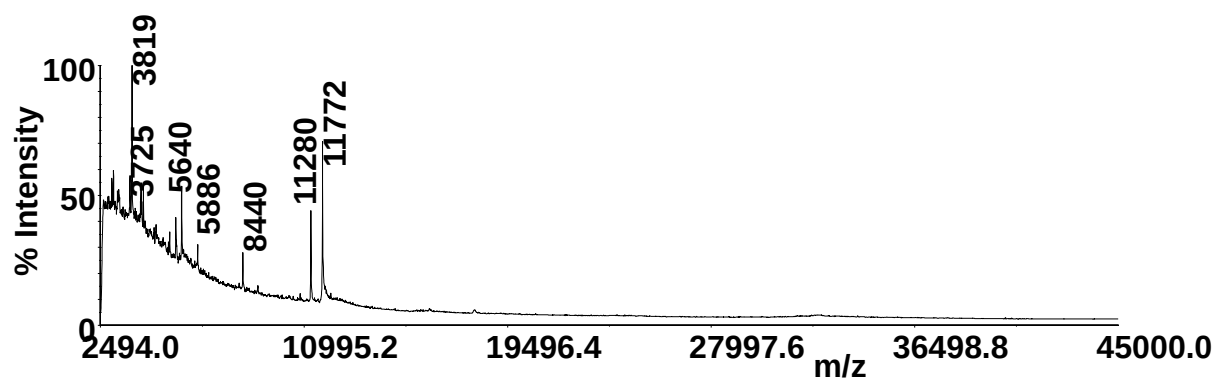


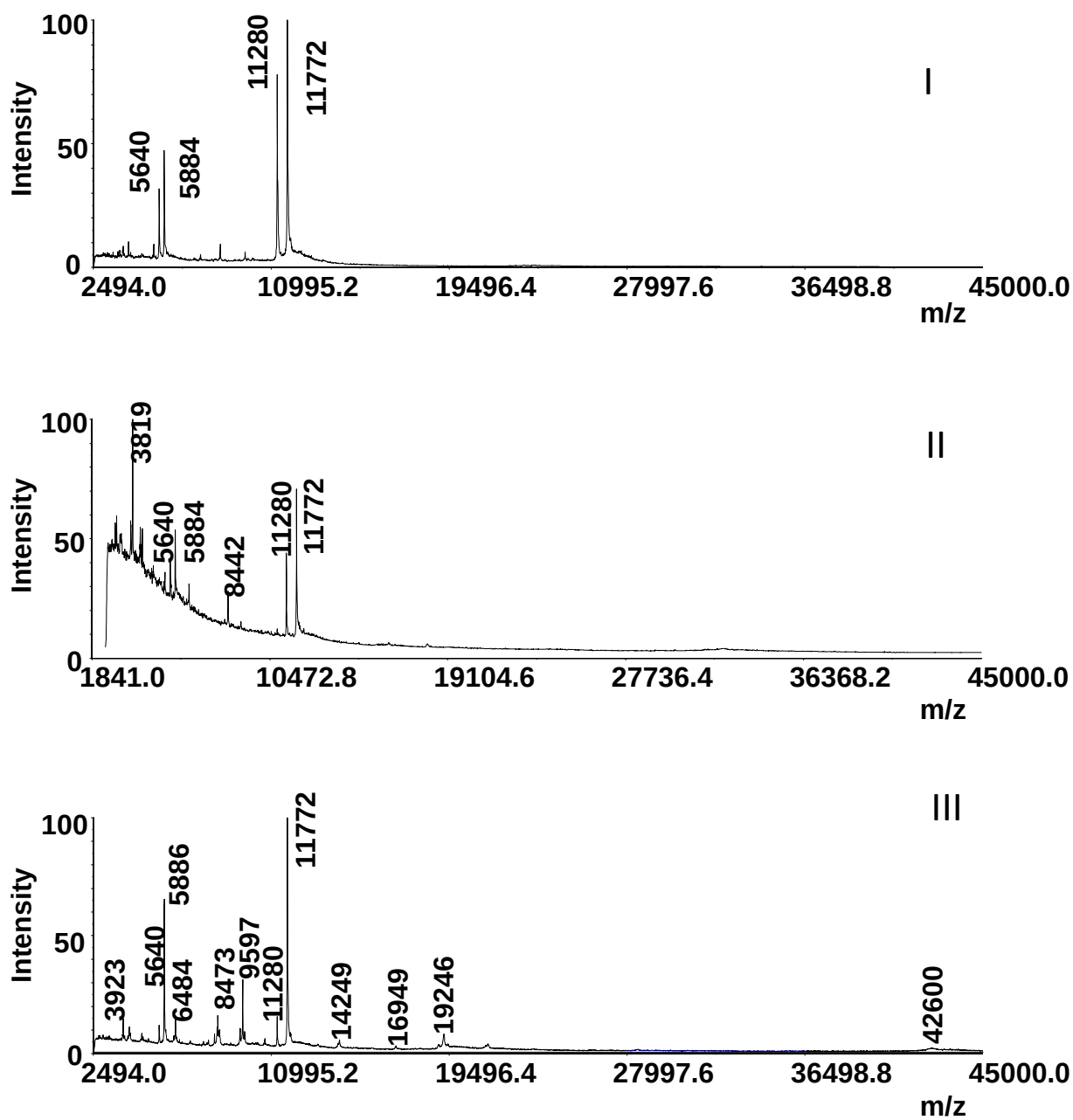
## **Electronic Supporting Information**

