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MASTERARBEIT

Identification of Phosphoproteins related to Mycoparasitism of *Trichoderma atroviride*

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Chemische Technologien und Analytik

der Technischen Universität Wien

Unter der Anleitung von

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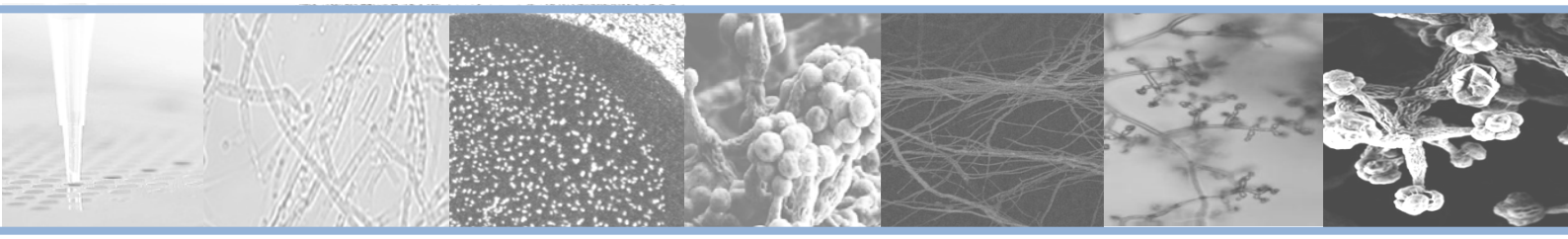

It is my earnest desire that some of you should carry on this scientific work and keep for your ambition the determination to make a permanent contribution to science.

Marie Curie (1867-1934)

ABSTRACT

Many species of the fungal genus *Trichoderma* are potent mycoparasites, which turns them into successful bio-fungicides for the biological control of plant diseases. Investigations on the underlying signal transduction pathways revealed that G protein signalling and pathways involving mitogen-activated protein kinases (MAPKs) play important roles in the recognition of the host fungus and activation of the mycoparasitic response. Mutants missing the MAPK-encoding *tmk1* gene show only reduced mycoparasitic abilities. To gain detailed knowledge on the phosphoproteome of *Trichoderma atroviride,* a workflow was established to identify phosphoproteins in different fungal samples (wild-type with induced and un-induced mycoparasitic activity, Δ*tmk1* mutant with reduced mycoparasitism) which may contribute to mycoparasitism. After careful investigation of different sample preparation methods like TiO_2 and IMAC enrichment of phosphorylated peptides and proper measurement conditions for mass spectrometric analysis, the phosphoproteome of *Trichoderma atroviride* was analyzed by means of matrix-assisted laser desorption/ionization – time of flight – mass spectrometry and the use of post source decay fragmentation of peptides to identify protein species. With this approach it was possible to identify phosphoproteins in all samples of interest and conclusions on their contribution to signaling events during the activation of the mycoparasitic cascade were drawn. The developed methodology allowed to gather a first overview of proteins, which are likely to be regulated by Tmk1 MAPK. Thus it can be stated, that there is a potential to gain further information on the phosphoproteome by following the proposed workflow which can subsequently lead to a better understanding of underlying mechanisms involved in mycoparasitism.

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1 INTRODUCTION

1.1 Motivation

Trichoderma species are used as biocontrol agents in agriculture which is due to two main mechanisms: a) their ability to exert beneficial effects directly on the plant and b) mycoparasitism of phytopathogenic fungi. The exact mechanism for recognition and attacking phytopathogenic fungi is still not completely understood [Grinyer et al., 2005].

Investigation on the underlying signal transduction pathways revealed that G protein signalling and pathways involving mitogen-activated protein kinases (MAPK) play important roles in the recognition of the host fungus and activation of the mycoparasitic response. Mutants missing the Tmk1 MAPK show reduced mycoparasitic activity against host fungi although they display an enhanced production of cell wall-degrading enzymes and antifungal metabolites [Reithner et al., 2007]. These findings suggest that still unknown proteins and processes contributing to *Trichoderma* mycoparasitism are regulated by Tmk1.

The aim of this study was to identify target proteins being regulated by theTmk1 MAPK which play key roles in mycoparasitism. Because MAPKs are serine/threonine-specific protein kinases involved in protein phosphorylation, the phosphoproteome of three different *Trichoderma atroviride* samples with varying mycoparasitic activities were compared (*T. atroviride*$_{wt}$ vs. *T. atroviride*$_{wt}$ (un-induced mycoparasitism), *T. atroviride*$_{wt}$ vs. *Rhizoctonia solani* (induced mycoparasitism) and *T. atroviride* $_{tmk1}$ vs. R. solani (reduced mycoparasitism)) to identify involved phosphoproteins.

1.2 The Fungus – *Trichoderma ssp.*

Trichoderma ssp. belongs to the fungal order of *Hypocreales*, more precisely to the *Hypocreaceae*, which are *Ascomycota* that are common in all types of soil. The anamorphic fungal genus *Trichoderma* (teleomorph *Hypocrea*) have hyaline phialides formed on exposed fertile branches and conidia that are generally smooth, typically ellipsoidal to nearly oblong and mostly green. If chlamydospores are formed, they are generally globose to subglobose and are within or at the tips of hyphae [Chaverri et al., 2003; Howell, 2003; Samuels, 2006]. Approximately 150 different *Trichoderma* species have already been identified and new species are still being analyzed each year. The website www.isth.info established by Irina Druzhinina & Alexey Kopchinskiy (2004-2008) provides an identification tool (TrichOKEY) and a search tool (TrichoBLAST), and also the possibility to

identify species via a morphological key (including descriptions and 500 images of the 32 most frequency *Trichoderma* species of the taxa found in temperate regions) [Druzhinina et al., 2005].

Species of *Trichoderma/Hypocrea* are filamentous fungi appearing on decaying woody substrata but also on other fungi. *Trichoderma* is universally found as a soil fungus. *Trichoderma atroviride,* a certain species of *Trichoderma* studied in this thesis, has been determined to be an effective mycoparasite of many phytopathogens [Druzhinina et al., 2011]. It is considered as a general biocontrol agent, especially in today´s focus to increase sustainable agriculture and biological control as a good alternative to chemical pesticides. The distribution of several phytopathogenic fungi such as *Rhizoctonia*, *Phythium*, *Phytophthora*, *Botrytis* and *Fusarium* has spread during the last few years due to changes introduced in farming with disadvantageous effects on crops, therefore the application of such biocontrol agents gains importance [Benitez et al., 2004]. The potential of *Trichoderma* for the protection and growth enhancement of a number of crops was first recognized in the early 1930s [Howell, 2003]. The preference to use *Trichoderma* species as biocontrol agents in agriculture is due to their ability to exert beneficial effects directly on the plant and their mycoparasitic activity against phytopathogenic fungi [Brotman et al., 2010; Samuels et al., 2002].

1.2.1 Mycoparasitism

Trichoderma species are economically important because of their antagonistic effect on disease-causing fungi. This antifungal activity has been extensively documented and suggestions have been made that this skill comprises three possible factors: mycoparasitism, antibiosis and nutrient competition [Brunner et al., 2005; Chaverri et al., 2003]. These mechanisms are complex, and what has been defined as “biocontrol” is the sum of mechanisms acting antagonistically and synergistically to achieve disease control [Benitez et al., 2004].

In this study, the main focus is on the mycoparasitistic activity, which enables the attack of phytopathogenic fungi. In general, fungi that parasitize other fungi are called mycoparasites and they can be grouped into two main categories a) the biotrophic and b) the necrotrophic mycoparasites, which are described below [Gruber and Seidl-Seiboth, 2012]

1.2.1.1 Biotrophic Mycoparasites

Biotrophic fungi establish a specialized relationship and have evolved to grow in living host tissue with minimum induction of host defense. Effectors, contributing to the relationship between the host and the biotrophic fungus are secreted through the fungal endoplasmic reticulum secretory pathway into the fungus-host interface [Druzhinina et al., 2011; Rafiqi et al., 2012]. Some fungi also

produce haustoria to penetrate and absorb nutrients from the living fungal hyphae (Figure 1.1) [Howell, 2003].

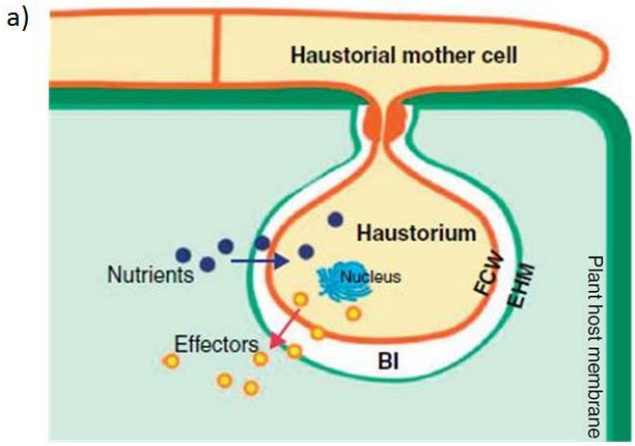


Figure 1.1 Specialized infection structure (haustorium) formed by effector- exporting biotrophic fungi to penetrate and adsorb nutrients from the living fungal hyphae. EHM…extrahaustorial membrane; FCW…fungal cell wall; BI…biotrophic interface

Modified from [Rafiqi et al., 2012]

1.2.1.2 Necrotrophic Mycoparasites

On the other hand, necrotrophic fungi including *Trichoderma atroviride* invade and destroy the host fungal cells and feed on the dead cell contents. The exact mechanism for the mycoparasitic activity is still not completely understood, but the process is a combination of host recognition, attachment to the host hyphae, followed by coiling around the hyphae (Figure 1.2) and also the secretion of antibiotic metabolites and cell-wall degrading enzymes [Grinyer et al., 2005; Howell, 2003; Omann et al., 2012].

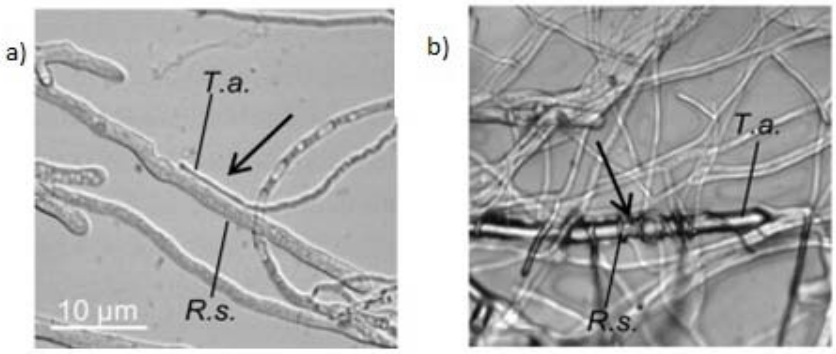


Figure 1.2 Mycoparasitic activity of *Trichoderma atroviride* in the presence of *Rhizoctonia solani* (a) recognition and (b) attacking by colling around the hyphae.

Adapted from [Omann et al., 2012]

In addition to the use of *Hypocrea/Trichoderma* as biocontrol agents, many species have the ability to break down cellulosic material through the production of cellulases. This ability has led to the commercial exploitation of some species in production of enzymes used to manufacture detergents for clothes washing, animal feed and fuel [Samuels et al., 2002]

1.3 Post-translational Modifications – The Phosphorylation

Phosphorylation is a key regulator of cellular signaling pathways such as cell division, growth and differentiation. It is one of the most widespread regulatory mechanisms in nature and the best understood posttranslational modification. Protein phosphorylation not only imparts structural changes on protein substrates but also affects their release (e.g. from the nucleus into the cytoplasm) via protein-protein interactions, protein translocations, protein activations or inactivations. MAP-kinases, acting as activators have such influences on the proteins and thus lead to the different abilities of organisms. Figure1.3 gives an overview of the effects of phosphorylation.

