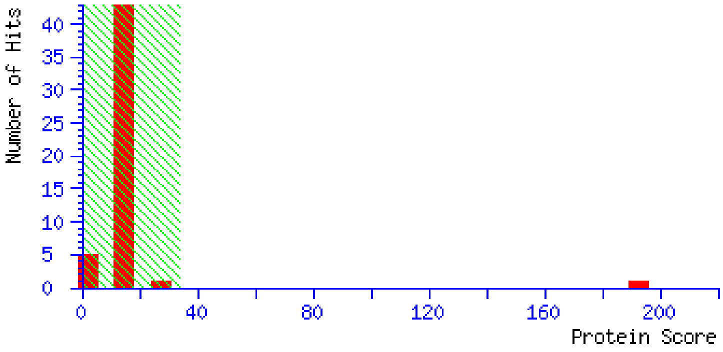
Calculated Mr: **23848** Calculated *p*I: **6.17**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **160**

NCBI accession No.: **cassava4.1_013921m|PACid:17992320**

Plant species: ***Manihot esculenta***

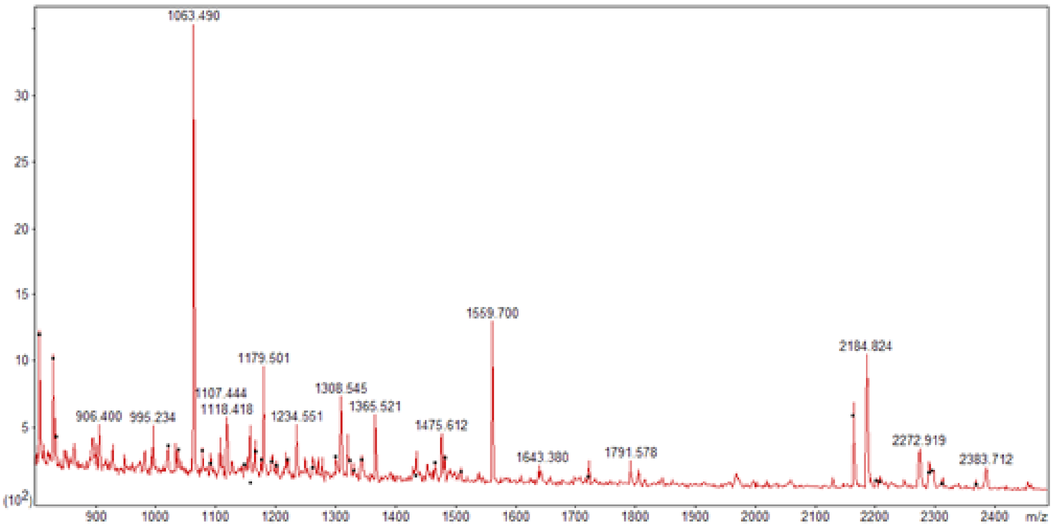
Protein name：**peroxiredoxin**

PFF Mascot score: **[79]** Sequence coverage %: **[9]**

Matched peptides No.: **[2]** p value: **1.4e-006**

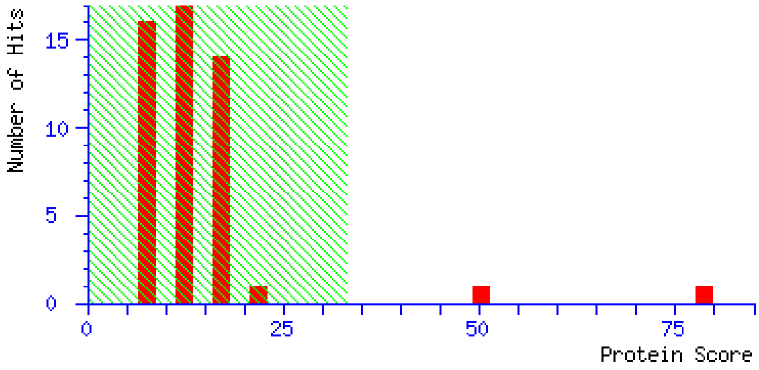
Calculated Mr: **29562** Calculated *p*I: **7.66**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **161**

NCBI accession No.: **cassava4.1_015116m|PACid:17987913**

Plant species: ***Manihot esculenta***

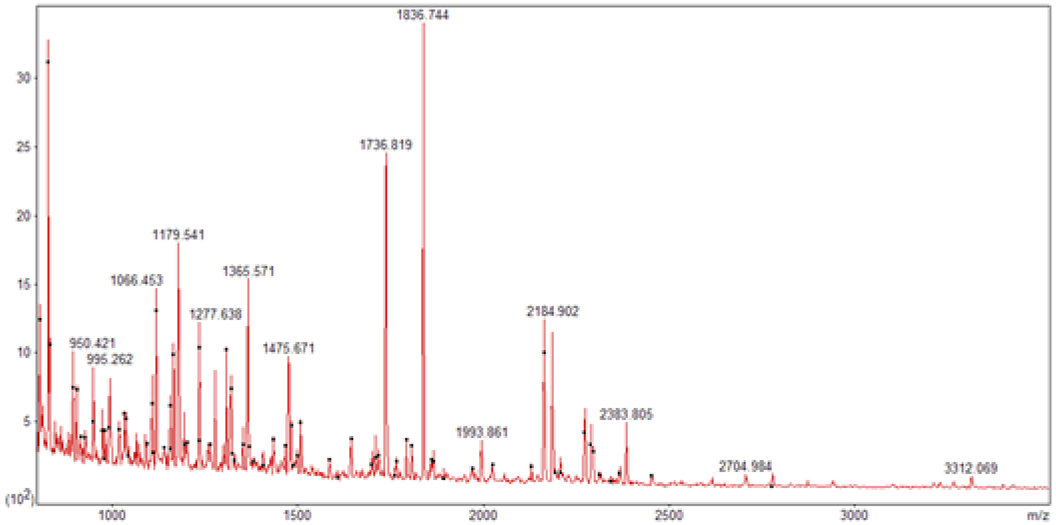
Protein name: **conserved hypothetical protein**

PFF Mascot score: **[173]** Sequence coverage %: **[13]**

Matched peptides No.: **[2]** p value: **2.7e-008**

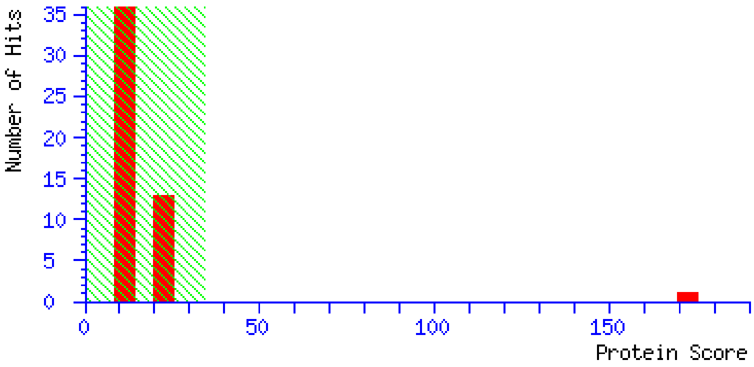
Calculated Mr: **26233** Calculated *p*I: **5.98**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **162**

NCBI accession No.: **cassava4.1_019468m|PACid:17983825**

Plant species: ***Manihot esculenta***

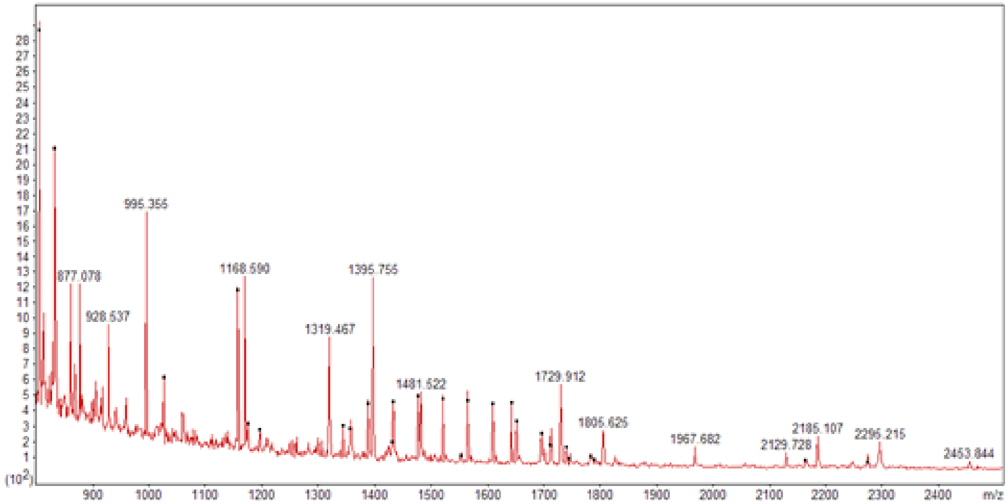
Protein name：**Small ubiquitin-related modifier**

PFF Mascot score: **[88]**　　　Sequence coverage %: **[22]**

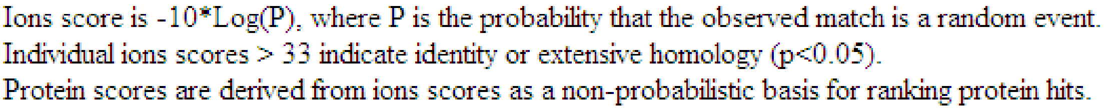
Matched peptides No.: **[2]**　　　p value: **0.00045**

Calculated Mr: **12426**　　　Calculated *p*I: **4.95**

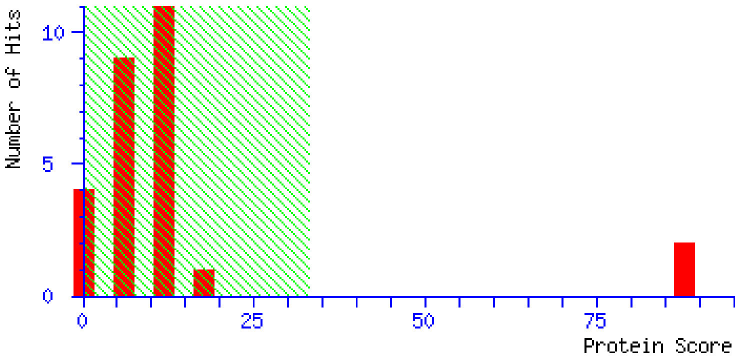
Annotated PMF **spectra:**



PFF Searched Score:



Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **163**

NCBI accession No.: **cassava4.1_009782m|PACid:17988600**

Plant species: ***Manihot esculenta***

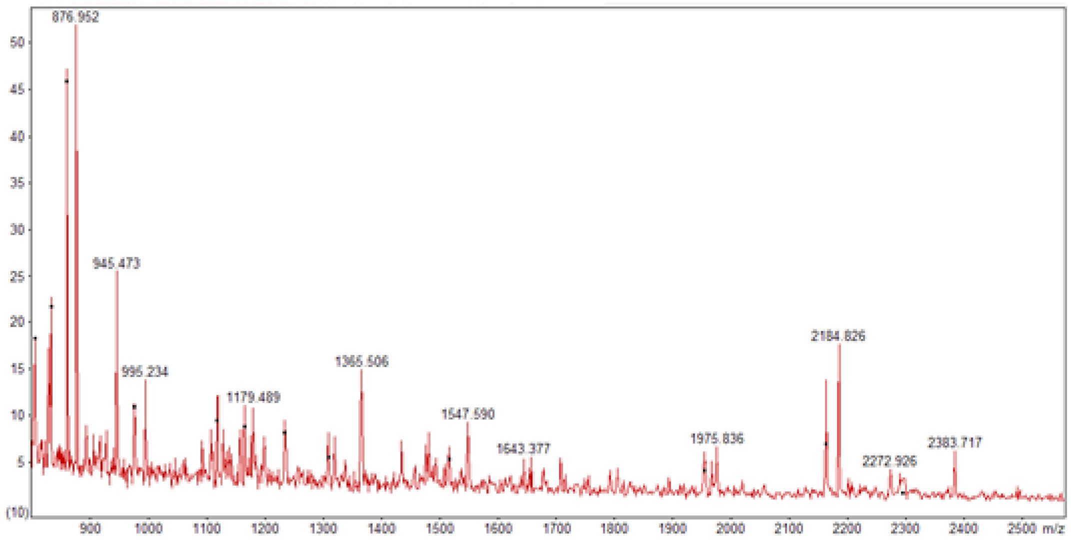
Protein name： **actin**

PFF Mascot score: **78** Sequence coverage %: **31**

Matched peptides No.: **8** p value: **0.0026**

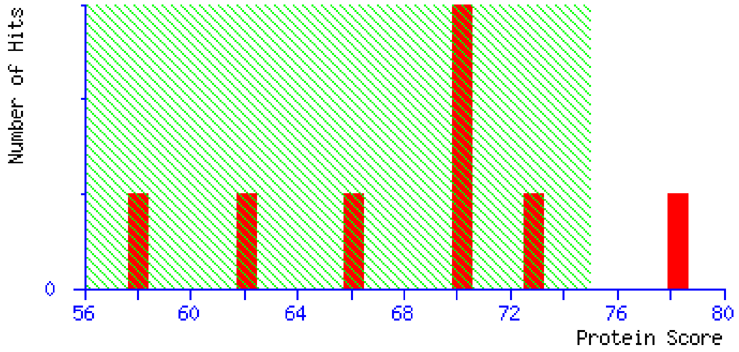
Calculated Mr: **32104** Calculated *p*I: **4.92**

Annotated PMF **spectra:**



PFF Searched Score:

Protein score is -10*Log(P), where P is the probability that the observed match is a random event.
Protein scores greater than 61 are significant ($p<0.05$).