**Major allergen in rainbow trout (*Oncorhynchus mykiss*): complete sequences of Parvalbumin by MALDI tandem mass spectrometry**

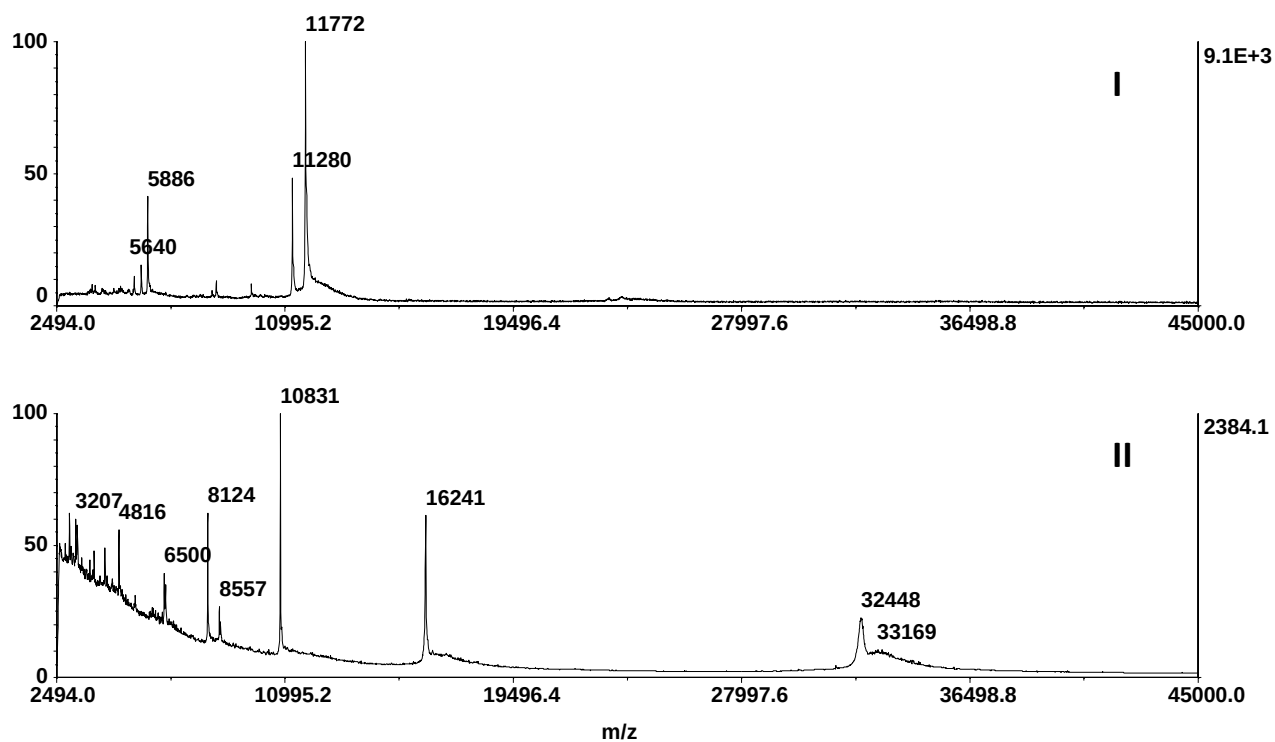
**Electronic Supporting Information Figure 1.** Linear MALDI MS spectrum of B<sub>w</sub> fraction



**Electronic Supporting Information Figure 2.** Linear MALDI MS spectra of (I) fraction A<sub>r</sub>, (II) fraction B<sub>r</sub> and (III) fraction C<sub>r</sub>



**Electronic Supporting Information Figure 3.** Linear MALDI MS spectra of fraction A after (a) 0 min, (b) 3 min of cooking (at 100°C) from homogenised white trout fleshes.