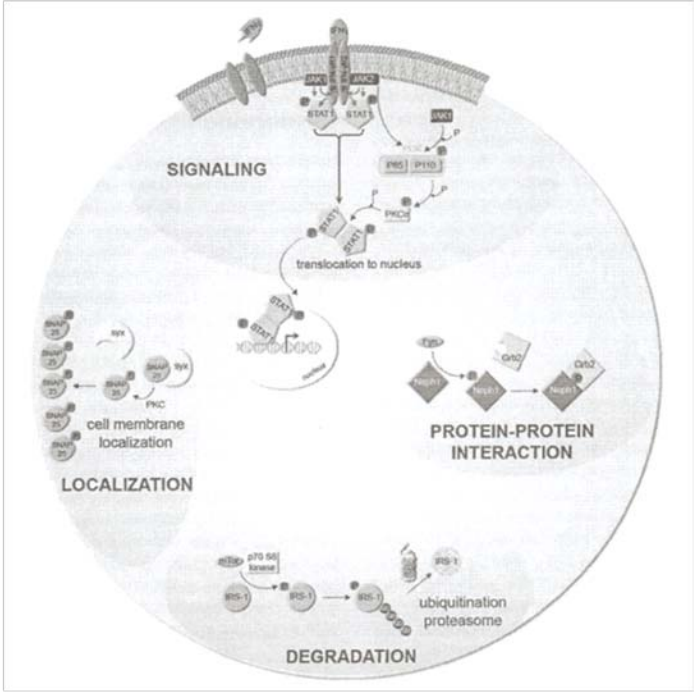


Figure1.3 Protein phosphorylation contribution to different cellular pathways playing an important role in cellular signaling pathways.
Adapted from[Trost et al., 2010]

The regulation of phosphorylation involves highly dynamic and very complex interactions between specific protein kinases and protein phosphatases to control (de-)phosphorylation events at specific sites in target proteins [Thingholm et al., 2009]. Most of the phosphorylations undergo O - phosphorylation on hydroxylated amino acids such as serine, threonine and tyrosine.

However, the phosphorylation rate of the three amino acids is not equal (serine:threonine:tyrosine = 1800:200:1), e.g. the phosphorylation of serine is nine fold higher than the phophorylation of threonine. N - phosphorylation on histidine and lysine, S - phosphorylation on cysteine and acyl-phosphorylation on aspartic and glutamic acid residues are also possible, but only rarely observed [Dunn et al., 2010]. Moreover the ratio of phosphorylated to non-phosphorylated proteins present in cells is an important factor, some residues are permanently phosphorylated and others may only be transiently phosphorylated. For proteins playing a key role in signaling pathways phosphorylation rates are very low, only 1 – 2 % [D'Ambrosio et al., 2007; Reinders and Sickmann, 2005; Trost et al.,

2010]. In general it can be said that one-third of all proteins in a eukaryotic cell are phosphorylated at any given time and that often more than one residue is phosphorylated. That means that the phosphorylation of proteins is heterogeneous [Han et al., 2008; Mann et al., 2002]

Complex phosphorylation regulation, dynamics and low stoichiometry make the analysis of phosphoproteins difficult. Nowadays, mass spectrometry (MS) is used to study protein phosphorylation, which is a challenging task due to several facts: First, phosphopeptides are negatively charged, making the ionization during an ionisation process like matrix-assisted laser desorption / ionization (MALDI), difficult (for detailed information about the MALDI – process, see chapter 1.5.1). Second, the hydrophilic character hinders the binding to chromatographic columns which are routinely used for purification and/or enrichment of proteins and peptides before MS analysis. Third, proteins/peptides without post-translational modifications are usually easier ionized than phosphorylated proteins resulting in less intensive signals for the modified species. And finally, the accurate detection of phospho residues itself is difficult as phosphogroups of phosphorylated threonine (pThr)and phosphorylated serine (pSer)are labile and easily get lost during the ionization process, whereas the phosphorylation on tyrosine (pTyr) is more stable and therefore the detection of pTyr more likely[Aebersold and Goodlett, 2001; Mann et al., 2002]. All these challenging facts put high demands on the analytical method required for the studies of phosphoproteins.

Next to phosphorylation, other post translation modifications exist. In sum, there are more than 300 known PTMs identified, evolutionarily conserved or species specific. The major post-translational modifications beside phosphorylations are acetylation (lysine, N – terminus), carboxylation (aspartic acid and glutamic acid), deamination (asparagines and glutamine), disulfide bond formation, glycosylation (asparagine, serine and threonine), hydroxylation (proline, asparagine, aspartic acid and lysine), methylation (aspartic acid and glutamic acid) and oxidation (methionine and cysteine) [Lottspeich and Engels, 2006].

1.4 Gel Electrophoresis

The determination of the phosphorylated proteins of interest is usually not possible without previous separation of the proteins [Reinders and Sickmann, 2005].The most important point in phosphoproteomic approaches is to minimize the loss of phospho groups during the whole analytical process. Gel electrophoresis is a proper method to simplify the analysis of a biological proteome due to the different electrophoretic mobilities of charged proteins in an electric field.

1.4.1 Sample Preparation for Gel Electrophoresis

The first step for protein analysis is total cell lysis to assess the total proteome. Nevertheless, cell lysis does not stop protein activity which means that many proteases, kinases and phosphatases are still active and the proteome is changed due to protein degradation. In addition, phosphorylation can be introduced or lost *post mortem* resulting in inadequate sample preparation artifacts. To avoid this, cell lysis and the protein extraction are carried out at 4 °C and protease and phosphatase inhibitors are added to all buffers used in the initial steps of cell disruption [D'Ambrosio et al., 2007; Thingholm et al., 2009]. In order to assess the complete (phospho-)proteome three steps are necessary: 1) lysis of the cells, 2) removal of the insoluble cell debris and 3) precipitation of the proteins. Different strategies for cell lyses are summarized in Table 1.1.

Table 1.1 Summary of the different lysis methods

Method	Application	Material
Weak shear force	Glass stirrer Compression through a sieve	Sensitive cells
Osmolysis	Hypotonic environment	Cells without cell wall
Freeze and thaw cycles	Repetitive freezing and thawing steps	Bacteria
Drying	3 days at 20 – 30 °C	Microorganisms and yeasts
Organic solvents	e.g. Acetone -15 °C (dehydration of the cells and extraction of lipids)	All biological material
Attrition	Mortar	Plants, stable bacteria and yeasts
Blade - homogenization	Rapidly rotating blades	Bacteria and yeasts
Vibrating cell mills	Shaking steel container with glass beads	Bacteria
Sonication	Pressure changes	Bacteria, yeasts, fungi

Modified from[Lottspeich and Engels, 2006]

Trichoderma atroviride samples were lysed by sonication and proteins were precipitated with acetone (-20 °C). The detailed protocol for the cell lysis is given in chapter2.1.

1.4.2 Protein Separation with1D – SDS – PAGE

As mentioned above (chapter 1.4), the basis of every electrophoretic method is the migration of charged particles in an electric field. The net charge and the size of the analyte play an important role in the migration behavior. The smaller the molecules and the higher the net charge, the faster the molecules migrate. This is shown in equation [1.5]. The derivation for this equation is described in the following chapter.

1.4.2.1 Electrophoresis – Theoretical Background

During electrophoresis, different forces affect a charged particle, namely an accelerating force F_e and a friction force F_{fr}, where the accelerating force is a function of the charge of the particle q and the strength of the electric field E. The friction force is defined by the frictional coefficient f_c(depending on the viscosity of the media and/or the pore size of the matrix) and the velocity of the migration$v$[Lottspeich and Engels, 2006].

So, the following equation [1.1] results:

[1.1] $$F_e = q \cdot E \text{and } F_{fr} = f_c \cdot v$$

Setting up a equilibrium between F_e and F_{fr}, the particle´s migration becomes constant (equ [1.2]).The electrophoretic mobility u (substance specific) is the proportionality factor between v and E(equ [1.3]):

[1.2] $$F_e = F_{fr}; \; q \cdot E = f_c \cdot v$$

[1.3] $$v = \frac{q \cdot E}{f_c} = u \cdot E$$

For small globular particles, the Stokes' Law can be applied to calculate F_{fr}:

[1.4] $$F_{fr} = 6 \cdot \pi \cdot r \cdot \eta \cdot v$$

r … Stokes radius from the hydratized ion
η … dynamic viscosity
ν…particle velocity

Including the Stokes'Law, the mobility *u* can be determined by the following equation:

[1.5] $$u = \frac{q}{f_c} = \frac{z \cdot e}{6 \cdot \pi \cdot r \cdot \eta \cdot v}$$

z… charge number
e…elementary charge

As proteins and peptides do not occur as globular particles, only an empiric relationship between the molecular mass *M* and the mobility *u* can estimate:

[1.6] $$u \approx \frac{q}{M^{\frac{2}{3}}}$$

1.4.2.2 Electrophoretic Techniques

Generally, three different electrophoretic techniques exist 1) zone electrophoresis (with our without carrier in a homogenous buffer system) 2) isotachophoresis (in a discontinuous buffer system) and 3) isoelectric focusing (using a pH gradient). Also a classification by using different media for

electrophoretic separation is possible and displayed in Table 1.2 for zone electrophoresis [Lottspeich and Engels, 2006].

Table 1.2 Classification of the electrophoretic methods based on the used media for separation for zone electrophoresis

	Carrier - free Electrophoresis	Gel Electrophoresis
System	using capillary tube or thin buffer layer	using membranes and gels as support material
Separation Principle	based on different charges	based on different charges and sizes
Comment	Development of Joule heat resulting in a failure of separation by convection	The matrix hampers the broadening of the zones (results as a consequence of convection)
Example*	Free – flow electrophoresis	Polyacrylamid gel electrophoresis

* These strategies are described in more detail due to the simple instrumental assembling

Carrier Free Electrophoresis – the example of Free – flow Electrophoresis

The principle of a free flow electrophoresis is shown in Figure 1.4. It is a method for separating large particles like mitochondria and other organelles [Kohlheyer et al., 2008; Zischka et al., 2003]. The basis of this technique is the laminar flow of a background electrolyte (BGE) between two narrowly spaced parallel plates. During continuously introducing the sample solution into the carrier buffer as a narrow zone, the charged sample components begin to deflect from the direction of the laminar flow as an orthogonal electric filed is applied and the particles are attracted by the oppositely charged electrodes and move towards the respective electrodes according to their electrophoretic mobilities. The different electrophoretic mobilities at different angles are responsible for the separation. At the outlet side of the chamber the separated sample compounds are continuously collected in the faction collector [Kasicka et al., 1998].

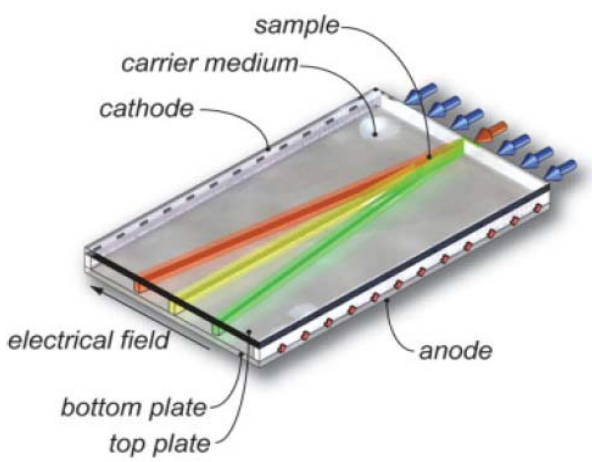


Figure 1.4 Separation in an orthogonal electric filed due to the molecule´s different migrations by means of a free flowelectrophoresis

Adapted from Kohlheyer et at.,2008

Carrier Electrophoresis – the example of Polyacrylamide gel electrophoresis:

Although the free-flow electrophoresis is advantageous for many analytic approaches, gel electrophoresis is often the method of choice for proteome approaches [Reinders and Sickmann, 2005; Thingholm et al., 2009; Tichy et al., 2011].

In general, gel electrophoresis can be carried out either in a vertical or horizontal system, depending on the direction of the gel camber and also different gel media are used, eg. polyacrylamide gel (also agarose gel is available). Polyacrylamide gels are stable and chemically inert. The gel is produced by co-polymerization of acrylamide monomers and a linker, mostly N,N´-Methylenbisacrylamide (Bis). The pore size depends on the total acrylamide concentration *T* and the degree of cross linking *C* [Lottspeich and Engels, 2006].

[1.6] $$T = \frac{m_{Acrylamide} + m_{Bis}}{100\ ml} * 100 \qquad C = \frac{m_{Bis}}{m_{Acrylamide} + m_{Bis}} * 100$$

T…total acrylamide concentration [%]
C…cross linking [%]
m…mass [g]

So, the separation principle is based on the different mobilities of the molecules, depending on their charge, size and shape. If the pore size of the gel is very small, the electrophoretic mobility is mostly dependent on the size of the molecules. Also gels with a gradient in the pore size are available and are received by continuously shift of the monomer concentration allowing the separation of proteins over a broader molecular mass range.