Spot No.: **164**

NCBI accession No.: **cassava4.1_018266m|PACid:17987264**

Plant species: ***Manihot esculenta***

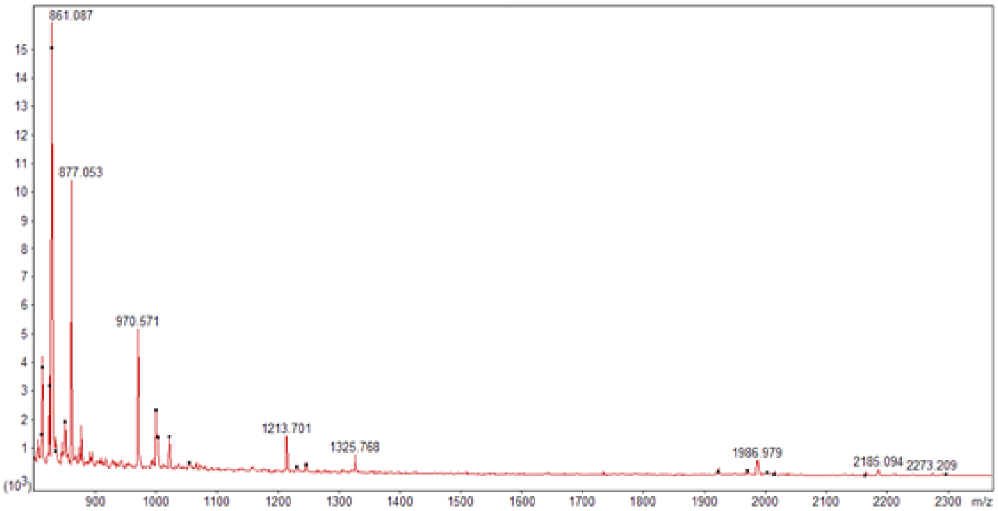
Protein name: **Ubiquitin-conjugating enzyme E2 35**

PFF Mascot score: **[88]**   Sequence coverage %: **[26]**

Matched peptides No.: **[5]**   p value: **0.00011**

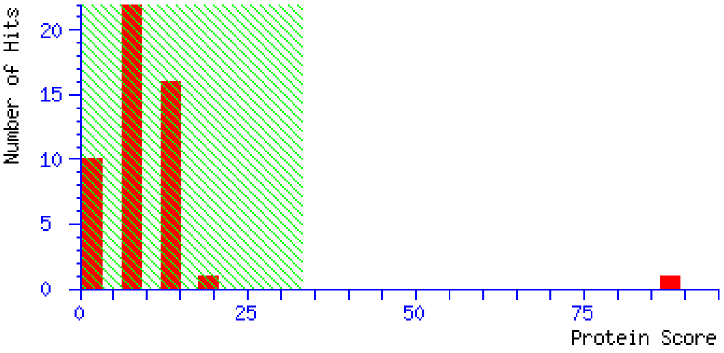
Calculated Mr: **17266**   Calculated *p*I: **6.74**

Annotated PMF **spectra:**



PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 33 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Spot No.: **165**

NCBI accession No.: **cassava4.1_018546m|PACid:17976766**

Plant species: ***Manihot esculenta***

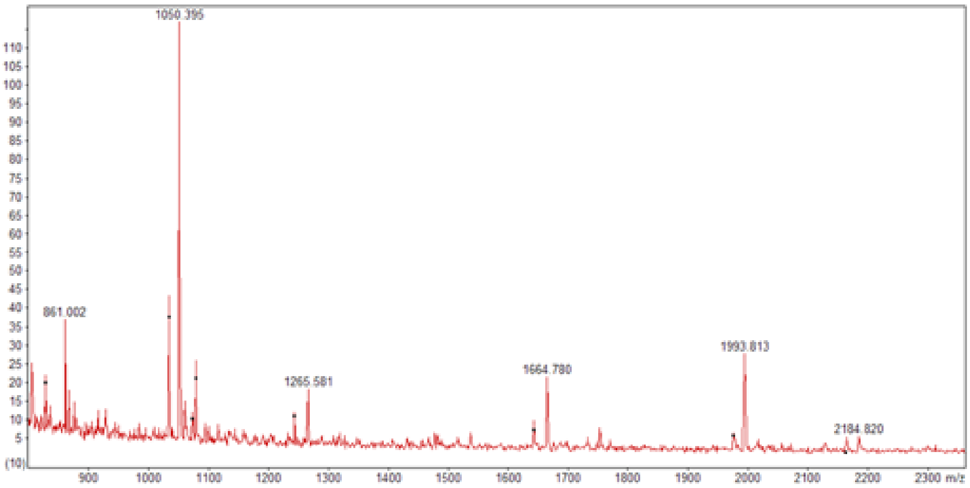
Protein name: **Putative uncharacterized protein At3g56490**

PFF Mascot score: **[153]** Sequence coverage %: **[17]**

Matched peptides No.: **[2]** p value: **1.3e-007**

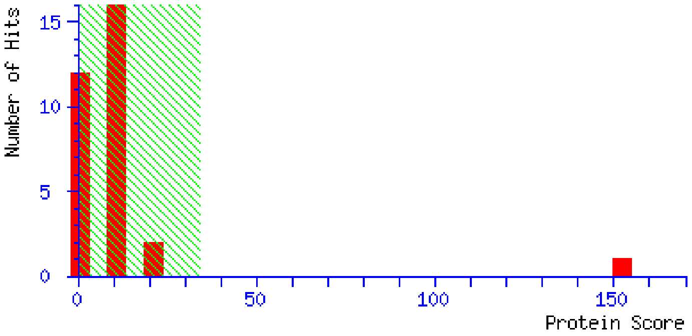
Calculated Mr: **15944** Calculated *p*I: **6.36**

Annotated PMF **spectra:**



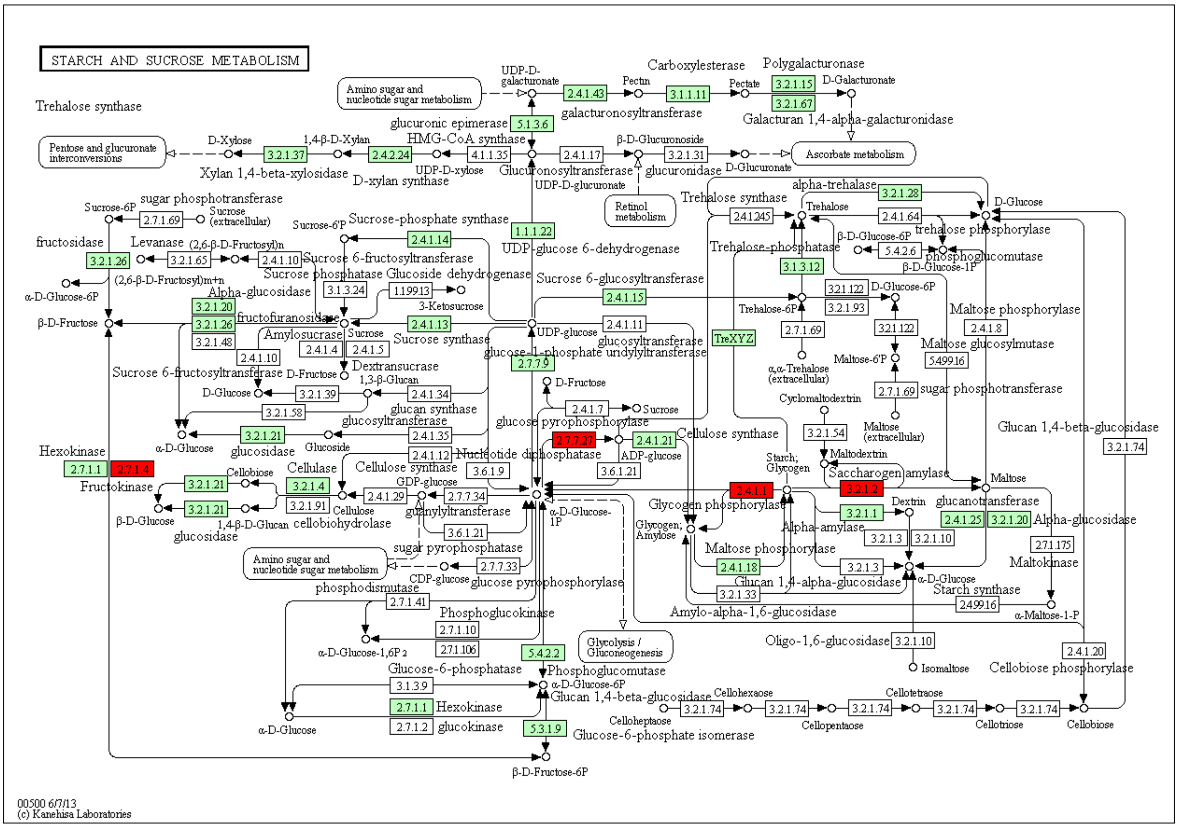
PFF Searched Score:

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 34 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Supplemental Figure S4: Main pathway ways overexpressed in all the differential proteins.

Enzymes exhibiting differential expression during tubernization are marked in green and red color. Marked in light green are enzymes that changed to some extent exhibit. Marked in red are the dramatically up-regulated enzymes. Marked in white are the not detected enzymes or general enzyme categories. Enzyme annotation was obtained from the protein sequence annotation and GO classification data.