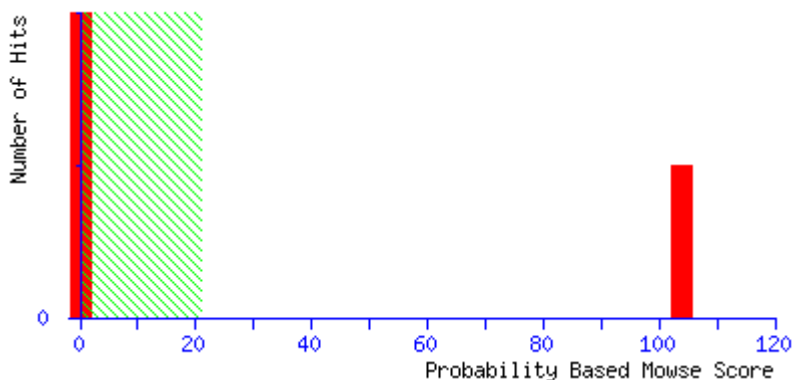
## Electronic Supporting Information Figure 4: MS/MS based sequence identification by data base search of the ion specie of m/z 2121.03.

### **MASCOT** Mascot Search Results

Search title : MSMS\_2121.03  
Database : SwissProt  
Taxonomy : Actinopterygii (ray-finned fishes)  
Significant hits: [Q91482](#) Parvalbumin beta 1 (Major allergen Sal s 1)

#### Probability Based Mowse Score

Score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores > 21 indicate identity or extensive homology ( $p < 0.05$ ).



#### Peptide Summary Report

1. [Q91482](#) Mass: 11881 Total score: 104 Peptides matched: 1 Parvalbumin beta 1 (Major allergen Sal s 1)

| Query             | Observed | Mr(expt) | Mr(calc) | $\Delta$ ppm | Miss Score | Rank | Peptide               |
|-------------------|----------|----------|----------|--------------|------------|------|-----------------------|
| <a href="#">1</a> | 2121.03  | 2120.02  | 2120.01  | 6.2          | 1 104      | 1    | AGDADGDGMIGIDEFAVLVKQ |

#### Search Parameters

Type of search : MS/MS Ion Search  
Enzyme : Trypsin  
Variable modifications : Oxidation (M)  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance :  $\pm 50$  ppm  
Fragment Mass Tolerance:  $\pm 0.20$  Da  
Max Missed Cleavages : 3  
Instrument type : MALDI-TOF-TOF

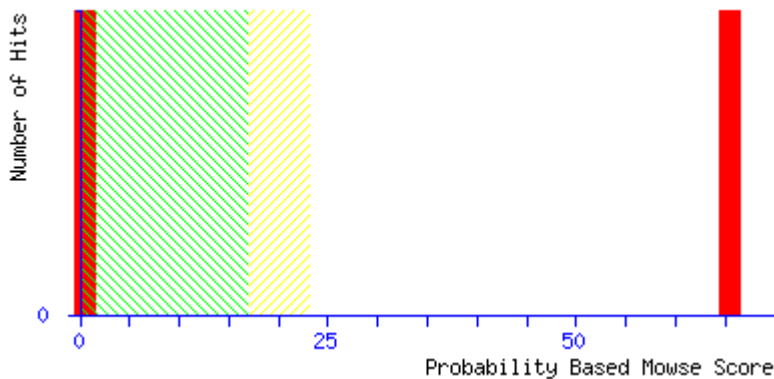
## Electronic Supporting Information Figure 5: MS/MS based sequence identification by data base search of the ion specie of m/z 2580.32

### **MASCOT** Mascot Search Results

Search title : MSMS\_2580.32  
Database : SwissProt  
Taxonomy : Actinopterygii (ray-finned fishes)  
Significant hits: [Q91482](#) Parvalbumin beta 1 (Major allergen Sal s 1)

### Probability Based Mowse Score

Score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event.  
Individual ions scores > 17 indicate peptides with significant homology ( $p < 0.05$ ).  
Individual ions scores > 23 indicate identity or extensive homology ( $p < 0.05$ ).



1. [gi|2493445](#) Mass: 11881 Total score: 65 Peptides matched: 1  
Parvalbumin beta 1 (Major allergen Sal s 1)

| Query    | Observed | Mr(expt) | Mr(calc) | $\Delta$ ppm | Miss | Score | Rank | Peptide                   |
|----------|----------|----------|----------|--------------|------|-------|------|---------------------------|
| <u>1</u> | 2580.32  | 2579.31  | 2579.29  | 7.75         | 2    | 65    | 1    | AFLKAGDADGDGMIGIDEFAVLVKQ |

### Search Parameters

Type of search : MS/MS Ion Search  
Enzyme : Trypsin  
Variable modifications : Oxidation (M)  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance :  $\pm 50$  ppm  
Fragment Mass Tolerance:  $\pm 0.20$  Da  
Max Missed Cleavages : 3  
Instrument type : MALDI-TOF-TOF