Within the presented thesis a **1**-**D**imensional – **S**odium-**D**odecyl-**S**ulfate – **P**oly-**A**crylamide – **G**el – **E**lectrophoresis (1D – SDS – PAGE) was used, which is very often used for protein research. SDS has different functions. First of all, SDS is a very strong anion detergent that can solubilized many proteins including some hydrophobic and denatured ones. Secondly, it disrupts the tertiary and secondary structure and leads to denaturation of the proteins by means of a heating step prior electrophoresis which is carried out with an excess of SDS at 95 °C. SDS masks the protein's own charge by forming protein/SDS micelles with a constant negative charge per unit mass (1.4 g SDS/g Protein).To completely unfold the protein, reduction of disulfide bridges between cysteine residues is necessary by means of Dithiothreitol (DTT). However, this step is optionally, depending on the experimental requirements [Lottspeich and Engels, 2006].

In a solution with an applied electric field all reduced proteins have the same electrophoretic mobility if properly covered with SDS. Using PAGE with 0.1 % SDS allows a linear correlation between the logarithm of the molecular masses and the migration distance in the gel. So, with the need of well-defined protein standards, the molecular masses of proteins can be determined.

Different buffer systems are available for SDS - PAGE. In this study the standard buffer system, described by Laemmli in 1970, was used, which is based on the discontinuous Tris-Chloride / Tris-Glycine system [Laemmli, 1970]. Other more often used buffer systems are Tris-Acetat / Tris-Tricine, Bis-Tris / Bis-Tris-Tricine and PPA-chloride / Tris-Glycin [Westermeier et al., 2008]. For proteins having an isoelectric point at acidic or neutral pH, buffers like Tris-Chloride or Tris-Glycine, both pH 9.1, and Tris-Tricin, pH 7.6, are used. For alkaline proteins, buffer systems with Glycin-acetate, pH 3.1, or Aluminum-lactate, pH 3.1, are preferable.

However, using gels with small pore sizes, proteins can aggregate and precipitate during entering into the gel. A possibility to avoid these effects is the use of discontinuous electrophoresis. For discontinuous electrophoresis, two gels are used, the stacking gel (larger pore size; formation of a protein – ion – stack in the electric field) and the resolving gel (smaller pore size; separation of the proteins; building of a sharp band separation) [Lottspeich and Engels, 2006] together with a combined buffer system. In Table 1.3, a selection of buffer systems used in discontinuous electrophoresis is shown.

Table 1.3 Selected buffer systems for discontinuous electrophoresis

Buffer	pH		Comments
	Stacking Gel	Resolving Gel	
Tris-Glycine	6.8	8.8	Universal (Laemmli)
Tris-Tricin	8.3	8.4	
Tris-Borate	8.3	8.3	Tris-Sulfate in the gel
Tris-Acetate		7.4	
Na-Phosphate	6.8	6.8	Salt sensitive
Tris-Phosphate		6.8	Urea/SDS
Phoshporic acid		2.4	

The Novex® 4 – 20 % Tris-Glycin Gels 1.5 mm, 12 wells were used for the separation of the *Trichoderma atroviride* samples with the 10x Novex® Tris-Glycin SDS Running Buffer.

1.4.3 Protein Detection – Staining of Gels

Staining is necessary to visualize separated proteins and is therefore an important step after the well-established electrophoresis techniques, such as SDS - PAGE. The interaction of the dye with amino acids is the principle. The appropriate method has to fulfill numerous requirements. It should be non-toxic, environment friendly, sensitive in detection, easy to use, have a high dynamic range and should not influence further analysis, like MS analysis [Winkler et al., 2007]. In Table 1.4 the different staining methods for the detection of proteins with their advantages and disadvantages are listed.

Table 1.4 Staining methods for electrophoretic gels

Method	Advantage	Disadvantage
Colloidal Coomassie brilliant blue staining	Steady state method, quantification possible, MS compatible	LOD: app. 20 ng of BSA (medium sensitive)
Coomassie brilliant blue staining	Steady state method, fast and good quantification, MS compatible	LOD: app. 100 ng of BSA (background destaining necessary)
Zinc imidazol reverse staining	LOD*: app. 15 ng of BSA, fast, MS compatible	Bad quantification, difficult documentation
Silver staining with silver nitrate	LOD: app. 0.2 ng of BSA, ev. MS compatible (adaption needed)	Poor reproducibility because of different destaining times (no endpoint), limited quantification possibilities, multistep procedure
Silver stainingwith silver diamine	LOD: app. 0.2 ng of BSA	Poor reproducibility because of different destaining times (no endpoint), limited quantification possibilities, multistep procedure, higher silver nitrate consumption
Fluorescent stainingwith RuBPS	LOD: app. 0.4 ng of BSA, very good quantification, wide dynamic range	Overnight procedure, additional equipment necessary (fluorescence imager), issues with MS, eventually problems with dye particles
Fluorescent staining with Deep Purple ™	LOD: app. 0.4 ng of BSA, very good quantification, wide dynamic range, MS compatible	Additional equipment necessary (fluorescence imager)
DIGE (fluorescent minimal labeling)	LOD: app. 0.5 ng of BSA, up to three samples comparable simultaneously in one gel, good quantification, wide dynamic range, MS compatible	Additional equipment necessary (fluorescence imager)
DIGE (fluorescent saturation labeling)	LOD: pg range, up to two samples comparable simultaneously in one gel, good for quantification, wide dynamic range, MS compatible	Optimizing of labeling protocols for different samples, additional equipment necessary (fluorescence imager)
Radioactive labeling	LOD: pg range, good quantification, wide dynamic range with phosphor imager	Radioactivity!, limited to living cells, gels have to be dried, additional equipment necessary (phosphor imager)

*Abbreviations: LOD = Limit of Detection; MS = mass spectrometry

Modified from Westermeier et al., 2008

To detect proteins without staining, Western Blotting is an opportunity. It is a highly selective and sensitive detection with specific antibodies. In an additional electrophoretic step, proteins separated by means of PAGE, can be transferred and immobilized on a nitrocellulose membrane. With specific antibodies or lectins the proteins can be detected on the membrane directly. However, the main disadvantages are the non uniform protein transfer on the blotting membrane and the limited compatibility of the membrane material to MS [Westermeier et al., 2008].

1.4.3.1 Coomassie Brilliant Blue Staining

For phosphoproteomics the access to the low abundant phosphoproteins is critical. Therefore usually as much protein as possible has to be applied to SDS-PAGE. This leads to a high overall protein concentration per applied sample on the SDS-PAGE and therefore Coomassie Brilliant Blue (CBB) staining was used to avoid saturation effects during staining. Either Coomassie Brilliant Blue G250 or Coomassie Brilliant Blue R250 (Figure 1.5) can be used [Diezel et al., 1971]. CBB – staining with solvents or a colloidal CBB staining is mostly used[Miller et al., 2006].

A) Coomassie Brilliant Blue G250 B) Coomassie Brilliant Blue R250

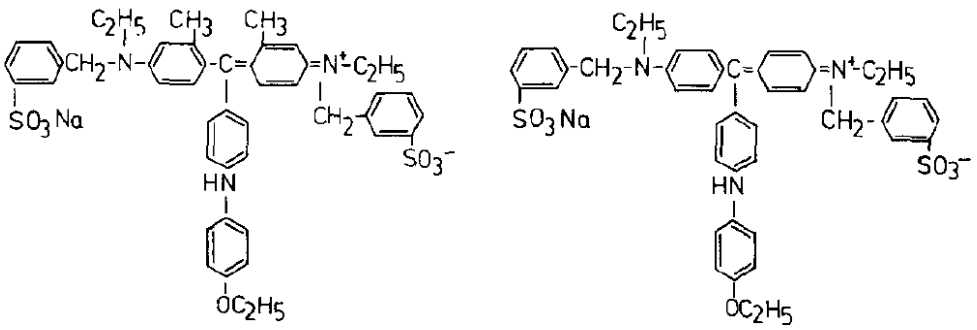


Figure 1.5 Chemical structure of Coomassie Brilliant Blue G250 and R250

CBB solutions with solvents:

CBB staining was first introduced by Neuhoff and contains alcohol (methanol, ethanol or isopropanol) like the classical CBB staining methods do. The component which is responsible for the staining is Coomassie Brilliant Blue R-250. It binds to positively charged amino acids like arginine, lysine, tyrosine and histidine by electrostatic and hydrophobic interactions [Neuhoff et al., 1988; Westermeier et al., 2008].Destaining the background is necessary with a similar solution devoid the dye. The gel matrices have a lower affinity for the dye than the proteins, therefore the proteins become visible. CBB – staining is easy to use and MS compatible which is very important for this approach. [Patton, 2002]

Colloidal CBB:

In the presence of 12.5 % TCA, CBB G250 converts into a colloidal state and results in a staining method with less background staining. Thus, makes the destaining of the background needless. Optimal staining of proteins with a clear background can be achieved with phosphoric acid and ammonium sulfate which transfers the dye completely into its colloidal form. During staining, equilibrium between colloidal CBB – G250 and low concentrated freely dispersed dye in solution is achieved. The proteins are stained by the entering of the free dye. The colloidal particles are excluded to avoid background staining. This staining method is more sensitive than staining by CBB R250 [Miller et al., 2006].

Keeping in mind to load high concentrations of the *Trichoderma atroviride* samples on the gel, it was decided to use the CBB – staining with CBB R250 due to lower sensitivity. The detailed CBB staining protocol is described in chapter2.4.

1.5 Mass–Spectrometry

MS is the method of choice for the detection and identification of posttranslational modifications. MS is an analytical approach to determine the mass-to-charge ratio of free ions in a high vacuum[Aebersold and Goodlett, 2001]. A mass spectrometer consists of an ion source, a mass analyser and a detector (Figure 1.6). The ion source is for the ionization of the sample. The mass analyzer separates the molecules according to their m/z values and the detector detects and transforms the ions pass through the mass analyzer into a usable signal. The single parts and their functions are described in the following chapter.

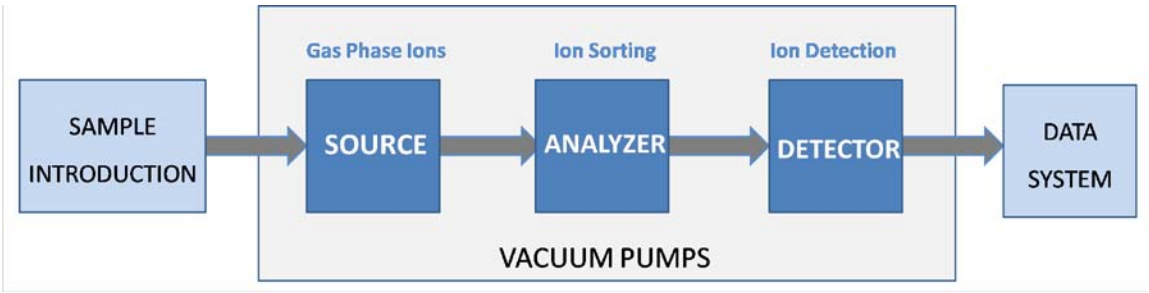


Figure 1.6 Schematic representation of the parts of a mass spectrometer
The dark blue quadrates display the three major parts of a mass spectrometer.

Adapted from Lottspeich and Engels, 2006.

Ions for MS can be produced by *electron impact* (EI), *chemical impact* (CI), *fast atom bombardment* (FAB), *electrospray ionization* (ESI) and *matrix assisted laser desorption/ionization* (MALDI). For the

mass analyzer, a *quadrupol* – analyzer (Q), a *magnetic sector*, an *electric sector*, an *iontrap* (IT), an *ioncyclotron, an orbitrap* and a *time-of-flight* analyzer are usually used. The ions are mostly detected by a *secondary electron multiplier* (SEM) but also a *faradycup*, a *scintillator* and a *microchannel plate* (MCP) can be used. The ionization methods that are used mostly for investigations of peptides and proteins are ESI - and MALDI - MS. The similarity of these techniques is the formation of stabile ions of the intact biological molecule and the absence of fragments. MALDI is especially used with TOF (Time-of-flight) analyzers. This instrumentation, MALDI – TOF – MS, was used in this approach and is described in the following chapters in more detail [Zenobi and Knochenmuss, 1998].