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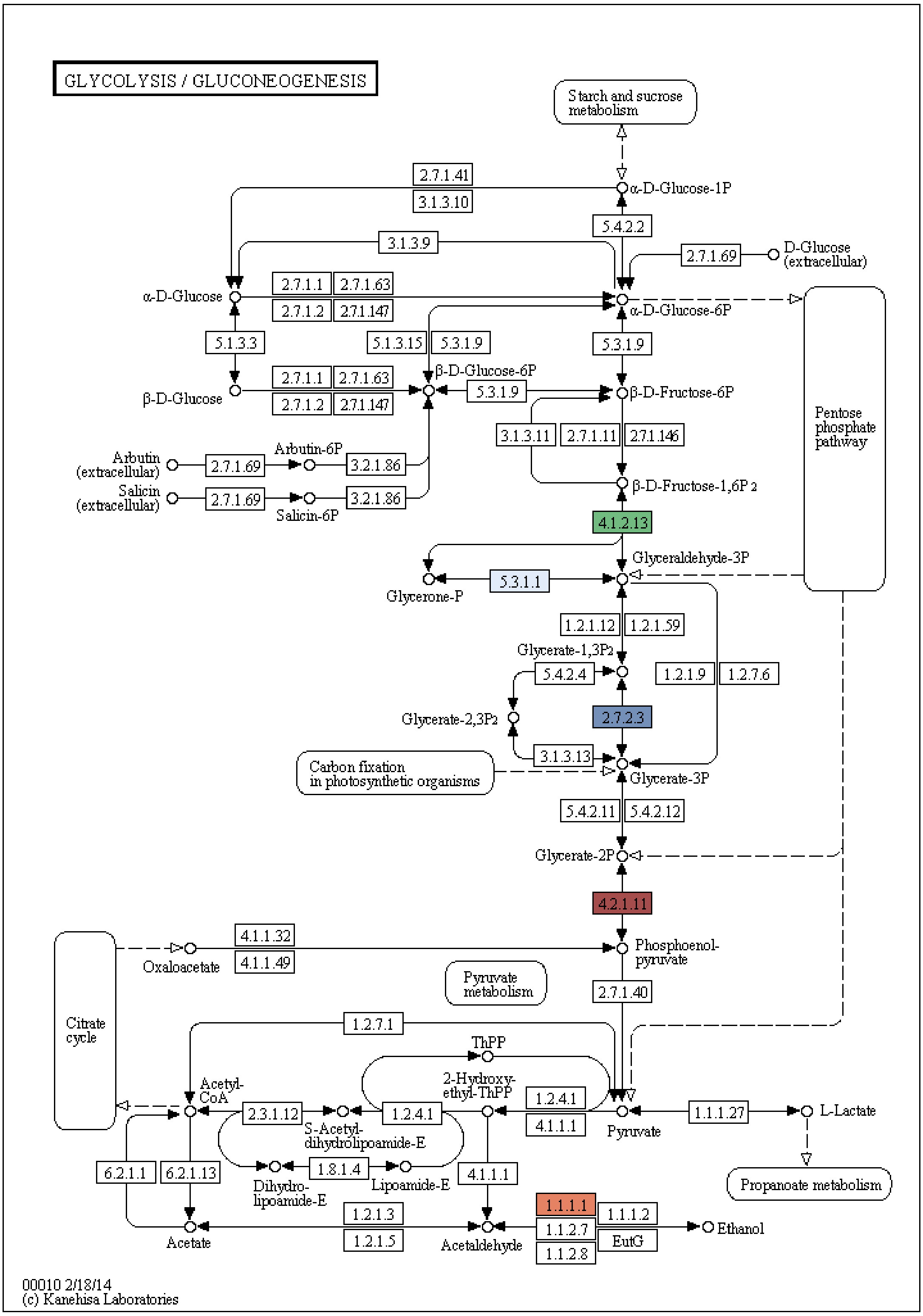
GLYCOLYSIS / GLUCONEOGENESIS
Starch and sucrose metabolism
2.7.1.41
3.1.3.10
α-D-Glucose-1P
5.4.2.2
3.1.3.9
2.7.1.69
D-Glucose (extracellular)
2.7.1.1
2.7.1.63
2.7.1.2
2.7.1.147
α-D-Glucose
α-D-Glucose-6P
5.1.3.3
5.1.3.15
5.3.1.9
5.3.1.9
β-D-Glucose-6P
2.7.1.1
2.7.1.63
2.7.1.2
2.7.1.147
β-D-Glucose
5.3.1.9
β-D-Fructose-6P
Pentose phosphate pathway
3.1.3.11
2.7.1.11
2.7.1.146
Arbutin (extracellular)
2.7.1.69
Arbutin-6P
3.2.1.86
Salicin (extracellular)
2.7.1.69
Salicin-6P
3.2.1.86
β-D-Fructose-1,6P2
4.1.2.13
Glyceraldehyde-3P
Glycerone-P
5.3.1.1
1.2.1.12
1.2.1.59
Glycerate-1,3P2
5.4.2.4
1.2.1.9
1.2.7.6
Glycerate-2,3P2
2.7.2.3
3.1.3.13
Carbon fixation in photosynthetic organisms
Glycerate-3P
5.4.2.11
5.4.2.12
Glycerate-2P
4.2.1.11
Citrate cycle
Oxaloacetate
4.1.1.32
4.1.1.49
Phosphoenol-pyruvate
Pyruvate metabolism
2.7.1.40
1.2.7.1
ThPP
Acetyl-CoA
2-Hydroxy-ethyl-ThPP
1.2.4.1
4.1.1.1
2.3.1.12
1.2.4.1
S-Acetyl-dihydrolipoamide-E
Pyruvate
1.1.1.27
L-Lactate
6.2.1.1
6.2.1.13
Dihydro-lipoamide-E
1.8.1.4
Lipoamide-E
4.1.1.1
Propanoate metabolism
1.2.1.3
1.2.1.5
1.1.1.1
1.1.1.2
1.1.2.7
EutG
1.1.2.8
Acetate
Acetaldehyde
Ethanol
00010 2/18/14
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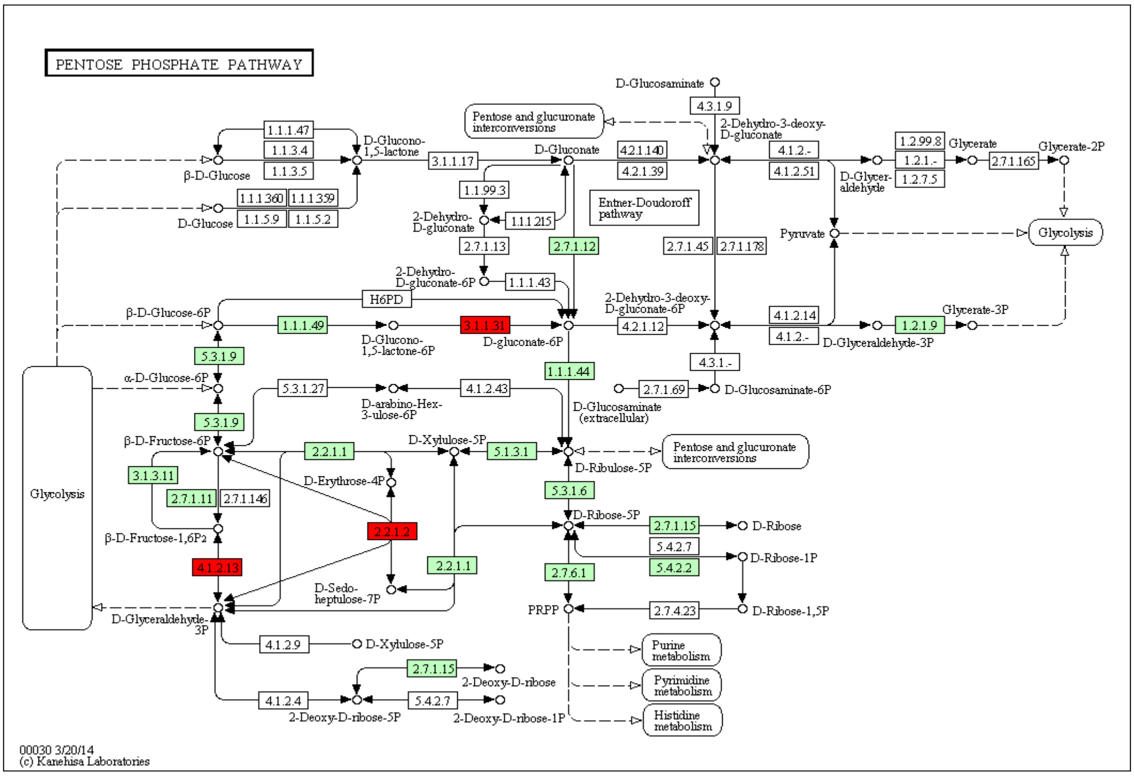
PENTOSE PHOSPHATE PATHWAY
D-Glucosaminate
4.3.1.9
Pentose and glucuronate interconversions
2-Dehydro-3-deoxy-D-gluconate
1.1.1.47
1.1.3.4
1.1.3.5
D-Glucono-1,5-lactone
β-D-Glucose
3.1.1.17
D-Gluconate
4.2.1.140
4.2.1.39
4.1.2.-
4.1.2.51
1.2.99.8
Glycerate
1.2.1.-
2.7.1.165
Glycerate-2P
D-Glycer-aldehyde
1.2.7.5
1.1.1.360
1.1.1.359
D-Glucose
1.1.5.9
1.1.5.2
1.1.99.3
2-Dehydro-D-gluconate
1.1.1.215
Entner-Doudoroff pathway
Pyruvate
Glycolysis
2.7.1.13
2.7.1.12
2.7.1.45
2.7.1.178
2-Dehydro-D-gluconate-6P
1.1.1.43
H6PD
β-D-Glucose-6P
1.1.1.49
3.1.1.31
2-Dehydro-3-deoxy-D-gluconate-6P
4.2.1.12
4.1.2.14
4.1.2.-
1.2.1.9
Glycerate-3P
D-Glucono-1,5-lactone-6P
D-gluconate-6P
D-Glyceraldehyde-3P
5.3.1.9
1.1.1.44
4.3.1.-
α-D-Glucose-6P
5.3.1.27
4.1.2.43
D-arabino-Hex-3-ulose-6P
2.7.1.69
D-Glucosamine-6P
D-Glucosamine (extracellular)
5.3.1.9
β-D-Fructose-6P
2.2.1.1
D-Xylulose-5P
5.1.3.1
Pentose and glucuronate interconversions
D-Ribulose-5P
D-Erythrose-4P
3.1.3.11
2.7.1.11
2.7.1.146
5.3.1.6
D-Ribose-5P
2.7.1.15
D-Ribose
β-D-Fructose-1,6P2
2.2.1.2
5.4.2.7
D-Ribose-1P
2.2.1.1
5.4.2.2
4.1.2.13
2.7.6.1
D-Sedo-heptulose-7P
PRPP
2.7.4.23
D-Ribose-1,5P
Glycolysis
D-Glyceraldehyde-3P
Purine metabolism
4.1.2.9
D-Xylulose-5P
2.7.1.15
2-Deoxy-D-ribose
Pyrimidine metabolism
4.1.2.4
5.4.2.7
2-Deoxy-D-ribose-5P
2-Deoxy-D-ribose-1P
Histidine metabolism
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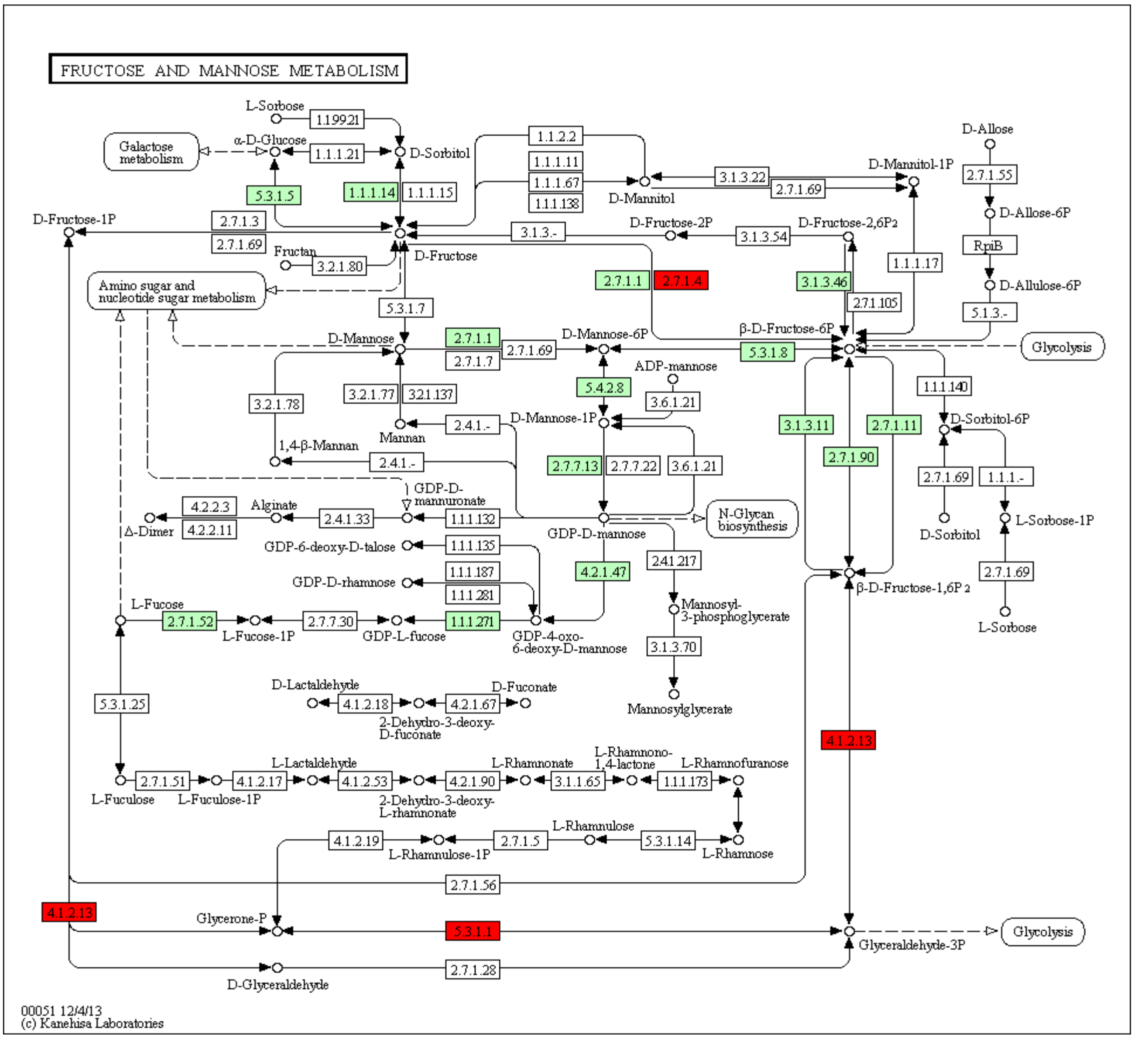
FRUCTOSE AND MANNOSE METABOLISM
L-Sorbose
1.1.99.21
Galactose metabolism
α-D-Glucose
1.1.1.21
D-Sorbitol
1.1.2.2
1.1.1.11
1.1.1.67
1.1.1.138
D-Allose
3.1.3.22
D-Mannitol-1P
2.7.1.69
D-Mannitol
2.7.1.55
5.3.1.5
1.1.1.14
1.1.1.15
D-Allose-6P
D-Fructose-1P
2.7.1.3
2.7.1.69
3.1.3.-
D-Fructose-2P
3.1.3.54
D-Fructose-2,6P2
RpiB
Fructan
3.2.1.80
D-Fructose
1.1.1.17
D-Allulose-6P
2.7.1.1
2.7.1.4
3.1.3.46
Amino sugar and nucleotide sugar metabolism
2.7.1.105
5.3.1.7
5.1.3.-
β-D-Fructose-6P
D-Mannose
2.7.1.1
D-Mannose-6P
2.7.1.69
5.3.1.8
Glycolysis
2.7.1.7
ADP-mannose
5.4.2.8
1.1.1.140
3.6.1.21
3.2.1.78
3.2.1.77
3.2.1.137
D-Mannose-1P
3.1.3.11
2.7.1.11
D-Sorbitol-6P
2.4.1.-
Mannan
1,4-β-Mannan
2.7.7.13
2.7.7.22
3.6.1.21
2.7.1.90
2.4.1.-
2.7.1.69
1.1.1.-
GDP-D-mannuronate
4.2.2.3
Alginate
2.4.1.33
1.1.1.132
N-Glycan biosynthesis
L-Sorbose-1P
Δ-Dimer
4.2.2.11
D-Sorbitol
GDP-D-mannose
GDP-6-deoxy-D-talose
1.1.1.135
2.4.1.217
1.1.1.187
4.2.1.47
2.7.1.69
GDP-D-rhamnose
β-D-Fructose-1,6P2
1.1.1.281
L-Fucose
Mannosyl-3-phosphoglycerate
2.7.1.52
2.7.7.30
1.1.1.271
L-Sorbose
L-Fucose-1P
GDP-L-fucose
GDP-4-oxo-6-deoxy-D-mannose
3.1.3.70
5.3.1.25
D-Lactaldehyde
D-Fuconate
Mannosylglycerate
4.1.2.18
4.2.1.67
2-Dehydro-3-deoxy-D-fuconate
4.1.2.13
L-Rhamnono-1,4-lactone
L-Lactaldehyde
L-Rhamnonate
L-Rhamnofuranose
2.7.1.51
4.1.2.17
4.1.2.53
4.2.1.90
3.1.1.65
1.1.1.173
L-Fuculose
L-Fuculose-1P
2-Dehydro-3-deoxy-L-rhamnonate
L-Rhamnulose
4.1.2.19
2.7.1.5
5.3.1.14
L-Rhamnulose-1P
L-Rhamnose
2.7.1.56
4.1.2.13
Glycerone-P
5.3.1.1
Glycolysis
Glyceraldehyde-3P
D-Glyceraldehyde
2.7.1.28
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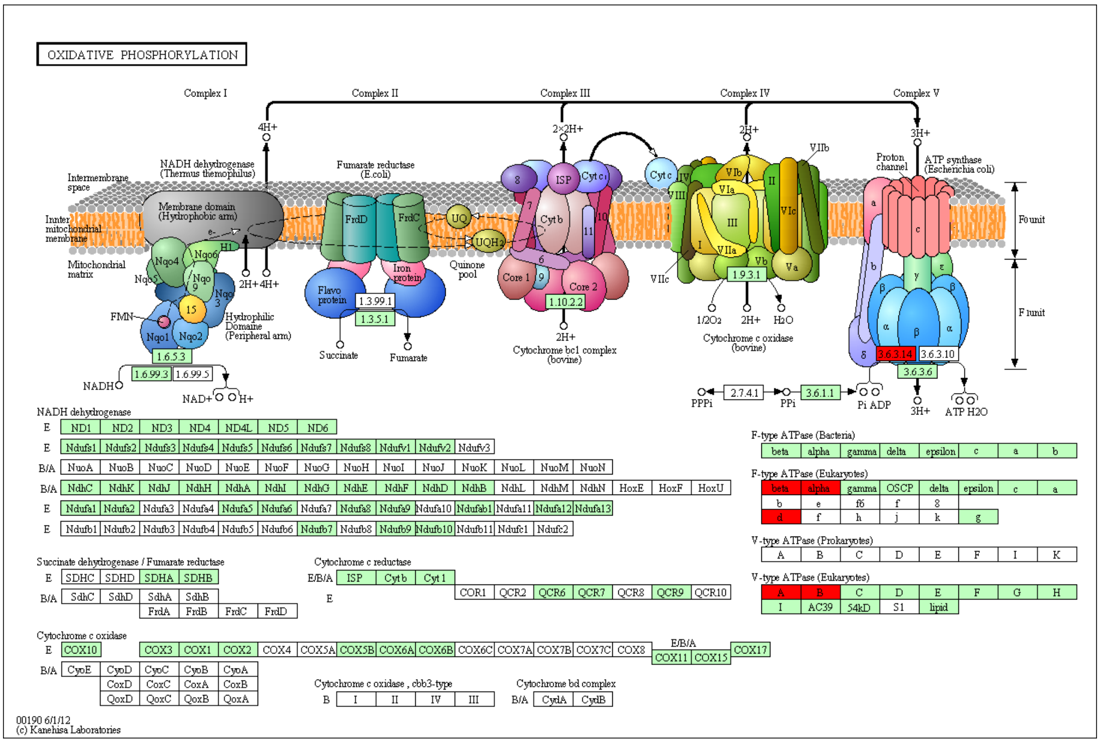
OXIDATIVE PHOSPHORYLATION
Complex I
Complex II
Complex III
Complex IV
Complex V
4H+
2×2H+
2H+
3H+
Intermembrane space
Inner mitochondrial membrane
Mitochondrial matrix
NADH dehydrogenase (Thermus thermophilus)
Membrane domain (Hydrophobic arm)
Hydrophilic Domain (Peripheral arm)
FMN
NADH
NAD+ H+
1.6.5.3
1.6.99.3
1.6.99.5
Fumarate reductase (E.coli)
FrdD
FrdC
Flavo protein
Iron protein
Succinate
Fumarate
1.3.99.1
1.3.5.1
UQ
UQH2
Quinone pool
ISP
Cyt c1
Cyt c
Cyt b
Core 1
Core 2
1.10.2.2
Cytochrome bc1 complex (bovine)
VIIb
VIb
VIa
VIIa
VIIc
Vb
Va
Vic
1.9.3.1
1/2O2
2H+
H2O
Cytochrome c oxidase (bovine)
Proton channel
ATP synthase (Escherichia coli)
F0 unit
F1 unit
3.6.3.14
3.6.3.10
3.6.3.6
PPPi
PPi
2.7.4.1
3.6.1.1
Pi ADP
ATP H2O
NADH dehydrogenase
E ND1 ND2 ND3 ND4 ND4L ND5 ND6
E Ndufs1 Ndufs2 Ndufs3 Ndufs4 Ndufs5 Ndufs6 Ndufs7 Ndufs8 Ndufv1 Ndufv2 Ndufv3
B/A NuoA NuoB NuoC NuoD NuoE NuoF NuoG NuoH NuoI NuoJ NuoK NuoL NuoM NuoN
B/A NdhC NdhK NdhJ NdhH NdhA NdhI NdhG NdhE NdhF NdhD NdhB NdhL NdhM NdhN HoxE HoxF HoxU
E Ndufa1 Ndufa2 Ndufa3 Ndufa4 Ndufa5 Ndufa6 Ndufa7 Ndufa8 Ndufa9 Ndufa10 Ndufab1 Ndufa11 Ndufa12 Ndufa13
E Ndufb1 Ndufb2 Ndufb3 Ndufb4 Ndufb5 Ndufb6 Ndufb7 Ndufb8 Ndufb9 Ndufb10 Ndufb11 Ndufc1 Ndufc2
Succinate dehydrogenase / Fumarate reductase
E SDHC SDHD SDHA SDHB
B/A SdhC SdhD SdhA SdhB
FrdA FrdB FrdC FrdD
Cytochrome c reductase
E/B/A ISP Cytb Cyt1
E COR1 QCR2 QCR6 QCR7 QCR8 QCR9 QCR10
Cytochrome c oxidase
E COX10 COX3 COX1 COX2 COX4 COX5A COX5B COX6A COX6B COX6C COX7A COX7B COX7C COX8
E/B/A COX11 COX15 COX17
B/A CyoE CyoD CyoC CyoB CyoA
CoxD CoxC CoxA CoxB
QoxD QoxC QoxB QoxA
Cytochrome c oxidase , cbb3-type
B I II IV III
Cytochrome bd complex
B/A CydA CydB
F-type ATPase (Bacteria)
beta alpha gamma delta epsilon c a b
F-type ATPase (Eukaryotes)
beta alpha gamma OSCP delta epsilon c a
b e f6 f 8
d f h j k g
V-type ATPase (Prokaryotes)
A B C D E F I K
V-type ATPase (Eukaryotes)
A B C D E F G H
I AC39 54kD S1 lipid
00190 6/1/12
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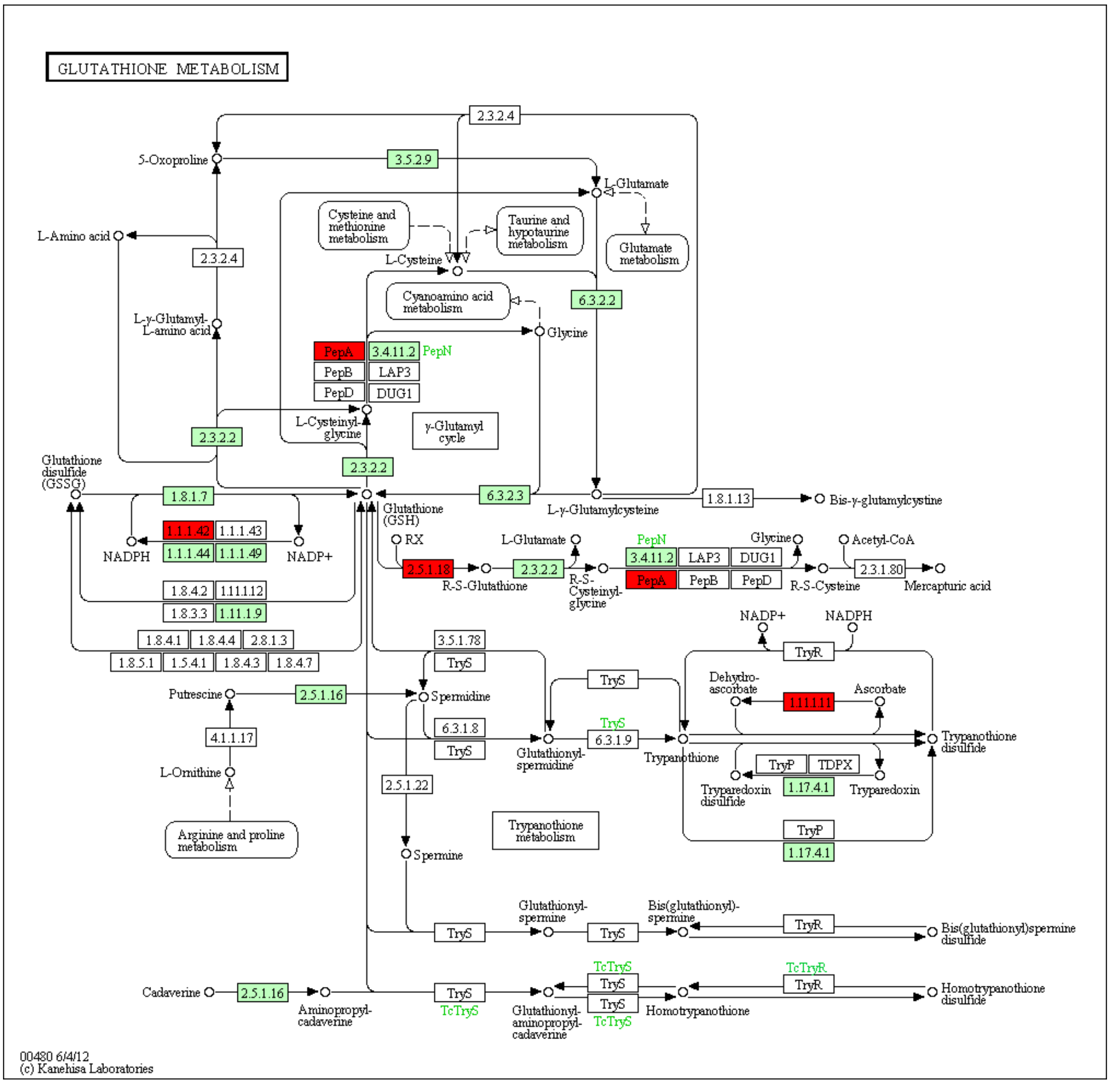
GLUTATHIONE METABOLISM
2.3.2.4
5-Oxoproline
3.5.2.9
L-Glutamate
L-Amino acid
Cysteine and methionine metabolism
Taurine and hypotaurine metabolism
Glutamate metabolism
L-Cysteine
2.3.2.4
Cyanoamino acid metabolism
6.3.2.2
L-γ-Glutamyl-L-amino acid
Glycine
PepA 3.4.11.2 PepN
PepB LAP3
PepD DUG1
L-Cysteinyl-glycine
γ-Glutamyl cycle
2.3.2.2
2.3.2.2
Glutathione disulfide (GSSG)
1.8.1.7
6.3.2.3
L-γ-Glutamylcysteine
1.8.1.13
Bis-γ-glutamylcysteine
Glutathione (GSH)
1.11.1.42 1.11.1.43
1.11.1.44 1.11.1.49
NADPH
NADP+
RX
2.5.1.18
R-S-Glutathione
L-Glutamate
2.3.2.2
PepN
3.4.11.2 LAP3 DUG1
PepA PepB PepD
R-S-Cysteinyl-glycine
Glycine
Acetyl-CoA
2.3.1.80
R-S-Cysteine
Mercapturic acid
1.8.4.2 1.11.1.12
1.8.3.3 1.11.1.9
1.8.4.1 1.8.4.4 2.8.1.3
1.8.5.1 1.5.4.1 1.8.4.3 1.8.4.7
3.5.1.78
TryS
NADP+
NADPH
TryR
Putrescine
2.5.1.16
Spermidine
TryS
Dehydro-ascorbate
1.11.1.11
Ascorbate
4.1.1.17
6.3.1.8
TryS
TryS
6.3.1.9
Glutathionyl-spermidine
Trypanothione
Trypanothione disulfide
L-Ornithine
2.5.1.22
TryP TDPX
Tryparedoxin disulfide
1.17.4.1
Tryparedoxin
Arginine and proline metabolism
Trypanothione metabolism
TryP
1.17.4.1
Spermine
Glutathionyl-spermine
Bis(glutathionyl)-spermine
TryS
TryS
TryR
Bis(glutathionyl)spermine disulfide
TcTryS
TryS
TryS
TcTryR
TryR
Cadaverine
2.5.1.16
Aminopropyl-cadaverine
TryS
TcTryS
Glutathionyl-aminopropyl-cadaverine
TcTryS
Homotrypanothione
Homotrypanothione disulfide
00480 6/4/12
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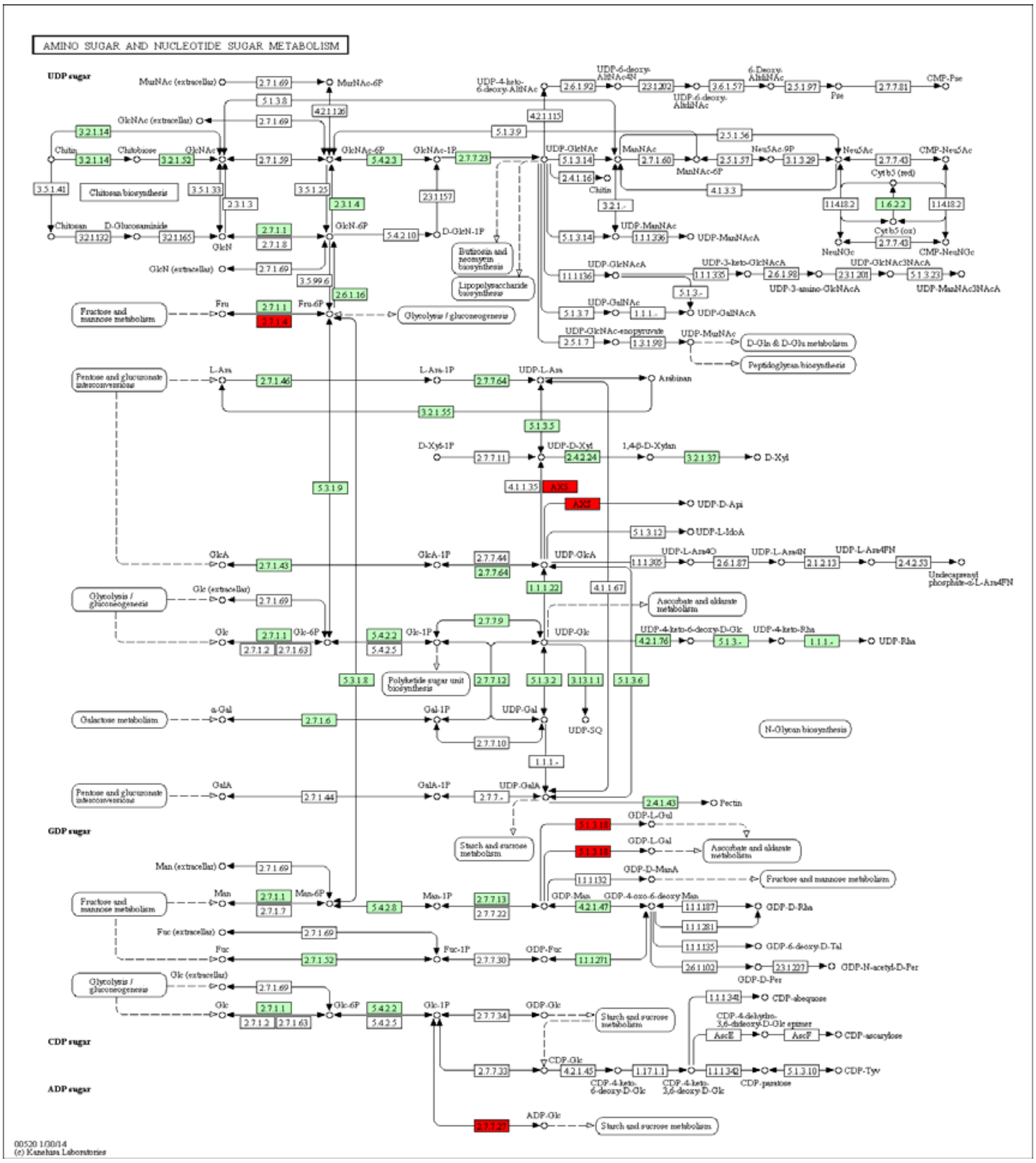
AMINO SUGAR AND NUCLEOTIDE SUGAR METABOLISM
UDP sugar
GDP sugar
CDP sugar
ADP sugar
MurNAc (extracellular)
MurNAc-6P
GlcNAc (extracellular)
Chitin
Chitobiose
GlcNAc
GlcNAc-6P
GlcNAc-1P
Chitosan biosynthesis
Chitosan
D-Glucosaminide
GlcN
GlcN-6P
D-GlcN-1P
GlcN (extracellar)
Fru
Fru-6P
Fructose and mannose metabolism
Glycolysis / gluconeogenesis
Butirosin and neomycin biosynthesis
Lipopolysaccharide biosynthesis
UDP-4-keto-6-deoxy-AltNAc
UDP-6-deoxy-AltNAc4N
UDP-6-deoxy-AltdiNAc
6-Deoxy-AltdiNAc
Pse
CMP-Pse
UDP-GlcNAc
ManNAc
ManNAc-6P
Neu5Ac-9P
Neu5Ac
CMP-Neu5Ac
Cyt b5 (red)
Cyt b5 (ox)
NeuNGc
CMP-NeuNGc
Chitin
UDP-ManNAc
UDP-ManNAcA
UDP-GlcNAcA
UDP-3-keto-GlcNAcA
UDP-3-amino-GlcNAcA
UDP-GlcNAc3NAcA
UDP-ManNAc3NAcA
UDP-GalNAc
UDP-GalNAcA
UDP-GlcNAc-enopyruvate
UDP-MurNAc
D-Gln & D-Glu metabolism
Peptidoglycan biosynthesis
Pentose and glucuronate interconversions
L-Ara
L-Ara-1P
UDP-L-Ara
Arabinan
D-Xyl-1P
UDP-D-Xyl
1,4-β-D-Xylan
D-Xyl
AXS
AXS
UDP-D-Api
UDP-L-IdoA
GlcA
GlcA-1P
UDP-GlcA
UDP-L-Ara4O
UDP-L-Ara4N
UDP-L-Ara4FN
Undecaprenyl phosphate-α-L-Ara4FN
Glc (extracellar)
Ascorbate and aldarate metabolism
Glc
Glc-6P
Glc-1P
UDP-Glc
UDP-4-keto-6-deoxy-D-Glc
UDP-4-keto-Rha
UDP-Rha
Polyketide sugar unit biosynthesis
Galactose metabolism
α-Gal
Gal-1P
UDP-Gal
UDP-SQ
N-Glycan biosynthesis
GalA
GalA-1P
UDP-GalA
Pectin
Starch and sucrose metabolism
GDP-L-Gul
GDP-L-Gal
Ascorbate and aldarate metabolism
GDP-D-ManA
Fructose and mannose metabolism
Man (extracellar)
Man
Man-6P
Man-1P
GDP-Man
GDP-4-oxo-6-deoxy-Man
GDP-D-Rha
Fuc (extracellar)
Fuc
Fuc-1P
GDP-Fuc
GDP-6-deoxy-D-Tal
GDP-D-Per
GDP-N-acetyl-D-Per
Glycolysis / gluconeogenesis
Glc (extracellar)
Glc
Glc-6P
Glc-1P
GDP-Glc
Starch and sucrose metabolism
CDP-abequose
CDP-4-dehydro-3,6-dideoxy-D-Glc epimer
AscE
AscF
CDP-ascarylose
CDP-Glc
CDP-4-keto-6-deoxy-D-Glc
CDP-4-keto-3,6-deoxy-D-Glc
CDP-paratose
CDP-Tyv
ADP-Glc
Starch and sucrose metabolism
00520 1/30/14
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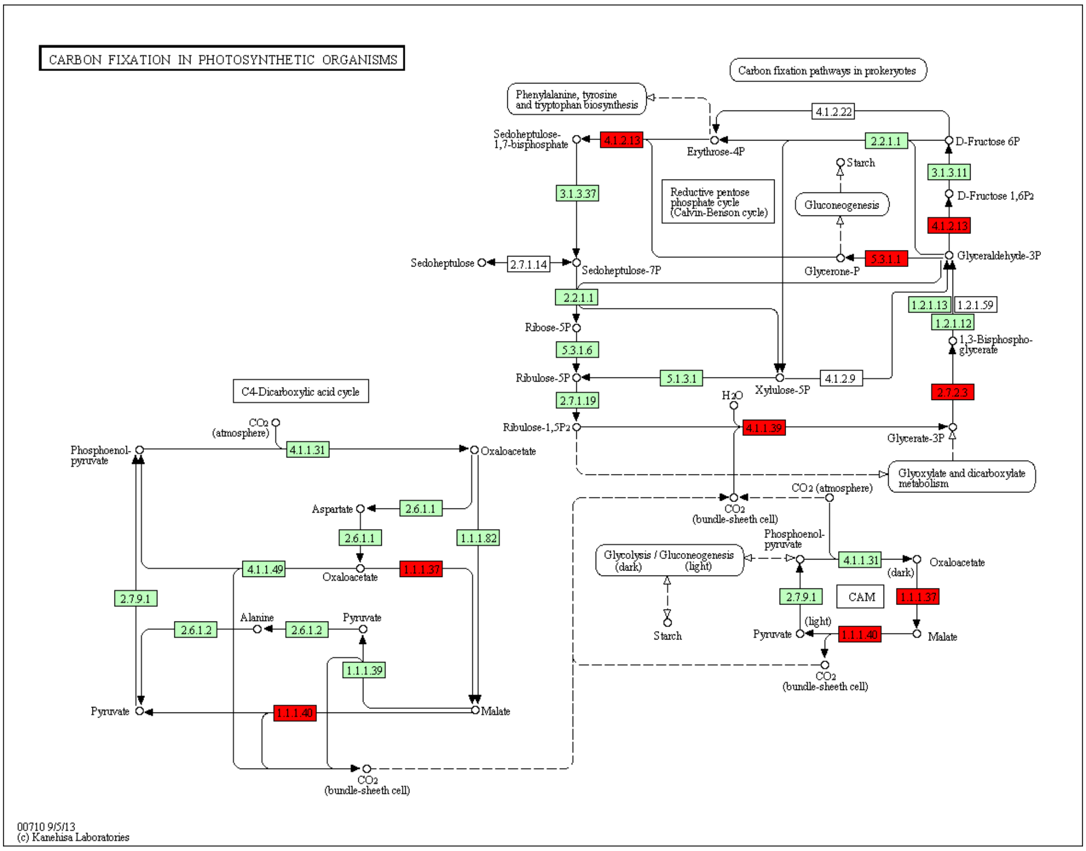
CARBON FIXATION IN PHOTOSYNTHETIC ORGANISMS
Carbon fixation pathways in prokaryotes
Phenylalanine, tyrosine and tryptophan biosynthesis
4.1.2.22
Sedoheptulose-1,7-bisphosphate
4.1.2.13
Erythrose-4P
2.2.1.1
D-Fructose 6P
Starch
3.1.3.11
D-Fructose 1,6P2
3.1.3.37
Reductive pentose phosphate cycle (Calvin-Benson cycle)
Gluconeogenesis
4.1.2.13
Sedoheptulose
2.7.1.14
Sedoheptulose-7P
Glycerone-P
5.3.1.1
Glyceraldehyde-3P
2.2.1.1
1.2.1.13
1.2.1.59
Ribose-5P
1.2.1.12
1,3-Bisphospho-glycerate
5.3.1.6
Ribulose-5P
5.1.3.1
Xylulose-5P
4.1.2.9
2.7.2.3
C4-Dicarboxylic acid cycle
H2O
2.7.1.19
CO2 (atmosphere)
Ribulose-1,5P2
4.1.1.39
Glycerate-3P
Phosphoenol-pyruvate
4.1.1.31
Oxaloacetate
Glyoxylate and dicarboxylate metabolism
CO2 (atmosphere)
CO2 (bundle-sheeth cell)
Aspartate
2.6.1.1
2.6.1.1
1.1.1.82
Phosphoenol-pyruvate
Glycolysis / Gluconeogenesis (dark) (light)
4.1.1.31
Oxaloacetate
4.1.1.49
Oxaloacetate
1.1.1.37
(dark)
2.7.9.1
2.7.9.1
CAM
1.1.1.37
Alanine
Pyruvate
2.6.1.2
2.6.1.2
Starch
(light)
Pyruvate
1.1.1.40
Malate
1.1.1.39
CO2 (bundle-sheeth cell)
Pyruvate
1.1.1.40
Malate
CO2 (bundle-sheeth cell)
00710 9/5/13
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Supplementary Table S1 Information for differential protein spots on 2-DE gels and their corresponding MS identities

