Mass Spectrometry Report

Jan 20, 2006

Hanson Institute
Protein Core Facility

Sample:  C:\MS Files\20-1-06\06-006-1.raw

Samples for identification by mass spectrometry were digested with trypsin under standardised conditions. The resulting peptides were reduced with TCEP and desalted through a C18 reverse phase silica column into the Q-Tof2 Mass Spectrometer, via a NanoSource.

The spectrometer was calibrated against the fragmentation pattern of [Glu]-Fibrino peptide B and found to be accurate to within 30 ppm.

Data was collected as intensity versus mass over charge (Th, Thompsons) and multiply charged ions (+2, +3, +4) were automatically detected and subjected to fragmentation.

The collected fragmentation data was the analysed using ProteinLynx software and searched against a FASTA protein database.

Protein identification matches were assigned if 2 or more sequenced peptides were identified from a protein in the database.

Regards,

[Signature]

Hanson Institute Protein Core Facility
Division of Human Immunology  Level 3
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**Workflow Template: Medium NCBI Search**

| Property          | Value                                |
|-------------------|--------------------------------------|
| Query Type        | Databank Search                      |
| Search Type       | PI.03                                |
| Databank          | NCBI0558-1.0                         |
| Fragment Tolerance| 0.1 Da                               |
| High MW Filter    | 200000                               |
| Low MW Filter     | 0                                    |
| High PI Filter    | 14.0                                 |
| Low PI Filter     | 0.0                                  |
| Mass Tolerance    | 100.0Da                              |
| Min Peptides      | 2                                    |
| Min Std. Deviation| 0.0050                               |
| Digestor 1        | Trypsin                              |
| Query Type        | Automod Search                       |
| Consider Mods     | true                                 |
| Consider Subs.    | true                                 |
| Max. Mods & Subs | 1                                    |
| Fragment Tolerance| 0.1                                 |
| Mass Tolerance    | 50.0 Da                              |
| Min. Mass Std. Deviation| 0.0050               |
| Digestor 1        | Trypsin                              |

Sample:  C:\MS Files\20-1-06\06-006-1.raw

| Acc #          | Protein Description                                      | Peptides | Coverage | Score  |
|----------------|----------------------------------------------------------|----------|----------|--------|
| 37999050       | essential protein for meiotic synapsis Oryza sativa japonica cultivar ... | 5        | 7.377    | 14.7098 |
**Protein Match Details**

**Sample:** C:\MS Files\20-1-06\06-006-1.raw  
**Accession:** 37999050  
**Name:** 37999050  
**Description:** essential protein for meiotic synapsis  *Oryza sativa japonica* cultiv  
**Confidence:** 100.0  
**Coverage:** 7.377  
**Matches:** 5  
**Score:** 14.7098

| Coverage Map |
|--------------|
| 37999050     |

|   | MVMAQKTEA | EITEQDSLLE | TRNLRIAICY | NISYIRLFP | EKYFNDKSVP |
|---|-----------|------------|-------------|-----------|------------|
| 1 | ALEMKIKKLMI | PMDETSRRLTI | DWMEKGVYDA | LQKKYLTLL | FCICKEEGP  |
| 51| MIEEYAFSFS | YPNTSGDEVA | MNLSRTGSKK | NSATTNAA  | EVTPDQMR    |
| 101| ACHMIRTLVS | LMTLDQPMFED | ERT1LMKLL | YDDVTEDYE | PFFKCCADN   |
| 151| EA1INIMKNP | LMMEVGNVNS | KHLVLALKVK | SVLDPCDDNN | VNSEDDNMSL  |
| 201| DNESDOQDONF | SDETRPSEA | ERYIVAEPNDG | TCKGQNGTIS | EDDTQDPVHE  |
| 251| EEILTAQREV | ICSRDTESLE | VSDVVLNPD  | ISEMWEDIM  | ERLKRDGILLS |
| 301| RAKKSYYNVS | KIADPPTPHI | KKEVIMQNSV | PTEGKNSNG  | DLMYMKALYH  |
| 351| ALPMNIVSVSG | LKHGKLDGEGA | SQNMVRKLI | KMVQDMGVRN | SANRRLGKAV  |
| 401| IHSEIVNRKL | LEIICLILEV | IAQMAIDTN  | AEPGEPEPKD | HLGSHMMDG   |
| 451| STMSCILQSVG | SDLTRTRELP | EPQQNVSMQS | GQEEASTVDK | PSRTPTSVRE  |
| 501| QASVCSLESG | VLGQKVRKSL | AGAGGTCSEQ | DKRFRKASTV | KEPILQYVKR  |
| 551| QKSQVQVQVQ |           |            |           |            |
| 601|            |            |            |           |            |
Peptide Match # 1
Sequence: EAEITEQDSLLLTR
Score: 220.5093
Mass: 1616.8258
Modifications: None

Precursor mass 809.3975, charge 2

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| Peptide | m/z | Prec |
|---------|-----|------|
| a       | 102.055, 173.093, 302.135, 415.219, 516.267, 645.31, 773.368, 888.395, 975.427, 1088.511, 1201.595, 1314.679, 1415.727 | – |
| b       | 130.05, 201.088, 330.13, 443.214, 544.262, 673.304, 801.363, 916.39, 1003.422, 1116.506, 1229.59, 1342.674, 1443.722 | – |
| v''     | – 1488.791, 1417.754, 1288.711, 1175.627, 1074.58, 945.537, 817.478, 702.451, 615.419, 502.335, 389.251, 276.167, 175.119 | – |
| z       | – 1471.765, 1400.727, 1271.685, 1158.601, 1057.553, 928.51, 800.452, 685.425, 598.393, 485.309, 372.225, 259.141, 158.093 | – |
Peptide Match # 2  
**Sequence:** SNAAEVTPDQMR  
**Score:** 106.0126  
**Mass:** 1333.5931  
**Modifications:** Hydroxyl *DKNP* (9)