1.5.1 MALDI - TOF – Mass Spectrometry

1.5.1.1 Matrix Assisted Laser Desorption Ionization

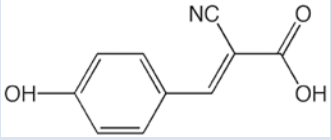
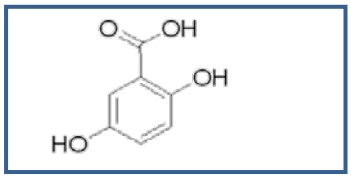
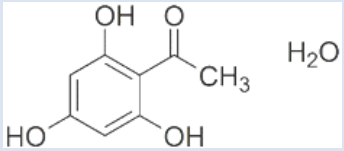
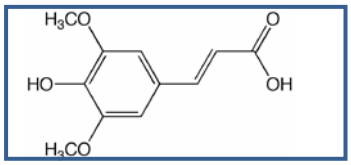
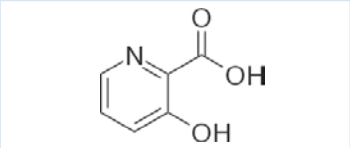
Among the many MS techniques available, the number of MALDI – MS applications is constantly increasing. MALDI is a soft ionization technique and has been applied to a large number of analytical problems such as the analysis of proteins, glycol-conjugates, poly-nucleotides and synthetic polymers. The sensitivity of the MALDI techniques is often in the low femtomole– rang[Gross and Strupat, 1998; Macha and Limbach, 2002]. MALDI – MS has both, advantages and limitations (see Table 1.5).

Table 1.5 Advantages and limitations of MALDI - MS

Advantages	Limitations
Femtomole sensitivity	Sensitivity/resolution drops with high mass range
Molecular ions formed at the time	Sample solution and matrix solution have to be miscible
Little fragmentation	Apolar compounds difficult
m/z up to 1 MDa	High chemical noise in low m/z
Ion doping supports desorption/ionization	Photochemical degradation
Low suppression effects	
High salt tolerance	
Re-analysis	
No time limitation for MS/MS	

Basis of the MALDI technique is desorption and ionization of molecules, which are imbedded in a matrix. The use of a MALDI matrix is the crucial factor for the process of this ionization method and different matrices are available for different applications (see Table 1.6).

Table 1.6 Overview of the most common MALDI matrices used in biological approaches

Matrix	Matrix Structure	Application
α-cano-4-hydroxy-cinnamic acid (CHCA)		UV laser: peptide analysis and protein digests. Analytes < 10 kDa
2, 5-dihydroxy-benzoic acid (DHB)		UV laser: protein digests and proteins, oligosaccharides released from glycoproteins.
6-trihydroxy-acetophenone (THAP)		UV laser: Oligonucleotides < 3 kDa
Sinapinic acid		Analysis of large polypeptides and proteins > 10 kDa
3-hydroxy picolinic acid		UV laser: Oligonucleotide > 3 kDa

Modified by [Westermeier et al., 2008; Zenobi and Knochenmuss, 1998

Principle of the Desorption/Ionization Process

The desorption/ionization process occurs in two steps. First, the samples have to be prepared for mass analysis by adding proteins or peptides to a concentrated solution containing a large molar excess of the matrix. The matrix has a strong absorption at the laser wavelength. After drying, the analyte molecules are embedded in the matrix. Second, by the means of intense laser pulses over a short duration, bulk portions of the matrix/analyte mixture are evaporated. The interaction of the laser pulse with the sample causes a fraction of the matrix/analyte mixture to be transferred into the gas phase during which the proteins/peptides become ionized. In short, during the ionization process a proton transfer occurs. Photon energy of the laser beam excites electrons at the outer shell of the matrix molecule. The neutral matrix molecules become positively charged by the removal of the electron. This matrix ions transfer their energy to the neutral analyte molecules, which leads to an ionic gas cloud [Zenobi and Knochenmuss, 1998]. The ions in the gas phase are then accelerated by an electrostatic field towards the analyzer [Chait and Kent, 1992; Gross and Strupat, 1998; Hillenkamp and Karas, 1991]. The figure below (Figure 1.7) shows schematically the desorption/ionization process.

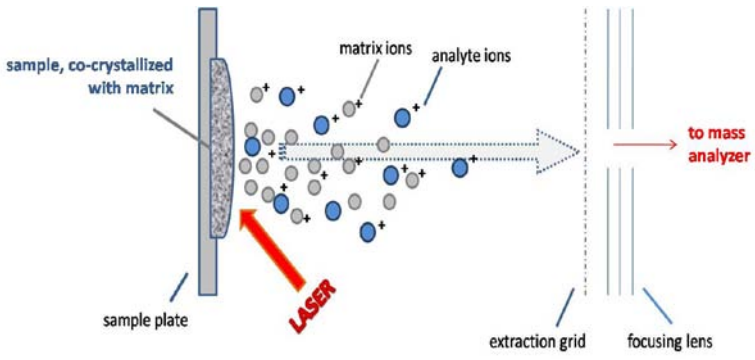


Figure 1.7 Schematic illustration of the desorption/ionization– process in MALDI – mass spectrometry.
modified from [de Hoffmann and Stroobant, 2008]

There are a variety of laser sources available, which can be divided into UV laser and IR laser. The plume, which is caused by UV laser beams, can be described as a very rapid, even explosive, solid-to-gas phase transition resulting in higher sensitivity and longer sample life due to short pulse width. The higher sensitivity is of course preferred in proteomics. IR lasers work at µm wavelengths and are mostly used in oligonucleotide analyses, due to their softer ionization behavior [Zenobi and Knochenmuss, 1998].

1.5.1.2 *Time-Of-Flight* (TOF) Mass Analyzer

The different mass analyzer types listed in chapter 1.5 on page 13 have unique properties, such as accessible mass range, analysis speed, mass resolution, sensitivity, ion transmission and dynamic range. Also a combination of more than one mass analyzer to give so called hybrid instruments is applicable [Soares et al., 2012].

For this thesis only TOF analyzers were used. In a linear TOF analyzer, ions were separated after their initial acceleration by an electric file, according to their velocities when they drift in a field free region that is called a flight tube.

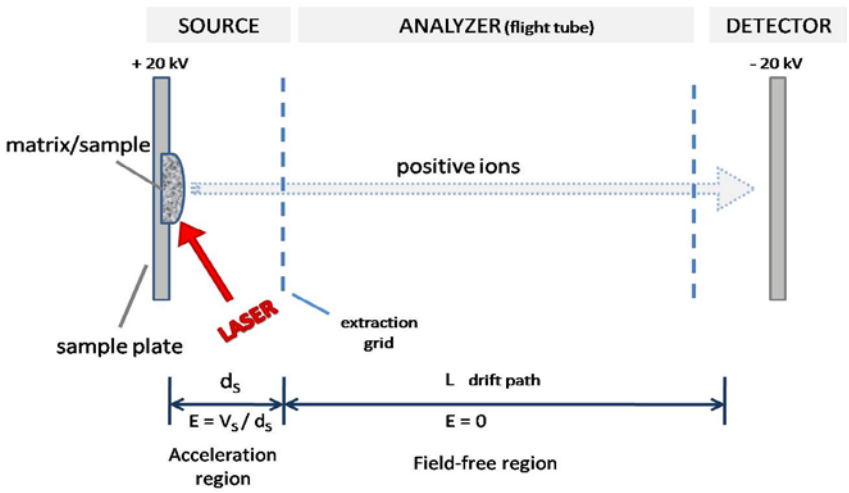


Figure 1.8 Principle of a linear TOF instrument for the separation of ions
Modified from [de Hoffmann and Stroobant, 2008]

Ions are expelled from the source in bundles, which are accelerated to a fixed kinetic energy by a difference of potential applied between an electrode and the extraction grid. The ions are then allowed to pass through a field-free region, where they are separated according to their velocities. A detector at the end of the field-free region produces a signal as each ion bundle strikes it[Hillenkamp and Karas, 1991]. The principle of a liner TOF instrument is displayed in Figure 1.8.

The difference between the start time, common to all ions, and the arrival time of an individual ion at the detector is proportional to $(m_i/z_i)^{1/2}$, as a result of the following considerations and derivations explained in equation [1.7] to [1.11]. Therefore it can be used to calculate the ion´s mass and convert the axis of the spectrum into a mass-to-charge ratio axis. Mass-to-charge ratios are determined by measuring the time that ions take to move through a field-free region between the ion source and the detector. The ion with mass m and charge [1.7] q ($q = z\ e$) is accelerated by a potential V_S before it leaves the source [Lottspeich and Engels, 2006]. Therefore, the kinetic energy of the ion is calculated by:

[1.8] $$E_k = \frac{m * v^2}{2} = q * V_s = z * e * V_s$$

E_k...kinetic energy m...mass of the ion
v ...velocity q...charge of the ion
q...charge of the ion V_S...applied electric field
z...number of charges e ...elementary charge

The velocity v is a result of the time t needed to cover the distance L, corresponding to the length of the field-free region of the flight tube.

[1.9] $$v = \frac{L}{t}$$

Combining equation [1.8] and [1.9] results in:

[1.10] $$\frac{1}{2} * m * \left(\frac{L}{t}\right)^2 = z * e * V_s$$

Therefore, the calculation of the m/z value is possible just by stopping the time how long an ion takes to pass the flight tube:

[1.11] $$\frac{m}{z} = \frac{2 * e * V_S}{L^2} * t^2$$

The resulting equation [1.11] shows, that the smaller the mass of an ion, the faster it will reach the detector (if all ions have the same charge).

To fully discuss the performance of TOF analyzers, it is necessary to define mass resolution R. This characteristic is the ability to separate two close masses in two separate signals, depending on the ratio of the mass m to Δm. It is expressed as the mass m divided by the full width of the signal Δm,

which is measured between the points of half maximum intensity for TOF instruments[de Hoffmann and Stroobant, 2008]:

$$R = \frac{m}{\Delta m} = \frac{m_1}{(m_2 - m_1)} \quad [1.12]$$

The resolution can be defined as 10 % valley, where two peaks of equal height are separated by a valley which is at its lowest point just 10 % of the height of higher peak. Another way to explain the resolution is the 50 % valley method. The 50 % value method based on the same principle, only the height of the point where two nearby peaks contact each other must be 50 % height of the higher peak. These two methods are mostly used either for magnetic sector mass spectrometers or for quadrupole MS. A common standard definition of resolution based upon Δ m being Full Width of the peak at Half of its Maximum height (FWHM)[Todd, 1991]

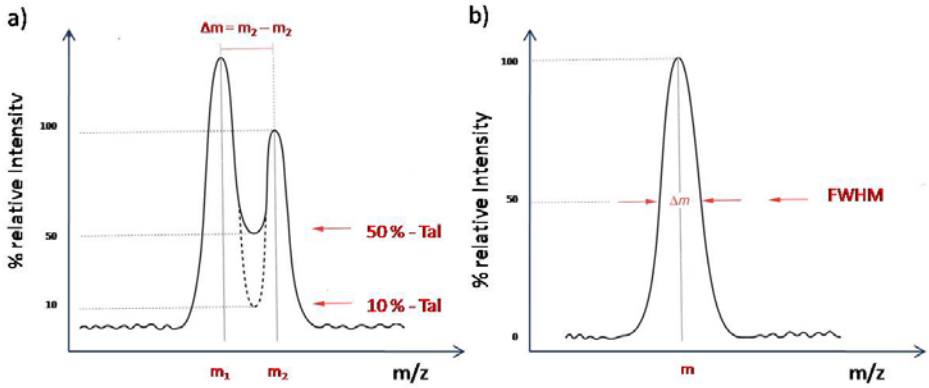


Figure 1.9 Mass resolution definitions for mass spectrometers
a)10 % and 50 % valley method and b) full width and half maximum method
Modified from [Lottspeich and Engels, 2006]

The practical limitation of the mass resolution obtained with the linear TOF mass spectrometer is the width of a signal observed for a single ion species. For a MALDI process the peak broadening is mainly affected by the ions initial velocity distribution which can be reduced by either using a delayed pulsed extraction or an instrumental configuration such as a reflectron [de Hoffmann and Stroobant, 2008; Mann and Talbo, 1996].

Delayed Pulsed Extraction

Generally, ions formed in the source are immediately extracted by a continuously applied voltage. Ions with the same m/z ratios but different kinetic energies reach the detector at slightly different times. Thus, leads to peak broadening. By the use of delayed pulsed extraction the ions are initially allowed to expand into a field-free region in the source and after a certain delay, a voltage pulse is applied to extract the ions outside the source. Ions with less initially energy receive more kinetic

energies and join the initially more energetic ions at the detector. Those ions with higher energy receive less kinetic energy resulting in a focusing of uneven energy distributions. So, the delayed pulsed extraction corrects the energy dispersion of the ions leaving the source with the same *m/z* ratio, resulting in improved resolution [de Hoffmann and Stroobant, 2008].