Spot No.[a]	Exper.[b] *p*I/M*r*	M.S.[c] Score	ABV S1[d]	ABV S2	ABV S3	ABV S4	ABV S5	ABV S6	ABV S7	ABV S8	ABV S9	Protein name
1	4.78/49	92	0.04	0.00	0.19	0.12	0.03	0.06	0.05	0.00	0.06	hypothetical protein
2	4.93/61	215	0.06	0.20	0.49	0.38	0.23	0.22	0.16	0.12	0.27	Chaperonin 60 subunit alpha 1
3	4.99/54	97	0.13	0.18	0.35	0.17	0.00	0.16	0.13	0.10	0.22	V-type proton ATPase subunit B1
4	5.14/54	187	0.07	0.10	0.21	0.13	0.16	0.15	0.08	0.00	0.13	V-type proton ATPase subunit B2
5	5.15/51	101	0.00	0.23	0.31	0.24	0.29	0.22	0.10	0.00	0.00	Tubulin alpha-6 chain
6	5.05/47	154	0.08	0.12	0.20	0.13	0.21	0.10	0.12	0.07	0.21	26S protease regulatory subunit 6A
7	5.19/70	115	0.34	0.35	0.55	0.40	0.43	0.35	0.23	0.28	0.43	RNA polymerase II transcription
8	5.21/70	98	0.57	0.52	1.01	0.58	0.68	0.51	0.45	0.35	0.53	RNA polymerase II transcription
9	5.23/70	128	0.11	0.25	0.56	0.51	0.48	0.38	0.36	0.36	0.34	RNA polymerase II transcription
10	5.30/67	127	0.15	0.35	0.27	0.41	0.22	0.18	0.43	0.27	0.21	Actin-7
11	5.24/60	147	0.24	0.30	0.31	0.22	0.22	0.19	0.17	0.16	0.15	Chaperonin 60 subunit beta 2
12	5.27/60	73	0.07	0.18	0.20	0.22	0.19	0.17	0.16	0.13	0.12	Chaperonin 60 subunit beta 1
13	5.28/60	143	0.30	0.19	0.15	0.13	0.13	0.12	0.11	0.11	0.09	Chaperonin CPN60, mitochondrial
14	5.18/53	87	0.04	0.30	0.36	0.30	0.57	0.28	0.24	0.22	0.13	Tubulin alpha-6 chain
15	5.18/51	103	0.08	0.52	0.92	0.59	0.78	0.62	0.38	0.29	0.15	Tubulin alpha-6 chain
16	5.23/53	89	0.05	0.06	0.13	0.23	0.24	0.25	0.19	0.23	0.18	Tubulin alpha-6 chain
17	5.31/51	173	0.19	0.12	0.07	0.37	0.03	0.08	0.05	0.02	0.00	Actin-7
18	5.50/52	190	0.47	0.53	0.33	0.23	0.30	0.26	0.24	0.37	0.15	ATP synthase beta subunit 1
19	5.78/53	175	0.52	0.33	0.38	0.26	0.46	0.60	0.43	0.75	0.34	ATP synthase subunit beta-3
20	5.75/49	182	0.15	0.34	0.15	0.06	0.08	0.13	0.05	0.06	0.00	Glucose adenylyltransferase
21	5.80/42	101	0.55	0.49	0.46	0.24	0.39	0.46	0.35	0.39	0.15	Glutamine synthetase
22	5.20/44	96	0.10	0.24	0.28	0.22	0.39	0.22	0.25	0.09	0.11	Actin-7
23	5.26/44	93	0.14	0.25	0.23	0.30	0.37	0.31	0.22	0.20	0.25	Actin-7
24	5.31/44	195	0.34	1.32	1.15	1.40	1.71	1.33	1.38	1.78	1.32	Actin-7
25	5.28/42	128	0.23	0.26	0.27	0.35	0.31	0.21	0.23	0.12	0.28	Succinyl-CoA ligase
26	5.29/42	107	0.26	0.26	0.39	0.34	0.30	0.16	0.18	0.26	0.17	Glutamine synthetase
27	5.30/40	[113]	0.27	0.35	0.18	0.13	0.16	0.13	0.13	0.12	0.12	Adenosine kinase 1
28	5.01/79	127	0.09	0.36	0.60	0.57	0.47	0.32	0.30	0.24	0.74	Heat shock protein 90-3
29	5.54/96	81	0.00	0.00	0.00	0.03	0.04	0.13	0.10	0.10	0.12	Alpha-glucan phosphorylase 1
30	5.60/96	[387]	0.00	0.03	0.04	0.07	0.08	0.16	0.20	0.12	0.19	Alpha-glucan phosphorylase 1
31	5.60/96	76	0.00	0.03	0.03	0.04	0.04	0.13	0.11	0.10	0.07	Alpha-glucan phosphorylase 1
32	5.59/102	[110]	0.00	0.02	0.00	0.00	0.00	0.00	0.00	0.12	0.00	Alpha-glucan phosphorylase 1
33	5.73/102	101	0.00	0.05	0.00	0.00	0.00	0.00	0.01	0.15	0.02	Alpha-glucan phosphorylase 1
34	4.62/29	115	0.35	0.27	0.55	0.48	0.38	0.18	0.24	0.25	0.97	14-3-3-like protein GF14 omega
35	4.68/28	159	0.57	0.12	1.08	0.79	0.56	0.25	0.32	0.36	0.88	14-3-3-like protein GF14 omega
36	4.75/29	111	0.37	0.11	1.09	0.61	0.72	0.14	0.21	0.25	0.56	14-3-3-like protein GF14 psi
37	5.16/37	[154]	0.24	0.18	0.34	0.19	0.21	0.14	0.13	0.18	0.24	Probable fructokinase-1
38	5.18/36	[147]	0.26	0.21	0.27	0.16	0.17	0.12	0.09	0.10	0.14	Probable fructokinase-1
39	5.21/34	151	0.65	0.73	0.99	0.62	0.90	0.39	0.48	0.39	0.70	Probable lactoylglutathione lyase