Precursor mass 667.7844, charge 2

|     | 0   | 25  | 50  | 75  | 100 |
|-----|-----|-----|-----|-----|-----|
| a   | 60.045 | 174.088 | 245.125 | 316.162 | 445.205 |
|     | (0.001) | (-0.003) | (-0.002) | (0.004) | (0.044) |
| b   | 88.04 | 202.083 | 273.12 | 344.157 | 473.2 |
|     | (0.001) | (-0.003) | (-0.005) | (-0.006) | (-0.002) |
|     |      |       |       | (-0.004) |       |

**ν"**  
|     | 0   | 25  | 50  | 75  | 100 |
|-----|-----|-----|-----|-----|-----|
| a   | -- | 1247.569 | 1133.526 | 1062.489 | 991.452 |
|     |     | (-0.024) | (-0.005) | (-0.006) | (-0.003) |
| b   | -- | 1230.542 | 1116.5 | 1045.462 | 974.425 |
|     |     | (-0.071) | (-0.004) | (-0.003) | (0.023) | (0.019) | (-0.011) |
**Peptide Match # 3**

**Sequence:**  IAIYNISYIR

**Score:**  86.9647

**Mass:**  1224.6866

**Modifications:**  None

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**Graphic Description**

- **Precursor mass:** 613.3324, charge 2
- **Peptide Sequence:** IAIYNISYIR
- **Score:** 86.9647
- **Mass:** 1224.6866
- **Modifications:** None

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**Diagram Details**

- **Y**
  - a: 86.097, 157.134, 270.218, 433.281, 547.324, 660.408, 747.44, 910.504, 1023.588
  - b: 114.092, 185.129, 298.213, 461.276, 575.319, 688.403, 775.435, 938.499, 1051.583
  - (y'')
  - z

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**Contact Information**

- **Dr Ian Milne**  ian.milne@imvs.sa.gov.au  (08) 8222 3716
- **Dr Chris Bagley**  chris.bagley@imvs.sa.gov.au  (08) 8222 3714
**Peptide Match # 4**

**Sequence:** SNAAEVTPDQMR

**Score:** 26.6958

**Mass:** 1317.5984

**Modifications:** None

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**Diagram:**

- Precursor mass: 659.7913, charge 2

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**Chromatogram:**

- **B**
  - 88.04
  - 202.083
  - 273.12
  - 344.157
  - 473.2
  - 572.268
  - 673.316
  - 770.368
  - 885.395
  - 1013.454
  - 1144.494

- **a**
  - 60.045
  - 174.088
  - 245.125
  - 316.162
  - 445.205
  - 544.273
  - 645.321
  - 742.373
  - 857.4
  - 985.459
  - 1116.5

- **b**
  - 202.083
  - 273.12
  - 344.157
  - 473.2
  - 572.268
  - 673.316
  - 770.368
  - 885.395
  - 1013.454
  - 1144.494

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**M+H**

- 500
- 1000
- 1500
- 1719

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**Values:**

- **v**
  - 1231.574
  - 1117.531
  - 1046.494
  - 975.457
  - 846.414
  - 747.346
  - 646.298
  - 549.246
  - 434.219
  - 306.16
  - 175.12

- **z**
  - 1214.548
  - 1100.505
  - 1029.468
  - 958.43
  - 829.388
  - 730.319
  - 629.272
  - 532.219
  - 417.192
  - 289.134
  - 158.093

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**PCF**

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Peptide Match # 5
Sequence: TLDQMPEER
Score: 25.8123
Mass: 1117.5074
Modifications: None

|  |  |
|---|---|
| a | 74.061 | 187.145 | 302.172 | 430.23 | 561.271 | 658.323 | 787.366 | 916.409 |
|   | (-0)  | (0.002) | (-0.028) |   |   |   |   |   |
| b | 102.056 | 215.14 | 330.167 | 458.225 | 589.266 | 686.318 | 815.361 | 944.404 |
|   | (-0.001) | (-0.004) |   |   |   |   |   |   |
| T |   |   |  |   |   |   |   |   |
| L |   |   |   |   |   |   |   |   |
| D |   |   |   |   |   |   |   |   |
| Q |   |   |   |   |   |   |   |   |
| M |   |   |   |   |   |   |   |   |
| P |   |   |   |   |   |   |   |   |
| E |   |   |   |   |   |   |   |   |
| E |   |   |   |   |   |   |   |   |
| R |   |   |   |   |   |   |   |   |

\[
\begin{align*}
\nu^* & \approx 1017.468 & 904.383 & 789.357 & 661.298 & 530.257 & 433.205 & 304.162 & 175.12 \\
& (-0.005) & (-0.015) & (-0.001) & (0) & (-0.085) & (-0.005) &   &   \\
z & \approx 1000.441 & 887.357 & 772.33 & 644.271 & 513.231 & 416.178 & 287.136 & 158.093 \\
& (-0.004) & (-0.034) & (-0.062) &   &   &   &   &   \\
\end{align*}
\]