Reflectron

The other possibility to improve the resolution is by means of a reflectron (also called reflector). In Figure 1.10the principle setup of a Reflectron – *time – of – flight* mass spectrometer (RTOF – MS) is illustrated. The reflector is placed behind the field-free region and creates a retarding field which acts like an ion mirror by deflecting the ions and sending them back through the flight tube. The detector is deposited on the source side of the ion mirror to capture the arrival of ions after reflection. The reason for implementation of a reflector is to correct the kinetic energy dispersion of the ions leaving the source with the same m/z ratio.The ions coming from the ion source leaved the sample holder with the same kinetic energies and travel along the linear field free drift tube with different velocities related to their *m/z* ratios. The reflector TOF – analyzer uses a static electric field to reverse the direction of travel of the ions and improves mass resolution by assuring that ions of the same m/z but different translational energy arrive at the detector at the same time. Ions having higher kinetic energies and therefore higher velocities will enter the reflector more deeply than ions with lower kinetic energy. Hence, the retentions time for fast ions are longer. Consequently, the slower ions and the ions which spend more time in the reflectron, both types having the same m/z ratios, will reach the detector at the same time [de Hoffmann and Stroobant, 2008; Soares et al., 2012].

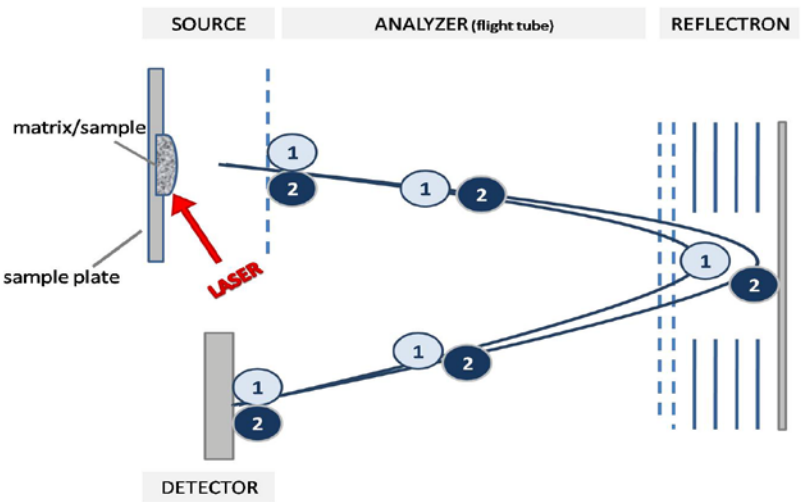


Figure 1.10 *time-of-flight* analyzer and the ion separation process using a reflectron
Modified from [Soares et al., 2012]

1.5.1.3 *TOF* – Analyzer for Tandem Mass Spectrometry

Analyzing proteins or peptides by means of MALDI MS can lead to fragmentations. These fragmentations result from the high energy transferred to the analyte during the

desorption / ionization process. The two different types of fragmentations that produce fragment ions are grouped according to the place where the fragmentation takes place. For detailed information on fragmentation pattern of peptides and proteins see chapter 321.7.3 on page 32.

On one hand, fragmentation taking place in the source is called in-source decay (ISD). This occurs, if the lifetime of an intact ion is shorter (prompt fragmentation) than its time spent in the ion source of the mass spectrometer. Only the fragments are accelerated towards the mass analyzer. On the other hand, fragmentation taking place after the ion source of a mass spectrometer is called post-source decay (PSD). These ions are stable enough to leave the source intact, but contain enough excess energy to allow fragmentation before they reach the detector [de Hoffmann and Stroobant, 2008].

ISD leads to product ions that are always apparent in the MALDI spectra, even when a linear TOF is used. The precursor ion and the fragment ions have the same kinetic energies after acceleration and thus they reach the detector separately according to their m/z ratios. In contrast, product ions from PSD fragmentation need certain instrumental conditions to be detected. The precursor molecule has to be selected. This precursor selection is often done by ion gating, where all ions passing the ion gate are deflected from the actual flight path except a certain mass window which is transmitted to the detector without deflection. The ion gate has to be set in a way that the majority of PSD ions have not yet been formed but also in a way that PSD fragments a sufficiently separated. The main consideration is that a precursor ion fragments after acceleration and before the entrance into the reflectron, which leads to the fact that the product ions and the precursor ion have the same velocity. Therefore, the flight time in the field-free region is the same. Consequently the survivor precursor ion, its fragment ions and neutral fragments reach the detector at the same time by means of a liner TOF. This leads to a broadening of the peaks with a loss of resolution and sensitivity. By using a reflectron mode, a produced fragment ion has the same velocity as its precursor but due to its lower mass a lower kinetic energy. As a consequence the fragment ions which have a lower kinetic energy penetrate the reflectron less deeply and thus are spending less time for passing the reflectron than the survivor precursor ions [Lottspeich and Engels, 2006; Spengler, 1997].So, these ions have different flight times depending on their masses, which reach the detector successively according to their m/z ratios, which can be proven by the following considerations:

The kinetic energies for the precursor E_{kp} with its mass m_p and the fragment E_{kf} with its mass m_f with the same velocity v_{ix} results in the following equation:

$$[1.13] \quad E_{kp} = \frac{m_p * v_{ix}^2}{2} \; and \; E_{kf} = \frac{m_f * v_{ix}^2}{2} \rightarrow {E_{kp}}/{E_f} = {m_p}/{m_f} \; or \; \boldsymbol{E_{kf} = E_{kp} * \frac{m_f}{m_p}}$$

If the penetration depth d in the reflectron (single stage, linear potential) is given by [1.14] $d = E_k/qE$, for the precursor and the fragment the relevant equations are:

$$[1.15] \qquad d_p = \frac{E_{kp}}{qE} \; and \; d_f = \frac{E_{kf}}{qE} = \frac{E_{kp} * (m_f/m_p)}{qE} \rightarrow \boldsymbol{d_f = d_p * \frac{m_f}{m_p}}$$

The respective flight times t in the reflectron are given by

$$[1.16] \qquad t_{rp} = \frac{4 * d_p}{v_{ix}} \; and \; t_{rf} = \frac{4 * d_f}{v_{ix}} \rightarrow t_{rf} = \boldsymbol{t_{rp} \frac{m_f}{m_p}}$$

This demonstrates, that the ratios of the respective flight times t are equal to the mass ratio. This equation also illustrates the relationship that the smaller the fragments are, the shorter the time spent in the reflectron.

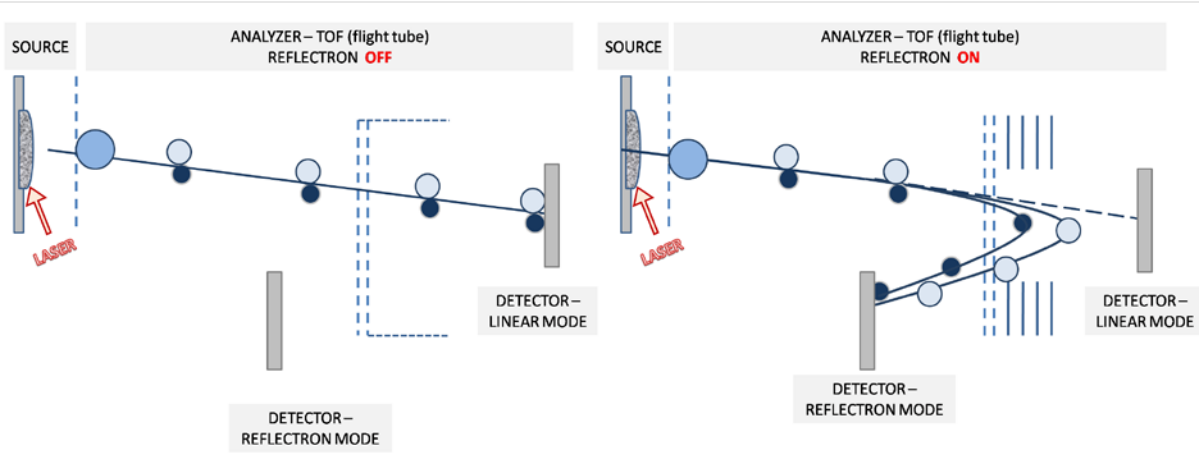


Figure 1.11 Combination of a linear and a reflectron TOF analyzing mode with the possibility to switch the reflectron on or off

Modified from [de Hoffmann and Stroobant, 2008]

BRUKER Daltonics provides theUltrafleXtrem™ which is a MALDI - TOF/RTOF –MS including a so called LIFT cell at the end of the TOF 1 analyzer [Suckau et al., 2003]. The additional LIFT cell has two main functions, the re-acceleration of fragments and remaining molecular ions and the re-focusing of the ions. Re-acceleration minimizes the energy spread of the metastable fragments and thus, to capture on the detector the complete fragment ion spectrum at one fixed reflectron voltage. The re-focusing increases the resolution.

1.5.1.4 Electron Multiplier for Detection of Signals

An electron multiplier (EM) is the most common used detector type for MALDI – MS [de Hoffmann and Stroobant, 2008; Lottspeich and Engels, 2006].The ions from the analyzer are accelerated to a high velocity in order to enhance detection efficiency. They reach a conversion dynode and

secondary particles are built. These secondary particles are converted to electrons at the first dynode. This process is then amplified a multiple times by a cascade effect in the electron multiplier to produce current and reach a signal increase by 10^6.

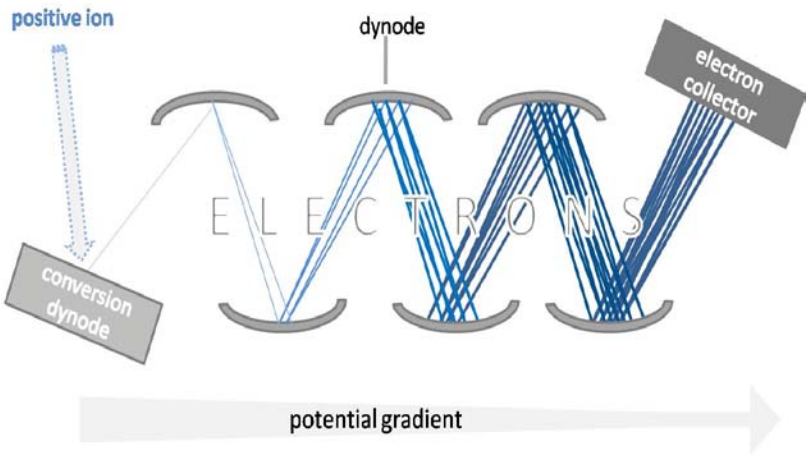


Figure 1.12 Electron multiplier as detector to convert gain usable signals
Modified from [de Hoffmann and Stroobant, 2008]

1.6 Sample Preparation for MALDI – TOF – MS

Due to the different challenges for the detection of phosphorylated proteins described in chapter1.3, namely low relative abundance of many phosphoproteins, low phosphorylation stoichiometry and the dynamic regulation of phosphoproteins, high demands on the analytical method are required for phosphoproteome studies. Even with recent advances in mass spectrometry instrumentation, the detection and identification of phosphorylation sites is challenging [Dunn et al., 2010]. Therefore a proper sample preparation is necessary to first, avoid the loss of phosphorylation during the ionisation process and second, to enrich the phosphorylated peptides selectively and hopefully remove un-phosphorylated ones.

1.6.1 Sample Preparation Techniques

Nowadays, different MALDI sample preparation recipes have been described, among which the most frequently used is the dried – droplet technique. However, the most frequently applied methods can be divided into four groups.

1.6.1.1 Dried – droplet Method

0.5 – 2 µl of sample is applied to the target and 0.5 – 1 µl of matrix solution is added and mixed direct on the target. The sample – matrix mixture is dried under ambient conditions. Also a gentle steam of air or argon is possible for drying [Kemptner et al., 2009].

1.6.1.2 Thin – layer Method

A thin layer of the matrix is applied on the target by pipetting 0.5 – 1 µl matrix solution. Then 0.5 µl of the sample solution is deposited on the dry, small, homogenous matrix crystal layer. After solvent evaporation, a sample washing procedure may follow. For instance by adding and removing up to three times 5 – 10 µl of 4 °C pre-cooled0.1 % TFA [Kemptner et al., 2009].

1.6.1.3 Thick – layer Method with Nitrocellulose as Matrix Additive

Nitrocellulose (NC) and matrix are equally dissolved in acetone (40 µg/µl) and each is diluted with 2-propanol to 20 µg/µl. After adding 1 % (v/v) of 0.1 % TFA to the solutions, 10 µl of each solution is deposited on a rotating target. To gain a uniform NC – matrix layer, the target is spin – dried. 0.5 µl of each, the sample solution and 4 °C pre-cooled 2 % TFA is placed on top of the NC – matrix layer and dried subsequently. A washing step for high contaminated samples is possible by adding 10 µl of 4 °C pre-cooled0.1 % TFA. Removal of the TFA is carried out after a few seconds by spinning. This washing step could be repeated tree three times. Last step is the deposition of another 0.5 µl of 2 % TFA and 0.5 µl matrix [Kemptner et al., 2009].