40	5.24/34	[73]	0.19	0.17	0.29	0.29	0.28	0.12	0.13	0.12	0.16	Probable lactoylglutathione lyase
41	5.27/32	[187]	0.14	0.17	0.19	0.19	0.24	0.16	0.19	0.20	0.27	Carboxypho-yruvate mutase
42	5.28/36	[146]	0.30	0.30	0.27	0.12	0.19	0.10	0.11	0.13	0.12	Probable fructokinase-1
43	5.45/37	[81]	0.44	0.42	0.19	0.39	0.45	0.32	0.35	0.26	0.30	NADP-dependent reductase P1
44	5.45/38	[99]	0.32	0.37	0.47	0.41	0.49	0.33	0.46	0.45	0.34	NADP-dependent reductase P1
45	5.31/35	[151]	0.13	0.15	0.14	0.14	0.17	0.13	0.15	0.19	0.15	DNA-damage-repair protein
46	5.77/36	[254]	0.55	0.24	0.19	0.11	0.14	0.11	0.12	0.13	0.08	NAD(P)H oxidoreductase
47	5.38/32	[133]	0.00	0.05	0.06	0.21	0.23	0.17	0.28	0.26	0.39	Thiamine thiazole synthase
48	5.18/30	[209]	0.00	0.17	0.29	0.14	0.27	0.11	0.13	0.07	0.14	Alpha-soluble NSF protein 2
49	5.21/24	125	0.16	0.14	0.34	0.36	0.42	0.17	0.23	0.20	0.37	Ferritin-4, chloroplastic
50	5.28/23	[172]	0.33	0.31	0.49	0.42	0.46	0.17	0.30	0.15	0.41	20 kDa chaperonin, chloroplastic
51	5.31/27	82	0.59	0.30	0.29	0.27	0.34	0.34	0.36	0.30	0.56	L-ascorbate peroxidase 1
52	5.55/28	133	1.79	1.21	2.47	1.99	3.21	2.10	1.51	2.58	3.37	L-ascorbate peroxidase 1
53	5.71/28	[96]	0.66	0.48	0.45	0.31	0.45	0.13	0.17	0.10	0.22	Actin-7
54	4.85/21	113	0.45	0.20	0.39	0.21	0.28	0.17	0.21	0.11	0.45	ATP synthase subunit d
55	5.15/19	184	0.32	0.18	0.31	0.15	0.25	0.13	0.12	0.08	0.17	ATP synthase subunit d
56	5.60/22	[137]	0.38	0.20	0.15	0.10	0.15	0.11	0.10	0.12	0.09	Proteasome subunit beta type
57	5.25/17	[133]	0.19	0.31	0.42	0.35	0.42	0.20	0.27	0.21	0.26	regulator of ribonuclease
58	5.60/17	[66]	0.00	0.08	0.17	0.52	0.57	0.38	0.47	0.32	0.63	Eukaryotic translation initiation factor
59	5.60/17	72	0.00	0.05	0.10	0.25	0.24	0.15	0.19	0.15	0.24	Eukaryotic translation initiation factor
60	5.78/16	[196]	0.13	0.18	0.16	0.45	0.35	0.55	0.49	0.48	0.32	heat-shock protein, putative
61	5.94/17	[112]	0.13	0.19	0.19	0.16	0.19	0.15	0.16	0.17	0.12	Actin-depolymerizing factor 3
62	5.99/18	[95]	0.54	0.98	1.38	0.79	1.71	0.58	0.89	0.62	0.36	class I heat shock protein
63	5.98/17	82	0.30	0.40	0.55	0.32	0.72	0.21	0.25	0.25	0.09	Eukaryotic translation initiation factor
64	6.17/18	[180]	0.69	1.23	1.26	1.03	1.26	0.60	1.11	0.60	0.54	Peroxiredoxin-2B
65	6.39/18	[164]	0.00	1.99	3.73	4.73	4.30	3.85	4.45	3.87	3.40	class I heat shock protein
66	6.60/15	[80]	0.45	0.36	0.32	0.16	0.19	0.25	0.32	0.20	0.00	Superoxide dismutase [Cu-Zn] 1
67	6.60/16	[147]	0.15	0.45	0.52	0.33	0.32	0.35	0.40	0.36	0.13	Actin-depolymerizing factor 3
68	6.84/17	119	0.34	0.41	0.28	0.18	0.20	0.21	0.14	0.22	0.10	Ubiquitin-conjugating enzyme E2
69	7.03/16	[195]	0.00	0.56	0.66	0.38	0.68	0.69	0.21	0.57	0.14	AT3g53990/F5K20_290
70	6.61/22	139	1.03	0.68	0.45	0.28	0.39	0.38	0.41	0.34	0.17	Superoxide dismutase [Mn] 1
71	6.60/23	[99]	0.31	0.13	0.15	0.10	0.15	0.12	0.13	0.17	0.05	Proteasome subunit alpha type-2-A
72	6.01/24	[94]	0.29	0.11	0.12	0.12	0.14	0.14	0.11	0.12	0.08	Superoxide dismutase [Fe] 2
73	6.55/26	[234]	0.35	0.32	0.26	0.13	0.22	0.21	0.20	0.22	0.20	L-ascorbate peroxidase 1
74	6.59/26	[194]	0.45	0.47	0.33	0.21	0.28	0.38	0.39	0.42	0.00	Triosephosphate isomerase
75	6.81/28	131	0.29	0.29	0.24	0.15	0.16	0.18	0.11	0.21	0.00	Proteasome subunit alpha type-6-A
76	5.86/32	[162]	0.00	0.04	0.09	0.14	0.20	0.21	0.22	0.27	0.16	Thiamine thiazole synthase
77	6.22/32	88	0.00	0.02	0.05	0.27	0.26	0.36	0.43	0.70	0.18	Thiamine thiazole synthase
78	6.10/48	119	0.26	0.44	0.32	0.14	0.21	0.15	0.11	0.13	0.06	S-adenosylmethionine synthase 1
79	6.64/39	108	0.89	0.46	0.28	0.17	0.24	0.34	0.29	0.35	0.10	malate dehydrogenase
80	6.44/46	163	0.06	0.09	0.07	0.06	0.06	0.13	0.11	0.16	0.03	UDP-D-apiose/-xylose synthase 1
81	6.49/45	115	0.07	0.12	0.08	0.06	0.07	0.12	0.09	0.13	0.04	Cytosolic isocitrate dehydrogenase
82	6.58/47	76	0.17	0.27	0.13	0.07	0.10	0.16	0.08	0.10	0.05	GDP-mannose 3,5-epimerase