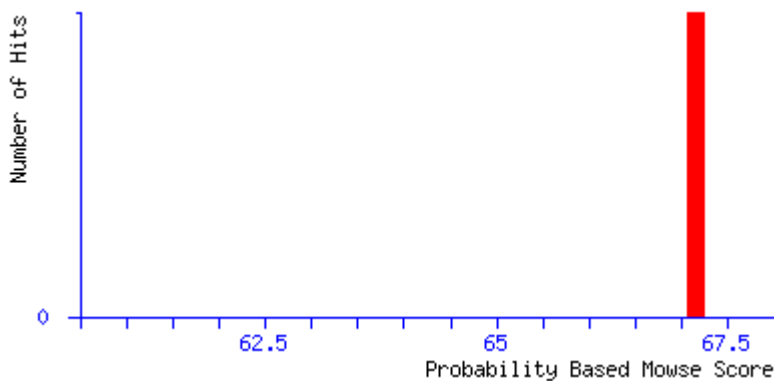
## Electronic Supporting Information Figure 6: MS/MS based sequence identification by data base search of the ion specie of m/z 1255.66

### ***{MATRIX}*** Mascot Search Results

Search title : MSMS\_1255.66  
Database : SwissProt  
Taxonomy : Actinopterygii  
Significant hits: [Q91482](#) PARVALBUMIN BETA 1

#### Probability Based Mowse Score

Score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores > 16 indicate identity or extensive homology ( $p < 0.05$ ).



#### Peptide Summary Report

1. [Q91482](#) Mass: 11881 Total score: 67 Peptides matched: 1  
PARVALBUMIN BETA 1 (CLONE 14.1) (MAJOR ALLERGEN) .

| Query             | Observed | Mr(expt) | Mr(calc) | $\Delta$ ppm | Miss | Score | Rank | Peptide     |
|-------------------|----------|----------|----------|--------------|------|-------|------|-------------|
| <a href="#">1</a> | 1255.66  | 1254.65  | 1254.64  | 7.8          | 0    | 67    | 1    | TFFHTIGFASK |

#### Search Parameters

Type of search : MS/MS Ion Search  
Enzyme : Trypsin  
Variable modifications : Oxidation (M)  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance :  $\pm 50$  ppm  
Fragment Mass Tolerance:  $\pm 0.20$  Da  
Max Missed Cleavages : 3  
Instrument type : MALDI-TOF-TOF

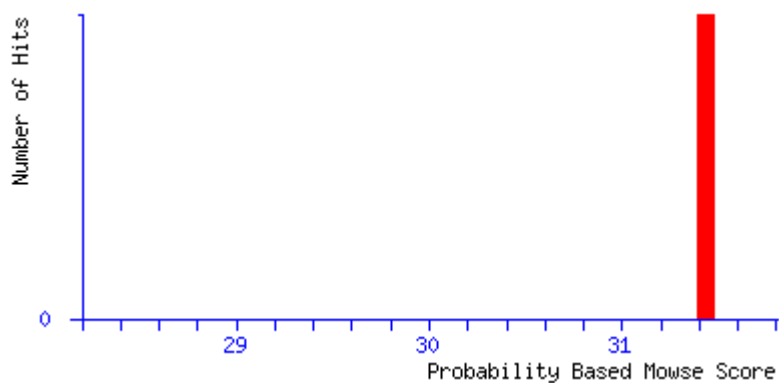
## Electronic Supporting Information Figure 7: MS/MS based sequence identification by data base search of the ion specie of m/z 1791.91

### ***MATRIX*** **SCIENCE** Mascot Search Results

Search title : F13\_MSMS\_1791.91  
Database : SwissProt  
Taxonomy : Actinopterygii  
Significant hits: [Q91482](#) PARVALBUMIN BETA 1

#### Probability Based Mowse Score

Score is  $-10 \cdot \log(P)$ , where P is the probability that the observed match is a random event. Individual ions scores > 19 indicate identity or extensive homology ( $p < 0.05$ ).



#### Peptide Summary Report

1. [Q91482](#) Mass: 11881 Total score: 31 Peptides matched: 1  
PARVALBUMIN BETA 1

| Query             | Observed | Mr(expt) | Mr(calc) | Δppm | Miss | Score | Rank | Peptide          |
|-------------------|----------|----------|----------|------|------|-------|------|------------------|
| <a href="#">1</a> | 1791.91  | 1791.36  | 1790.89  | 6.0  | 0    | 31    | 1    | VIDQDASGFIEVEELK |

#### Search Parameters

Type of search : MS/MS Ion Search  
Enzyme : Trypsin  
Variable modifications : Oxidation (M)  
Mass values : Monoisotopic  
Protein Mass : Unrestricted  
Peptide Mass Tolerance :  $\pm 50$  ppm  
Fragment Mass Tolerance :  $\pm 0.20$  Da  
Max Missed Cleavages : 3  
Instrument type : MALDI-TOF-TOF