1.6.1.4 Sandwich Method

The first step is to gain a thin layer of matrix, described as above in 1.6.1.2. After that, 1 – 2 µl of 4 °C pre-cooled 0.1 % TFA, 0.5 µl of sample solution and 0.5 µl of matrix solution is added consecutively including a drying step at ambient air after each and every solution application. So, a matrix – sample – matrix sandwich results.

The dried – droplet technique is our choice, because it is compatible with almost of the matrix-variations described in this work. For more detailed information about the matrices used in this study see chapter 1.6.4 on page29. Kussmann et al. [Kussmann et al., 1997]summarized the preferences of matrix selection dependent on the analyte and the matrix compatibility with the sample preparation techniques. The modified summary with relation to peptide analysis is given in Table 1.7.

Table 1.7 Preference of sample preparation techniques and their compatibility with different matrices for peptide mapping

Sample Preparation Technique	Matrix		
	CHCA	DHB	THAP
Dried - droplet Method	1	2	2
Thin – layer Method	1	n. c.	2
Thick – layer Method	1	n. c.	n. c.
Sandwich – Method	1	n. c.	n. c.

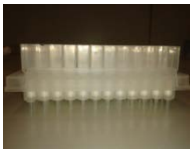
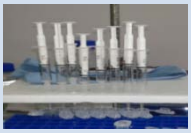
Preferences are given in numbers whereat “1” for high priority and “2” for low priority signals. n. c. = not compatible

1.6.2 Desalting Methods

Samples often need to be preprocessed to ensure their compatibility for MS analyses. Desalting reduces the salt concentration to generate an artifact free mass spectrum by MALDI. This section describes the mechanism of a desalting process utilizing reversed phase material and the different methods used in this work. The stationary phase is a non-polar silica material with covalently linked alkyl residues (C_4– C_{18}; the longer the alkyl residue the higher the hydrophobicity). Typically, C_{18} materials are used for desalting peptides. The sample is first in an aqueous solvent for binding. After peptide binding the stationary phase is washed with aqueous solvents and last organic solvents are used for peptide elution. Due to hydrophobic interaction, the analyte molecules bind to the stationary phase. [Lottspeich and Engels, 2006].

Table 1.8 listed the three different desalting methods and their characteristics.

Table 1.8 Characteristica of the different desalting methods

Method	Binding Capacity	Resin Material	Advantages	Disadvantages	Picture
ZipTip ® C_{18} (Milliipore)	Typically 5 µg	Silica, 15 µm, 200Å pore size	Commercially available	High costs	
HyperSep-96 C_{18} Plate (Thermo Scientific)	Up to 2mg	Silica, 40-63 µm, 60 Å pore size	Commercially available, high through-put (96 well plate), quick method	Contamination of unused cartridges during desalting is possible	
Self made Strata-X column* (4 layers of C_{18}Empore ™ Extraction Discs)	No information	Silica, 12µm, 60 Å pore size	Low costs	Not reproducible, time consuming, inaccurate	

*The Strata-X tips were made of four layers of C_{18}Empore ™ Extraction Discs, which were positioned in the top of an Eppendorf – tip. The eluates were collected in a sample tube.

1.6.3 Enrichment strategies

As mentioned above, only a fraction of the total proteins in a proteome is phosphorylated at any given time and these proteins are difficult to analyze by MS, especially in the presence of non-phosphorylated peptides. This is mainly due to lower ionization efficiencies of phosphopeptides resulting in lower signal intensities. Thus, efficient enrichment of phosphorylated peptides prior MS resulting in increased sensitivity is essential. Specific enrichment of phosphorylated peptides (or proteins) is possibly the most widely used approach in phosphoproteomics [D'Ambrosio et al., 2007;

Reinders and Sickmann, 2005; Trost et al., 2010].A survey of the different strategies for phosphopeptide enrichment is shown in Figure 1.13.

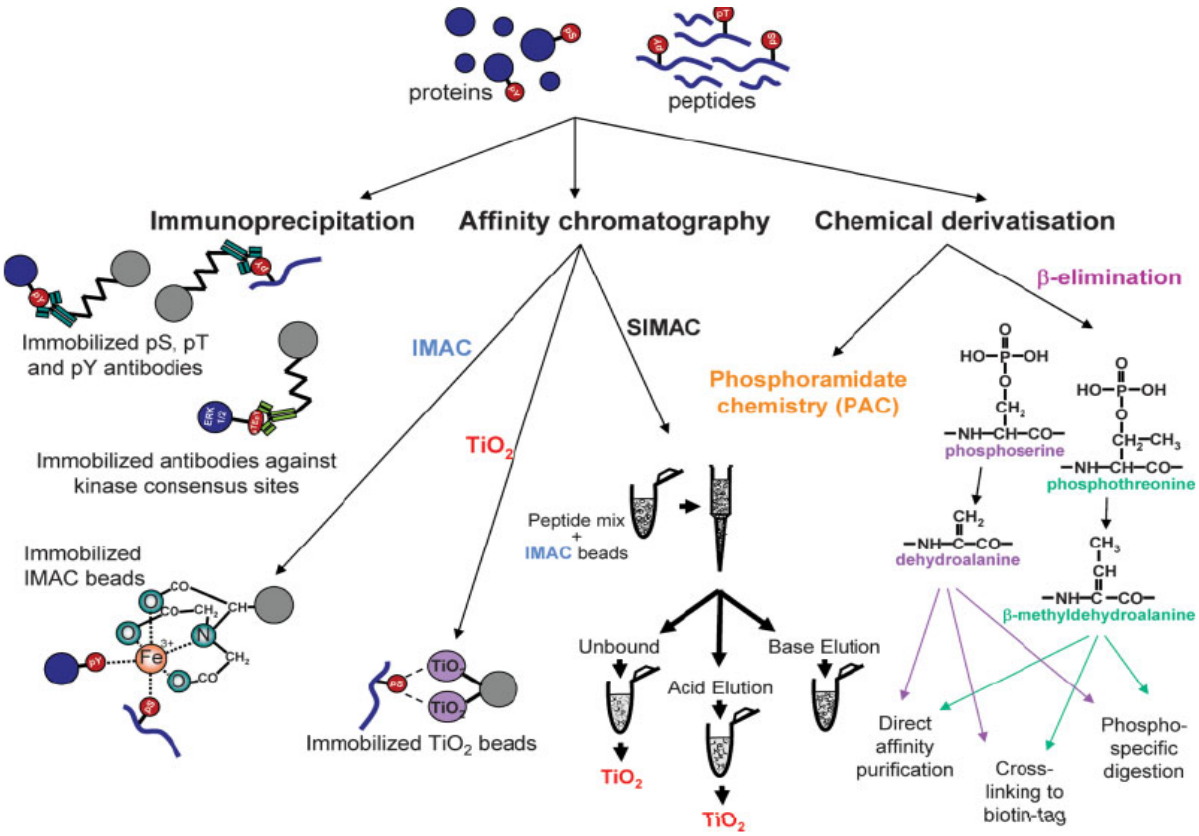


Figure 1.13 Different strategies for the specific phosphopeptide/phophoprotein enrichment
Adapted from [Howell, 2003; Thingholm et al., 2009]

1.6.3.1 Immunoprecipitation

The enrichment of phosphate group containing molecules can be performed either on the protein or the peptide level. Successful application of immunoprecipitation methods relies on the availability of antibodies recognizing specific epitopes with high affinity. A wide range of phoshpospecific antibodies are commercially available, but only a few have been described for large-scale phosphoproteomic studies [Blagoev et al., 2004; Oda et al., 2001; Rikova et al., 2007; Villen et al., 2007]. Immunoprecipitation of phosphotyrosine-containing proteins (anti pTyr, that tightly bind to pTyr in a generic fashion) is still much more frequent than immunoprecipitation [Rush et al., 2005; Steen et al., 2002; Zhang et al., 2002] using the more expensive mixtures of anti-phosphoserine or anti-phoshpothreonine. However, Antibodies against pSer, pTyr and pThr residues can be used for the overall enrichment of phosphoproteins from a complex sample, though, this method is limited by the specificity of the antibodies [Macek et al., 2009; Thingholm et al., 2009].

1.6.3.2 Affinity Chromatography

Other commonly used strategies for selective enrichment are, as can be seen in Figure 1.14., affinity chromatographic methods. In the following, immobilized metal ion affinity chromatography (IMAC) and titanium dioxide chromatography are described in more detail.

Immobilized metal ion affinity chromatography – IMAC

In general, IMAC prefers the binding of multiply phosphorylated peptides. Phosphopeptides are bound to the stationary phase by electrostatic interactions of the negatively charged phosphate moiety with positively charged metal ions like Fe^{3+}, Ga^{3+}, Al^{3+}, Co^{3+} or Zr^{4+}. These ions are chelated to nitrilotriacetic (NTA) acid or iminodiacetic acid (IDA) coated beads, representing the stationary phase [Porath, 1992]. Three different principles for the elution of the bond peptides are used (1) competitive elution, (2) stripping elution or (3) pH adjustment [Chaga, 2001; Paunovic et al., 2005]

Various ready-made boxes providing all necessary consumables are commercially available (e.g. Pierce®*Fe-NTA Phosphopeptide Enrichment Kit*).The major disadvantage of this strategy is the high level of nonspecific binding of non phosphorylated peptides containing multiple acidic amino acid residues that co-purify with the phosphorylated peptides [Dunn et al., 2010; Reinders and Sickmann, 2005].

Titanium Dioxide Chromatography

The TiO_2 chromatography is a suitable alternative to IMAC with a bias to mono and di phosphorylated peptides and belongs to the group of metal oxide affinity chromatography (MOAC) strategies. Thingholm et al [Thingholm et al., 2008] propose that TiO_2 is able to bind multiply phosphorylated peptides as well as mono phosphorylated ones, nevertheless multi phosphorylated peptides are difficult to elute form the TiO_2 material due to the high binding affinity. However, TiO_2 has an acceptable affinity for phosphate ions from aqueous solutions and turned out to be a robust method to enrich phosphopeptides.

Peptides are loaded under acidic conditions on porous, spherical TiO_2particles using various organic acids (e.g. phthalic acid or glycolic acid). The binding is based on the interaction of the π-orbital of the TiO_2 and the phosphor group of the phosphopeptide. The acidic pH value eliminates effectively the unspecific binding of non-phosphorylated, acidic peptides to the resin. After washing steps to remove the non-phosphorylated peptides, the phosphopeptides are eluted from the TiO_2 column under alkaline conditions using e.g. ammonia solution. The strategy provides a high selectivity towards phosphopeptide [Macek et al., 2009; Tichy et al., 2011]. Similar to IMAC, ready-made boxes

for TiO_2 enrichment are commercially available (e.g. Pierce®*Magentic Titanium Dioxide Phosphopeptide Enrichment Kit* or *TiO_2 Mag Sepharose* from GE Healthcar**e**).

Analog to TiO_2, ZrO_2 is positively charged at acidic pH and has a higher binding affinity towards phosphate than carboxylated anions (i.e. acidic peptide residues). Previously, ZrO_2 has been used as a chromatographic resin due to its physical and thermal stability. Kweon and Hakanson found out in 2006 [Kweon and Hakansson, 2006], that TiO_2 based phosphor enrichment preferentially enriches multiply phoshporylated peptides, whereas more selective isolation of singly phosphorylated peptides was observed using ZrO_2. However, TiO_2 shows better reproducibility and is more selective for phoshpoeptides with less nonspecific binding.

Sequential Elution from IMAC - SIMAC

The presence of mono- and non-phosphorylated peptides in samples prepared for MS analysis may suppress the ionization of multiply phosphorylated peptides. Hence detection efficiency decreases for these peptides. Therefore new phosphoproteomics approaches are developed to study multiple phosphorylations. SIMAC, developed by Thingholmen et al in 2008 [Thingholm et al., 2008], is a straightforward method to improve large scale phosphoproteomics. It combines the strengths of IMAC with the strength of TiO_2 chromatography and represents a strategy in which mono and multiply phosphorylated peptides are efficiently enriched from highly complex samples into separate pools, which can be analyzed using different MS/MS settings. In SIMAC, the digested phosphopeptides are bound to IMAC beads. Unbound peptides, including unbound phosphopeptides, are collected for further enrichment using TiO_2 chromatography. First, mono phosphorylated peptides are eluted from the IMAC beads using acidic conditions (pH 1.0). Then, a subsequent elution of the multiple phosphorylated peptides is carried out by using basic conditions (pH 11.3). Due to the limited selectivity of the IMAC material for highly complex samples, the first elution fraction using acidic conditions is subsequently enriched using TiO_2 chromatography. The basic elution fraction contains a relatively low level of non-phosphorylated peptides and thus no further enrichment is necessary and MS analysis can be carried out.