83	6.24/54	124	0.13	0.30	0.31	0.18	0.19	0.26	0.28	0.39	0.11	Bifunctional enolase 2
84	6.21/52	100	0.00	0.20	0.21	0.12	0.14	0.22	0.14	0.27	0.13	Bifunctional enolase 2
85	6.32/55	151	0.25	0.31	0.09	0.20	0.21	0.32	0.26	0.33	0.10	ATP synthase F1 subunit 1
86	6.45/64	177	0.08	0.11	0.10	0.10	0.14	0.18	0.20	0.19	0.08	malic enzyme, putative
87	6.43/54	[150]	0.09	0.33	0.29	0.16	0.18	0.40	0.39	0.26	0.14	Bifunctional enolase 2
88	6.41/52	160	0.07	0.24	0.20	0.14	0.17	0.28	0.25	0.25	0.10	Bifunctional enolase 2
89	5.45/69	234	0.02	0.04	0.04	0.01	0.01	0.04	0.02	0.04	0.01	V-type proton ATPase
90	5.55/69	194	0.07	0.07	0.12	0.06	0.06	0.06	0.04	0.11	0.04	V-type proton ATPase
91	5.60/49	81	0.02	0.07	0.15	0.06	0.06	0.06	0.08	0.86	0.06	Glucose-adenylyltransferase
92	6.61/64	154	0.04	0.11	0.03	0.06	0.03	0.03	0.05	0.03	0.02	malic enzyme, putative
93	4.52/50	[114]	0.47	0.13	0.27	0.18	0.17	0.17	0.14	0.04	0.09	Triosephosphate isomerase
94	5.72/101	[278]	0.05	0.09	0.17	0.08	0.09	0.20	0.20	0.14	0.15	Alpha-glucan phosphorylase 1
95	5.05/33	[108]	0.12	0.34	1.36	1.08	1.21	0.45	0.38	0.32	1.02	Actin-7
96	4.93/33	[77]	0.13	0.09	0.48	0.53	0.87	0.15	0.07	0.07	0.19	Actin-7
97	5.32/35	[165]	0.71	0.33	0.17	0.17	0.17	0.09	0.13	0.11	0.07	nitrile-specifier protein 5-like
98	5.53/28	[190]	0.09	0.07	0.15	0.14	0.22	0.10	0.19	0.09	0.27	Abscisic acid receptor PYR1
99	5.18/24	[210]	0.21	0.22	0.35	0.25	0.35	0.18	0.18	0.12	0.36	Triosephosphate isomerase
100	5.28/26	[161]	0.61	0.41	0.35	0.30	0.30	0.15	0.16	0.16	0.16	Dienelactone hydrolase
101	5.51/23	[67]	0.18	0.25	0.23	0.20	0.23	0.07	0.07	0.06	0.06	UMP-CMP kinase 3
102	5.31/25	[189]	0.37	0.38	0.07	0.11	0.00	0.05	0.06	0.05	0.00	Actin-7
103	5.50/22	[158]	0.41	0.29	0.25	0.22	0.28	0.15	0.13	0.18	0.17	Proteasome subunit type-3
104	5.62/18	[61]	0.37	0.38	0.35	0.46	0.78	0.41	0.50	0.43	0.56	Superoxide dismutase [Cu-Zn] 1
105	6.25/17	[142]	0.00	0.47	0.77	0.59	0.53	0.27	0.39	0.21	0.00	class I heat shock protein
106	6.36/16	[130]	0.31	0.19	0.23	0.18	0.13	0.11	0.12	0.10	0.00	Superoxide dismutase [Cu-Zn] 1
107	6.95/27	[257]	0.39	0.40	0.31	0.35	0.40	0.22	0.06	0.09	1.59	glutathione S-transferase GST
108	5.56/24	[166]	0.22	0.10	0.12	0.09	0.11	0.11	0.14	0.15	0.05	Triosephosphate isomerase
109	5.86/25	[77]	0.15	0.35	0.26	0.18	0.19	0.19	0.25	0.16	0.12	6-phosphogluconolactonase
110	6.25/26	[298]	0.43	0.42	0.37	0.23	0.23	0.40	0.36	0.42	0.13	Triosephosphate isomerase
111	6.87/37	[298]	0.24	0.54	1.10	0.14	0.99	0.58	0.26	0.53	0.29	annexin
112	6.23/41	[343]	0.14	0.69	0.76	0.39	0.58	0.93	0.78	0.95	0.30	alcohol dehydrogenase
113	5.63/41	[440]	0.00	0.08	0.20	0.17	0.16	0.44	0.26	0.47	0.15	Actin-7
114	6.65/38	[349]	1.05	0.72	0.68	0.37	0.33	0.66	0.31	0.76	0.23	Malate dehydrogenase
115	6.23/53	[399]	0.20	0.31	0.22	0.34	0.33	0.41	0.48	0.39	0.19	Leucine aminopeptidase 3
116	6.35/52	[173]	0.21	0.18	0.18	0.15	0.19	0.42	0.48	0.31	0.27	Bifunctional enolase 2
117	5.65/58	[345]	0.12	0.32	0.21	0.26	0.38	0.42	0.32	0.36	0.21	Betaine aldehyde dehydrogenase 1
118	5.84/57	[214]	0.12	0.24	0.19	0.32	0.33	0.32	0.21	0.13	0.13	Ketol-acid reductoisomerase