1.6.3.3 Chemical Derivatization

Chemical derivatizations have been used for the tagging of phosphate groups on both, proteins and peptides. β-elimination of phosphate groups, present only on serine and threonine residues, producedehydroalanine and β-methyldehydroalanine [McLachlin and Chait, 2003].By Michael addition, a dithiol is formed in the peptide after adding a chemical compound containing a free sulfhydryl group (e.g ethanedithiol, or EDT [Oda et al., 2001]), which can furthermore act as a cross linker to a biotin tag for direct affinity purification. The general drawback of β-elimination is the of

other post-translational modifications that also undergo β-elimination (*O*-glycosylation) [Thingholm et al., 2009].

Another chemical derivatization strategy is called phosphoramidatechemistry (PAC) and is a multistep chemical modification strategy introduced by Zhou in 2001 [Zhou et al., 2001], which can be applied to all phosphorylated residues. The workload of this strategy is extensive due to the many chemical reactions and sample may be lost at each step.

1.6.3.4 Other Enrichment Methods

Beside the techniques described above, many other enrichment strategies are described. On plate enrichment is an advantageous technique to enrich phosphopeptides prior MALDI - MS analysis [Dogruel et al., 1995; Hutchens and Yip, 1993; Nelson et al., 1995]. It provides high throughput capabilities, minimal sample loss and minimal sample handling. This method includes incubation with the sample on the plate. Different plates modified with IMAC functionalities and metal oxides described. IMAC MALDI plates are available as a commercial MALDI affinity chip [Cardone et al., 1998; Tang et al., 2004], as monolayer of metal-ion complexes immobilized on MALDI surfaces [Ataka et al., 2006] or as polymer-modified MALDI plate [Xu et al., 2004]. Zirconium oxide-functionalized MALDI surfaces [Blacken et al., 2007] or immobilized titanium dioxide on MALDI plates [Lin et al., 2006] are used for MALDI plates modified for MOAC approaches The MALDI plate is coated with material which employs the principles described above. Only rinsing of the sample on the plate and addition of matrix are necessary prior MS analysis. However, there are other strategies like calcium phosphate precipitation [Reynolds et al., 1994] or charge-based fractionation [Nuhse et al., 2003] (strong anion/cation exchange, hydrophilic interaction chromatography)are available, but these are rather pre-separation techniques used to reduce sample complexity.

To detect proteins without staining, Western Blotting is an opportunity. It is a highly selective and sensitive detection with specific antibodies. In an additional electrophoretic step, proteins separated by means of PAGE, can be transferred and immobilized on a nitrocellulose membrane. With specific antibodies or lectins the proteins can be detected on the membrane directly. However, the main disadvantages are the non uniform protein transfer on the blotting membrane and the limited compatibility of the membrane material to MS

Nowadays, there are also several strategies to characterize the phosphoproteom on the protein level. Western blotting operates by means of specific antibodies against pSer, pThr and pTyr on a nitrocellulose membrane but no information of specific phosphorylation sited can be concluded [Kaufmann et al., 2001]. Another possibility to visualize phosphoproteins directly after electrophoretic separation without the need of antibodies is the use of specific fluorescent stains

(e.g. Pro-Q Diamond from *Invitrogen*) [Eymann et al., 2007] or highly selective Zn^{2+} ion chelators coupled to a fluorophor (*Wako Pure Chemical Industries, Ltd, Osaka*, Japan, provides a ready-made box called Phos-tag) [Nakanishi et al., 2007]. Also radioactive labeling via ^{32}P and ^{33}Pduring metabolic studies and visualization after gel electrophoretic or chromatographic separation is feasible and one of the most sensitive alternatives, called autoradiography. However, MS still remains the method of choice for detailed characterization of phosphorylated proteins. [Macek et al., 2009; Tichy et al., 2011].

1.6.4 Matrix choice for Phosphoproteomics using MALDI-TOF and TOF/TOF-MS

After enrichment, phosphopeptides are subsequently transferred to a sample plate, in the case of a MALDI approach. It is generally accepted that factors such as matrix solvent compositions highly affect the ionization efficiency of analyte molecules, respectively phosphopeptides. So the selection of an appropriate matrix is an important point to gain high quality mass spectra. [Cohen and Chait, 1996; Tichy et al., 2011].

Several matrices have been employed in phosphopeptide analysis including the matrices like [Zenobi and Knochenmuss, 1998] α – cyano – 4 - hydroxycinnamic acid (CHCA), 2,5 - dihydroxybenzoic acid (DHB) and 6 - trihydroxyacetophenone (THAP).Table 1.6 gives an overview of common MALDI matrices used in biological applications. Also the combination of matrices, e.g. CHCA and DHB, are reported in the literature [Lau et al., 2012]. In addition, ammonium salts, including diammonium hydrogen citrate (DAHC), ammonium acetate and ammonium phosphate [Asara and Allison, 1999; Zhang et al., 2008]as well as phosphoric acid [Kjellström and Jensen, 2004]have been used as matrix additives with respect to enhance ionization and improve the ion response of phosphopeptides during MALDI MS analysis. The additives appear to lower the charge state of the analyte, making detection easier. In case of ammonium salts, the ammonium cations form complexes with the negatively charged phosphate groups. During desorption/ionization, ammonia is completely evaporated, leaving the charged group in a neutral form containing protons as the counter ions $(H^+)_n$(phosphate^{-n}) [Zhu et al., 1996]. Therefore, the desorption/ionization efficiency for phosphopeptides is improved [Asara and Allison, 1999; Hou et al., 2010]. On the other hand, Kjellström and Jensen[Kjellström and Jensen, 2004] investigate the application of phosphoric acid as additive. They observe the presence of singly charged phosphopeptide dimer ions, singly charged phosphopeptide ions and doubly charged phosphopeptide ions in the same mass spectrum, and suggest that phosphoric acid improves the overall ionization efficiency and/or increases ion stability. However, the exact mechanism is not known and further investigations have to be done.

1.7 Mass Spectrometric Proteome Analysis using MALDI – MS

Identification of phosphorylated residues within proteins is very often done by MS. For this purpose, two complementary analysis strategies are currently used: bottom up and top down analyses. The bottom up approach deals with peptides derived from protein digests (e.g.tryptic digestion) and the resulting peptides are analyzed by MS. In the top down approach, intact protein ions are introduced into the gas phase, usually by ESI, and are then fragmented and analyzed, giving therefore the molecular mass of the intact protein as well as protein ion fragment ladders [Reinders and Sickmann, 2005]. The two different approaches are visualized in Figure1.14.

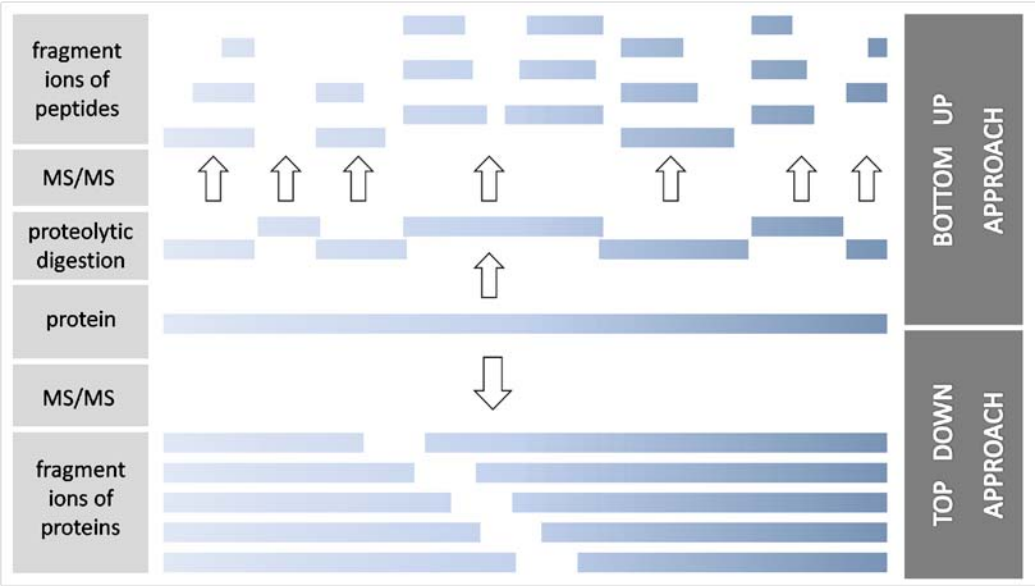


Figure 1.14 Strategy of Bottom Up and Top Down approaches

The bottom up approach is widely used for identification of proteins and the determination of details of their sequence and posttranslational modifications. In the bottom up approach, the peptide fragments, generated by an enzymatic digestion (e.g. trypsin) are analyzed in the gas phase by mass spectrometry in two stages. First, the masses of the peptides are determined and second, the peptide ions are fragmented to produce information on the sequence of the protein as well as its modifications. In the top down approach, the intact protein ions are under investigations. If a sufficient number of informative fragment ions are observed, this analysis can provide a complete description of the primary structure of the protein and its modifications. Although the molecular masses of intact proteins have been successfully measured by MALDI MS for some time [Chait and Kent, 1992; Han et al., 2006], it has proved difficult to produce extensive gas-phase fragmentation of intact protein ions, especially from large proteins. However, there are major challenges to deal with in a top down approach. A highly purified protein is usually necessary to get conclusive results which

means that the separation of protein isoforms or the isolation from complex samples is sometimes necessary if even possible [Chait, 2006]. In this research a bottom up approach was used.

1.7.1 Enzymatic Digestion

For an effective bottom up approach by MS, enzymatic protein degradation, a so called enzymatic digestion, is necessary. Prior digestion, the proteins were reduced and alkylated. In the reduction step, chemicals including a sulfhydryl or phosphin group (e. g. dithiotreitol) cleave disulfide bonds of cystine and cysteine to gain an optimal decay of the secondary and tertiary structure. During the alkylation, free SH – groups were converted with iodoacetamide into stable S-carboxy-amido-methylcysteine [Hale et al., 2004]. In this study, digestion was carried out using trypsin for accomplishing this task. However, digestion using alternative proteases such as AspN, chymotrypsin, GluC, or LysC is possible to gain peptides resulting from different specificities. Trypsin is a sequence specific serine protease and cuts the amino acid sequence after lysine or arginine. Trypsin is the most commonly used enzyme as Lys and Arg are quite frequent amino acids in proteins (5.5 % Arg and 5.8 % Lys -calculated from the UniProtKB/Swiss-Prot databank) [Gasteiger et al., 2005] giving therefore a high number of well defined peptides helpful for protein identification. The digestion can be carried out either directly in the gel (in-gel digestion) or in solution.

1.7.2 Peptide Mass Fingerprint for Protein Identification

After tryptic digestion the peptides are commonly analyzed by MALDI – MS, because it is fast, robust, easy to perform, sensitive, accurate, and tolerant to a certain level of various contaminants and can be performed automated. Protein identification can be performed using peptide mass fingerprint PMF.

After digestion, the generated peptides are investigated by MS determining their molecular masses (peptide mass fingerprint, PMF) or generating peptide fragments (peptide sequencing) [Aebersold and Goodlett, 2001]. High mass accuracy is mandatory in any case. In the case of a PMF, the list of experimentally obtained peptide masses are compared to theoretical peptide masses deduced from an *in-silico* digest of proteins stored in databases (e.g. NCBI database) [Thiede et al., 2005]. This can be done in an automated way by using freely accessible, web-based search programs like Mascot [Perkins et al., 1999],MS-Fit [Clauser et al., 1999]or Profound [Zhang and Chait, 2000]. The input of the used enzyme, the number of expected missed cleavage sites and fixed and variable artificial and biologically relevant modification, like oxidation, phosphorylation (at Ser, Thr, Tyr), pyro-glutamine formation or alike, the database search can be specified[Johnson et al., 2005]. By use of iodoacetamide, carboamidomethyl has to be considered as fixe modification

PMF is an effective tool for the identification of relatively pure proteins. Protein mixtures reduce the significance of the statistical result for the protein identification. Thus, the application of PMF in combination with proteins separated by 1D SDS – PAGE often fails, due to the presence of different proteins in one gel band. Therefore, protein identification cannot be performed by means of PMF for SDS PAGE separated samples and information for protein identification has to be gathered from– peptide sequences.