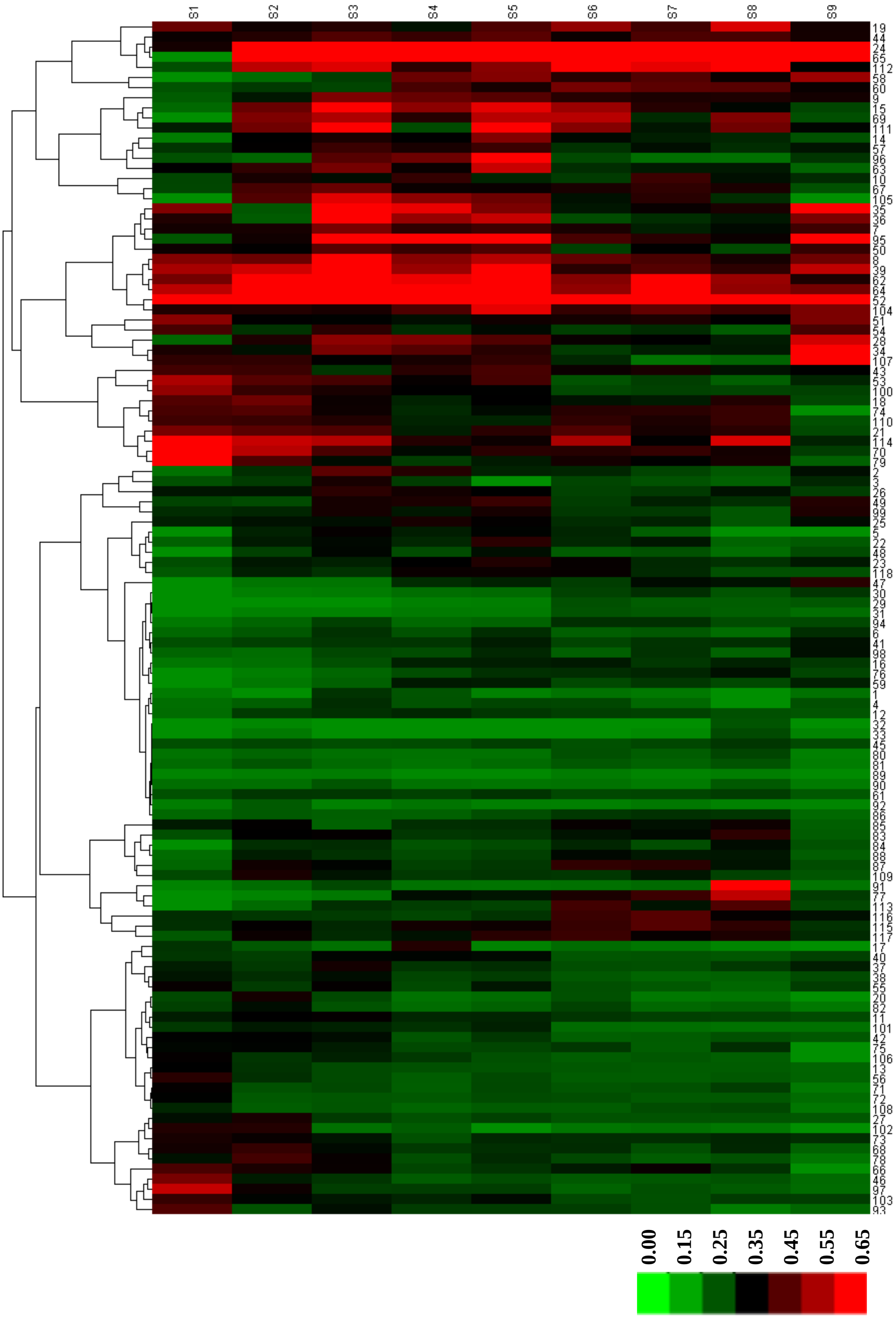
Note: [a]Assigned spot number (S1-S118) for the 118 differential proteins as indicated in Fig. 2.

[b]The experimental values for the mass (kDa) and *p*I of identified proteins.

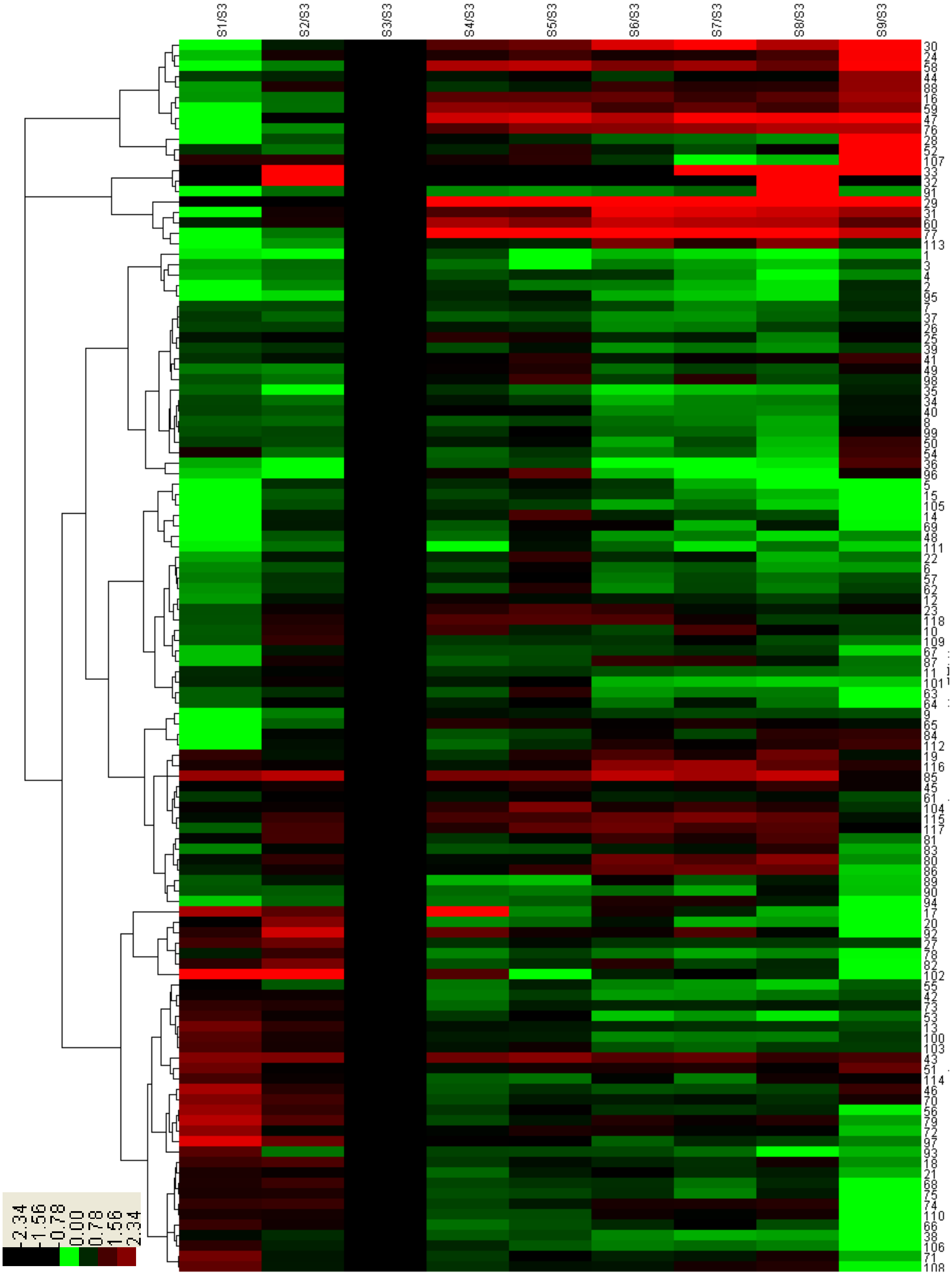
[c]Mascot searched scores (M.S.) against cassava genome for MS and [MS/MS] searched results.

[d]The average abudance of the statistical percent of volue (ABV) value (Vol%) in 2-DE gels for protein spots in different development stages (S1-S9) of cassava roots produced by ImageMaster.

Supplementary Table S1-continued Detai information for the hierarchical cluster of abundance volume% of the protein spots in Figure 5A was presented in the following. The high- or low-abundance proteins were indicated in red or green, respectively.



Supplementary Table S1-continued Detai information for the hierarchical cluster of the relative abundance volume ratios for the protein spots with S3 on 2-DE gels in Figure 5B was highlighted. The log values for the induced or reduced relative abundance volume ratios were indicated in red or green, respectively.



Supplementary Table S2. Information for differential proteins on 2-D DIGE gels and the corresponding MS identities.

Spot No.[a]	**Exper.**[b] ***p*I/M*r***	**Ther.**[c] ***p*I/M*r***	**MP/ TP**[d]	**SC**[e] **(%)**	**M.S.**[f] **Score**	**Av. R.**[g] **S4/S3**	**Av. R. S5/S3**	**Av. R. S5/S4**	**Protein name**
2	5.34/62.3	4.93/61	29/64	47	215	1.53	1.19	-1.12	Chaperonin 60 subunit alpha 1
5	4.95/48.3	5.15/51	15/65	51	101	2.42	3.63	1.55	Tubulin alpha-6 chain
6	4.99/47.7	5.05/47	29/93	59	154	-1.56	-1.26	-1.55	26S protease regulatory subunit 6A
15	4.95/48.3	5.18/51	18/79	48	103	12.27	18.41	1.55	Tubulin alpha-6 chain
21	6.27/47.5	5.80/42	14/54	33	101	-1.37	-1.54	-1.65	Glutamine synthetase
23	5.31/41.9	5.26/44	18/87	52	93	1.53	1.55	1.61	Actin-7
27	5.38/38.1	5.30/40	[2]	[7]	[113]	-1.21	-1.24	-1.58	Adenosine kinase 1
28	4.99/80.3	5.01/79	33/77	37	127	2.62	2.55	-1.53	Heat shock protein 90-3
29	8.50/81.9	5.54/96	24/95	24	81	1.73	1.63	-1.56	Alpha-glucan phosphorylase 1
30	8.5/81.9	5.60/96	[7]	[12]	[387]	1.75	1.59	-1.13	Alpha-glucan phosphorylase 1
31	6.71/80.6	5.60/96	16/58	32	76	1.56	1.02	-1.53	Alpha-glucan phosphorylase 1
34	4.77/29.4	4.62/29	16/46	44	115	-1.63	1.05	-1.57	14-3-3-like protein GF14 omega
35	4.76/29.5	4.68/28	21/56	54	159	-1.76	-1.11	-1.59	14-3-3-like protein GF14 omega
36	4.75/29.9	4.75/29	16/67	60	111	-1.36	-1.12	-1.56	14-3-3-like protein GF14 psi
39	5.17/32.8	5.21/34	19/77	55	151	1.30	1.18	-1.53	Probable lactoylglutathione lyase
40	5.17/32.8	5.24/34	[2]	[7]	[73]	1.30	1.08	-1.58	Probable lactoylglutathione lyase
42	5.29/35.5	5.28/36	[3]	[11]	[146]	-1.22	-1.10	-1.87	Probable fructokinase-1
44	5.41/38.8	5.45/38	[2]	[7]	[99]	1.28	1.22	1.54	NADP-dependent reductase
46	5.47/33.9	5.77/36	[3]	[15]	[254]	-1.54	-1.33	-1.56	NAD(P)H oxidoreductase
47	6.07/37.6	5.38/32	[2]	[8]	[133]	3.53	2.78	-1.25	Thiamine thiazole synthase
49	5.30/29.5	5.21/24	18/68	61	125	-1.55	-1.28	1.23	Ferritin-4, chloroplastic
50	7.79/26.7	5.28/23	[3]	[21]	[172]	1.23	1.02	-1.56	20 kDa chaperonin, chloroplastic
51	5.31/27.8	5.31/27	13/78	40	82	1.57	1.00	1.53	L-ascorbate peroxidase 1
53	5.31/41.9	5.71/28	[2]	[7]	[96]	1.58	-1.09	1.52	Actin-7
57	5.61/18.3	5.25/17	[2]	[16]	[133]	1.59	1.15	-1.63	regulator of ribonuclease
58	5.60/17.7	5.60/17	[2]	[18]	[66]	2.12	1.32	-1.55	Eukaryotic translation initiation factor
61	6.60/16.3	5.94/17	[2]	[11]	[112]	2.65	1.35	-1.92	Actin-depolymerizing factor 3
64	5.7/17.4	6.17/18	[10]	[22]	[180]	1.85	1.03	-1.63	Peroxiredoxin-2B
65	7.93/18.8	6.39/18	[5]	[25]	[164]	3.11	1.33	-1.56	18.1 kDa class I heat shock protein
68	5.73/17.2	6.84/17	12/37	72	119	-1.62	-1.54	-1.56	Ubiquitin-conjugating enzyme E2
69	6.14/18.0	7.03/16	[3]	[21]	[195]	-1.51	-1.09	-1.64	AT3g53990/F5K20_290
71	6.13/29.8	6.60/23	[2]	[8]	[99]	-2.58	-1.34	1.96	Proteasome subunit alpha type-2-A
77	7.10/36.9	6.22/32	17/70	38	88	7.84	4.62	-2.23	Thiamine thiazole synthase
78	5.68/43.7	6.10/48	16/54	55	119	-2.18	-2.11	1.06	S-adenosylmethionine synthase 1
79	6.09/36.2	6.64/39	18/67	54	119	1.62	-1.02	1.58	malate dehydrogenase
86	6.03/65.3	6.45/64	35/90	47	200	1.51	1.54	1.03	malic enzyme, putative
88	5.86/47.9	6.41/52	25/78	62	160	1.43	1.14	-1.67	Bifunctional enolase 2
89	5.29/69	5.45/69	41/95	61	234	1.78	1.08	1.23	V-type proton ATPase subunit A
92	6.03/65.3	6.61/64	28/71	37	174	1.52	1.53	1.12	malic enzyme, putative

94	8.50/81.9	5.72/101	[7]	[12]	[278]	1.62	1.18	-1.54	Alpha-glucan phosphorylase 1
97	5.49/35.8	5.32/35	[7]	[24]	[165]	1.51	-1.10	-1.59	nitrile-specifier protein 5-like
105	7.93/18.8	6.25/17	[5]	[23]	[142]	1.51	-1.21	-1.80	18.1 kDa class I heat shock protein
113	5.31/41.9	5.63/41	[9]	[36]	[440]	1.56	1.17	1.51	Actin-7
118	5.50/58.5	5.84/57	[4]	[9]	[214]	1.53	1.20	-1.58	Ketol-acid reductoisomerase
130	5.86/95.0	6.71/83	[7]	[10]	[184]	1.59	1.14	-1.66	At1g56070/T6H22_13
131	4.99/80.2	5.12/85	[4]	[7]	[181]	1.69	1.64	1.56	Heat shock protein 90-3
132	5.20/75.3	4.46/73	[9]	[16]	[516]	1.70	1.19	-1.61	Heat shock 70 kDa protein 7
133	5.24/75.5	4.48/73	[7]	[12]	[386]	1.59	1.21	-1.59	Heat shock 70 kDa protein 7
134	4.99/59.3	4.85/72	[6]	[14]	[305]	1.56	1.15	-1.55	Putative S9 Tyrosyl aminopeptidase
135	6.31/80.9	6.05/68	[2]	[7]	[78]	1.62	1.04	1.53	Transketolase-2, chloroplastic
136	4.91/54.5	4.78/52	[2]	[8]	[78]	-1.54	-1.12	-1.61	V-type proton ATPase subunit B3
137	4.77/50.7	5.05/47	[5]	[11]	[193]	-1.53	-1.04	-1.66	Tubulin beta-6 chain
138	5.30/59.7	5.56/63	[4]	[13]	[195]	1.52	1.20	0.92	Importin subunit alpha-1
139	4.68/50.7	4.78/51	[4]	[10]	[170]	2.98	3.42	1.15	Tubulin beta-6 chain
140	5.86/53.9	6.35/52	[4]	[10]	[65]	-1.51	-1.64	1.02	Adenosylhomocysteinase 1
141	5.70/51.9	6.34/53	[3]	[7]	[153]	1.57	1.18	0.86	ribulose carboxylase-oxygenase
142	6.19/48.5	6.65/44	[4]	[10]	[94]	-1.63	-1.09	0.89	Aldolase-type family protein
143	6.02/38.3	6.45/45	[5]	[20]	[152]	-1.53	-1.64	1.01	Alcohol dehydrogenase class-P
144	5.50/26.4	5.35/45	[2]	[6]	[61]	1.54	1.15	0.93	acetylornithine deacetylase-like
145	5.64/42.2	5.11/37	[2]	[6]	[115]	-1.65	-1.79	1.29	Actin-7
146	5.82/41.6	5.71/41	[2]	[8]	[73]	-1.65	-1.02	-1.53	UDP-arabinopyranose mutase 3
147	8.26/50.4	4.89/41	[4]	[9]	[103]	1.67	1.22	1.51	Phosphoglycerate kinase 1
148	8.63/43.1	6.68/40	[7]	[20]	[380]	1.61	1.06	1.52	fructose-bisphosphate aldolase 3
149	8.93/24.6	6.76/38	[4]	[15]	[118]	-4.15	-2.33	1.81	fructose-bisphosphate aldolase
150	7.72/15.2	6.36/39	[2]	[10]	[69]	1.70	-1.10	-1.66	aldo/keto reductase AKR
151	5.12/35.6	5.11/34	[4]	[16]	[110]	1.58	1.05	1.62	Probable fructokinase-1
152	4.75/34.9	4.63/33	[3]	[14]	[125]	1.92	1.16	-1.62	late embryogenesis abundant proteins
153	5.31/41.9	5.28/25	[3]	[7]	[62]	1.54	1.06	-1.61	Actin-7
154	4.93/30.9	4.88/28	[7]	[37]	[343]	-1.57	-1.17	-1.64	26S proteasome non-ATPase
155	5.77/27.7	6.32/24	[2]	[10]	[107]	-1.61	-1.14	-1.57	Triosephosphate isomerase
156	4.70/26.2	4.56/27	[3]	[10]	[123]	-1.51	-1.15	-1.75	Proteasome subunit alpha type-5
157	6.42/24.9	6.16/23	[2]	[8]	[61]	-1.51	-1.07	-1.68	Proteasome subunit beta type-1
158	6.52/26.9	5.56/30	[4]	[26]	[292]	-5.22	-2.39	2.23	3-isopropylmalate dehydratase
159	6.17/23.8	6.88/23	[4]	[24]	[192]	-2.57	-2.64	1.03	glutathione-s-transferase theta
160	7.66/29.6	4.68/25	[2]	[9]	[79]	-1.56	-1.13	-1.65	peroxiredoxin
161	5.98/26.2	5.21/22	[2]	[13]	[173]	-1.52	-1.20	-1.65	conserved hypothetical protein
162	4.95/12.4	4.75/15	[2]	[22]	[88]	-1.53	-1.02	1.51	Small ubiquitin-related modifier
163	4.92/32.1	4.98/15	8	31	78	-5.57	-1.36	4.17	actin
164	6.74/17.3	6.76/12	[5]	[26]	[88]	-1.62	-1.54	1.14	Ubiquitin-conjugating enzyme E2 35

Note:

[a] Assigned spot number (S2-S164) for the 80 differential proteins in 2-D DIGE gelss of cassava

root proteins as indicated in Fig. 3.

[b, c] The experimental (b) and theoretical (c) values for the mass (kDa) and *p*I of identified proteins. The theoretical values were retrieved from the protein database, and the experimental values were produced by ImageMaster.

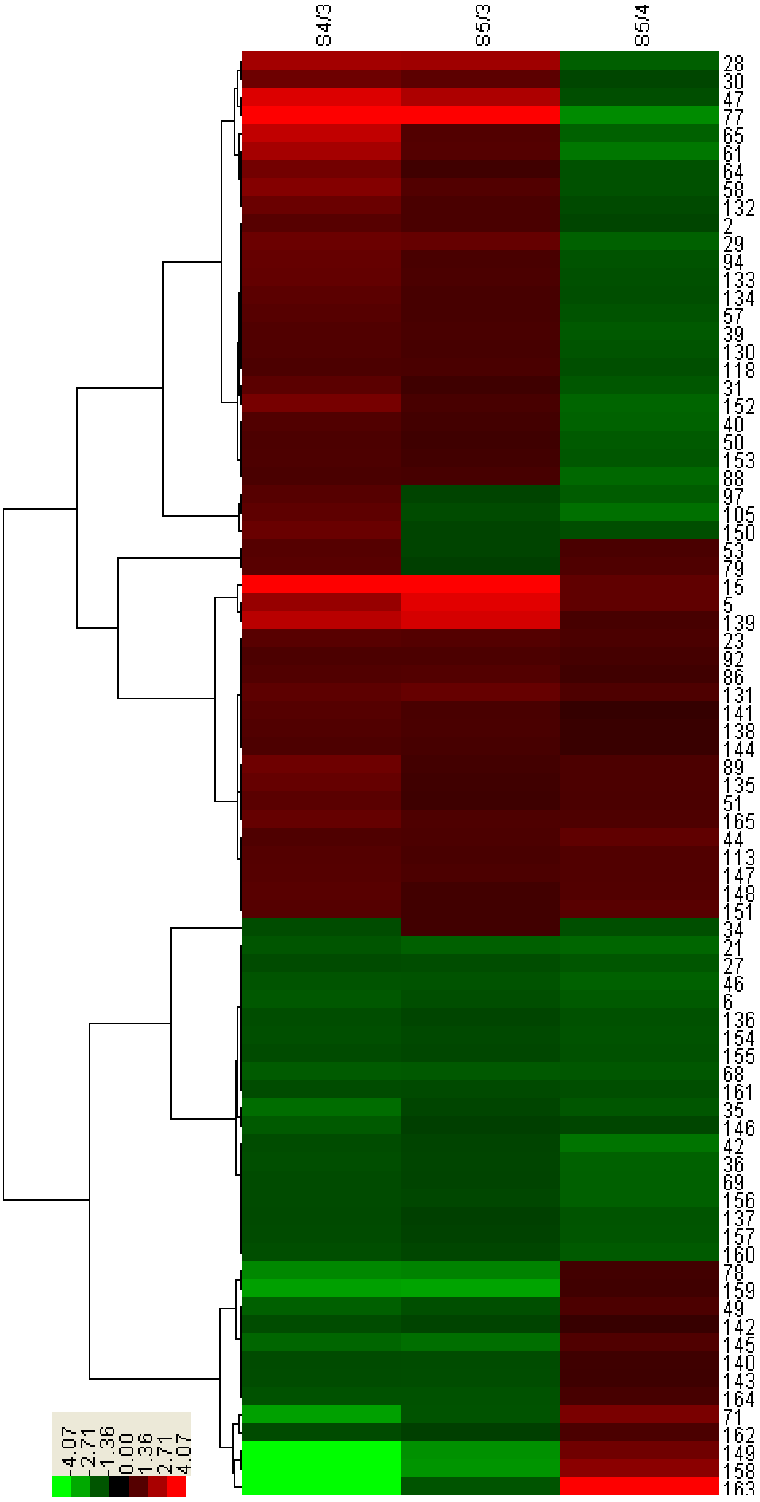
[d] The number of matched peptides (MP) and total searched peptides (TP) for the proteins identified for MS. The number of matched peptides for MS/MS was presented in square bracket.

[e] Sequence coverage (SC) of the identified proteins by MS and [MS/MS].

[f] Mascot searched scores (M.S.) against cassava genome for MS and [MS/MS] searched results.

[g] The average changed ratios of the target protein spots in 2-D DIGE gels of the stage 3 (S3), 4 (S4) and 5 (S5) of cassava roots.

Supplementary Table S2-continued Detai information for the hierarchical cluster of the average changed abundance ratios of the identified protein spots on 2-D DIGE gels in Figure 5C was also highlighted. The log values for the induced or reduced relative abundance volume ratios were indicated in red or green, respectively.



Supplementary Table S3. Primers used for RT and Q-PCR analysis.

14-3-3 protein (Spots 34, 35, 36):

5’- GAGCAAGATTTGTGATGGGATC-3’

5’-TAGGAGCGAGATCAGCAAGG-3’

Ascorbate peroxidase APX2 (Spots 51, 52, 73):

5’-GTTTCATCGCTGAGAAAGGC-3’

5’-ATCTCAACGGCAACAACACC-3’

Superoxide dismutase (Spots 66, 72, 104, 106):

5’-GGCTGAAGCTGTTCTTACCA-3’

5’-TGATCTTTGCCAGAAGGGTT-3’

Initiation factor eIF5-A:

5’-GATATTGTTCCTTCATCCCACA-3’

5’-CCTCAGCAAACCCATCTTTA-3’

S-adenosylmethionine synthetase 4:

5’-AAGACGCAGGTTTAGGTGGAAGAT-3’

5’-GATGGGTTTAGGTGGAAGAT-3’

Malate dehydrogenase (Spots 79, 114):

5’-CAAATGCGTTGATTCTAAGGG-3’

5’-GCGTGATTGACATGTGGGTAC-3’

UDP-D-apiose/UDP-D-xylose synthase:

5’-TCTGGCGGCTATTTGTACTC-3’

5’-TCTCTGCTTCTCAATGGGTC-3’

Enolase (Spots 83, 87, 88, 116):

5’- TGCTGGAAATAAACTTGCTATG -3’

5’-AACCACCTTCATCACCAACAT-3’

ADP-glucose pyrophosphorylase small subunit (Spots 20, 91):

5’- TTCATTCTTGTAGCCACCCA-3’

5’- ATTATTCTTGGAGGCGGTGC-3’

Starch phosphorylase 1 precursor:

5’- GAGGTTGCTGAAGATTGGCT-3’

5’- CCCAGCATTGAAAGCAGACA-3’

18sRNA: 5’- CCTGAGAAACGGCTACCAT -3’

5’- CGTGTCAGGATTGGGTAAT -3’

Primers specific for the vector:

S1300F, 5’-GCCTTGCTTCCTATTATATCTTCC-3’;

S1300R, CCCATCTCATAAATAACGTCATG.

Primers specific for 14-3-3 gene in the transgenic plants for Southern blotting:

P1300-1433F, 5’- TGCTGATCTCGCTCCTACCCAC -3’;

P1300-1433R, 5’- AACCACCAGATGATGGCATCTACTC -3’.