1.7.3 Peptide Sequencing for Protein Identification

As mentioned in chapter1.5.1.3 on page 19, PSD analysis allows the observation and identification of structurally informative fragment ions from decay taking place in the field-free region after the moment a selected precursor ion left the ion source. The goal of PSD analysis is to detect characteristic product ions and deduce the primary structure of the precursor molecule from that mass information. After selecting a precursor ion, different kinds of fragments are generated, according to the location of the cleavage relative to the peptide bond and the energy transferred to the peptide[Papayannopoulos, 1995]. The nomenclature of this fragmentation was defined by Roepstorff and Fohlman [Roepstorff and Fohlman, 1984] and is represented in Figure 1.15

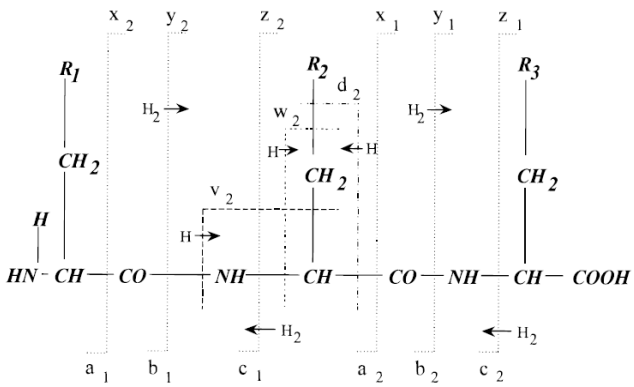


Figure 1.15 Nomenclature of peptide fragmentation described by Roepstorff and Fohlman in1984
Adapted from [Roepstorff and Fohlman, 1984]

The cleavage can occur on three bond types , the C_α-C, the C-N and the N-C_α bond, which yields six types of fragments that are respectively labeled a_n, b_n and c_n when the positive charge is kept on the N – terminus of the peptide and x_n, y_n or z_n when the positive charge is kept on the C-terminal side[Paizs and Suhai, 2005; Papayannopoulos, 1995]. The mass difference between the ions within a series allows the identification of the consecutive amino acids and thus the detection of the peptide sequence due to the characteristic elemental compositions and consequently characteristic masses (see Table 1.9).

Table 1.9 Monoisotopic and average mass of each one of the 20 common amino acids

Amino Acid	Code	Chemical Formula	Monoisotopic Mass [Da]	Average Mass [Da]
Glycine	G	C_2H_3ON	57.02146	57.0519
Alanine	A	C_3H_5ON	71.03711	71.0788
Serine	S	$C_3H_5O_2N$	87.03203	87.0782
Proline	P	C_9H_9ON	97.05276	97.1167
Valine	V	C_5H_9ON	99.06841	99.1326
Threonine	T	$C_4H_7O_2N$	101.04768	101.1051
Cysteine	C	C_3H_5ONS	103.00919	103.1388
Isoleucine	I	$C_6H_{11}ON$	113.08406	113.1594
Leucine	L	$C_6H_{11}ON$	113.08406	113.1594
Asparagine	N	$C_4H_6O_2N_2$	114.04293	114.1038
Aspartate	D	$C_4H_5O_3N$	115.02694	115.0886
Glutamine	Q	$C_5H_8O_2N_2$	128.05858	128.1307
Lysine	K	$C_6H_{12}ON_2$	128.09496	128.1741
Glutamate	E	$C_5H_7O_3N$	129.04259	129.1155
Methionine	M	C_5H_9ONS	131.04049	131.1926
Histidine	H	$C_6H_7ON_3$	137.05891	137.1411
Phenylalanine	F	C_9H_9ON	147.06841	147.1766
Arginine	R	$C_6H_{12}ON_4$	156.10111	156.1875
Tyrosine	Y	$C_9H_9O_2N$	163.06333	163.1760
Tryptophan	W	$C_{11}H_{10}ON_2$	186.07931	186.2132

Modified from [de Hoffmann and Stroobant, 2008]

For PSD experiments the predominant ions are a-, b-type, y-and z-type ions. In PSD sometimes also amino acid specific immonium ions occur with a molecular mass below 200 Da. This is especially helpful for interpretation as they provide a first indication of the amino acid composition of the peptide of interest.

As it is done for a PMF, also a peak list is submitted to protein database using web-based platforms, like Mascot or ProteinProspector. Again theoretically derived fragment ions are compared to actually measured ones, based on available fragmentation rules, and the protein or peptide search results are ranked according to statistical criteria as potential matches for the peptide of interest [Purcell and Gorman, 2001].

1.7.4 Phosphopeptide Analysis and Identification by Mass Spectrometry

The MS detection of phosphopeptides can be achieved in the negative as well as in the positive ion mode, but the unpredictable nature of negative ion fragmentation and the limited sequence information obtainable from the dissociation of peptide anions make the analyses very challenging [Savitski and Fälth, 2007]. So the method of choice is the fragmentation of positively charged ions for sequencing and the determination of modification sites. In case of the bottom up approach, peptides are subjected to PSD experiments for the identification of phosphorylated peptides [Trost et al., 2010].

During fragmentation modified peptides produce sequence specific fragments and also sometimes characteristic fragment ions that are specific for a defined type of modification (=reporter ions). Corresponding to this, it has been widely demonstrated that during fragmentation in the positive ion mode the labile pSer and pThr containing phosphopeptides will typically undergo β-elimination of phosphoester bond [Annan and Carr, 1996; Jornvall et al., 1991; Liao et al., 1994; Steen et al., 2001; Wang et al., 1993; Weijland et al., 1997]. pSer and pThr can be identified by MALDI –MS because they tend to loosephosphoric acid (- H_3PO_4), unlike pTyr residues, which are more stable and primarily lose meta-phosphoric acid (- HPO_3). Due to metastable decay of phosphorylated peptides, the mass differences Δ- 80 Da and Δ- 98 Da indicate the loss of either HPO_3 or H_3PO_4.

2 Materials and Methods

2.1 Cell Lysis

2.1.1 Chemicals

PRODUCT	COMPANY	QUALITY
Tris (Tris(hydroxymethyl) aminomethane)	Merck (Darmstadt, Germany)	99.8-100.1 %
HCl (Hydrochloric acid)	Merck (Darmstadt, Germany)	36 %
DL-DTT (dithiothreitol)	Sigma (St. Louise, MO, USA)	≥ 99.0 %
Glycerol	Merck (Darmstadt, Germany)	≥ 99.5 %, p.a.
Tween 20	Sigma (St. Louise, MO, USA)	no declaration
Toluol	Fluka Chemie AG (Buchs, Switzerland)	> 99.7 %
Phosphatase Inhibitor Kit: HALT™ Protease and Phosphatase Inhibitor Cocktail (100x) and 0.5 M EDTA solution (100x)	Thermo Scientific(Rockford, IL, USA)	no declaration (Lot. Nr.: ND170705)*
		no declaration
TCA (trichloroacetic acid)	Merck (Darmstadt, Germany)	≥ 99.5 %, p.a.
Urea	Merck (Darmstadt, Germany)	p.a.
Thiourea	Sigma (St. Louise, MO, USA)	≥ 99 %
CHAPS	Merck (Darmstadt, Germany)	≥ 99.0 %
Acetone	Merck (Darmstadt, Germany)	p.a.
Ultra high quality water (UHQ)	Millipore (Billerica, MA, USA)	Conductivity parameter = 18.2 mΩ.cm (at 25 °C)

* Lot Nr. is only mentioned for chemicals playing critical roles in the process (not mentioned for consumables).

2.1.2 Working Solutions

Lysis buffer (in total 10 ml):

50 mM Tris/HCl pH=8.0	0.0605 g
2 mM DTT	0.020 ml (1 M)
10 % (v/v) Glycerol	1.0 ml
0.5 % (v/v) Tween 20	0.05 ml
10 % Toluol (after pH adjustment)	1 ml
0.5 % Phosphatase Inhibitor/EDTA (10 µl/ml) (before use)	0.05 ml (per solution)

TCA - solution (in total 13ml):

TCA	10 g
UHQ	7 ml

DIGE buffer (10 ml):

30 mM Tris/HCl pH=9.5	0.0365 ml
7 M Urea	4,2 g
2 M Thiourea	1.52 g
4 % CHAPS	0.4 g
1 % Phosphatase Inhibitor/EDTA (10 µl/ml) (before use)	0.1 ml (per solution)

2.1.3 Protocol

The different *Trichoderma atroviride* samples were provided by the Institute of Chemical Engineering, TU Vienna. For the cultivation of the fungi, Potato – dextrose – agar (PDA) covered with cellophane was used. Incubation was carried out at 28 °C for up to five days, depending on the strain (*Trichoderma atroviride* $_{wt}$ grew faster than the Δ*tmk1* mutant). After harvesting the *Trichoderma* mycelia from the confrontation area (before the fungi contact each other) the mycelia were frozen with liquid nitrogen and then stored at - 80 °C. To gather 50 mg total dry weight, up to five plates of cultivated mycelia had to be collected.

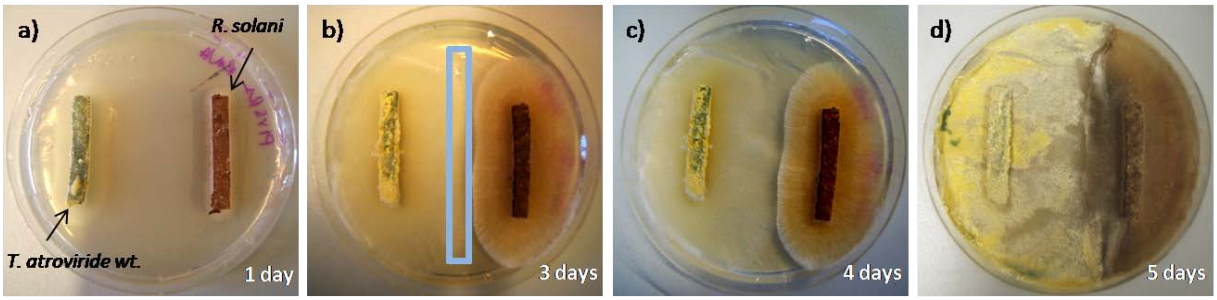


Figure 2.1 Different growth states of the confrontations on PDA
On the left side of the petridish *T. atroviride*$_{wt}$ was cultivated and on the opposite side *R. solani*. Pictures a) to d) show the growth behavior over five days. In b) the sample area is highlighted via a blue frame. There, the samples for the phosphoproteome analysis were taken, just before the two fungi contact each other (see c). After five days incubation at 28 °C, *T. atroviride*$_{wt}$ parasitizes *R.solani* and began to overgrow the phytopathogenic fungi (d).

50 mg of the dried cell mycelia were suspended in 0.8 ml of lysis buffer in a 15ml centrifuge tube and lysed under the assistance of sonication at 4 °C on an ice bath (intensity: 60 %; duration: two times for three seconds and one time for 10 seconds, *Branson Sonifier 250; Branson Ultrasonics, Danbury, CT, USA*). Lysed cells were centrifuged at 14 000 x g for 10 minutes at 4 °C to deplete cell debris. After centrifugation, three phases were separated, the toluol phase, an aqueous interphase and further depleted cell debris. The interphase was collected, divided into three equal parts (volume) and transferred into fresh centrifuge tubes (15 ml). For protein precipitation pre-cooled (- 80 °C) acetone was added (8 times the volume of the aqueous phase) and TCA solution (same volume as aqueous phase). This solution was left for 60 minutes at -20 °C. After centrifugation at 14 000 x g for 15 min at 4 °C the supernatant was removed and the protein precipitates were first washed with 20 ml of 80 %

acetone (-20 °C) and subsequently, two times with 2 ml acetone. Between the washing cycles centrifugation steps were carried out at 14 000 x g for 15 min at 4 °C for pellet formation. Finally the pellets were dried either at ambient conditions or in the vacuum centrifuge (*UNIVAPO 100 H, Uniquip Gemany*). After this, proteins were solubilized in approximately 100 µl of DIGE buffer at 4 °C over night. The three aliquots were combined and centrifuged a last time to remove insoluble particles.

2.2 Determination of the Protein Concentration – Bradford Assay

2.2.1 Chemicals

PRODUCT	COMPANY	QUALITY
Bovine serum albumin (BSA)	Sigma (St. Louise, MO, USA)	≥ 96 % (Lot Nr.: 129K197)*
Coomassie Brilliant Blue G 250	Fluka Chemie AG (Buchs, Switzerland)	no declaration
Phosphoric acid	Sigma (St. Louise, MO, USA)	≥ 85 %
Ethanol	Merck (Darmstadt, Germany)	p.a.

* Lot Nr. is only mentioned for chemicals playing critical roles in the process (not mentioned for consumables).

2.2.2 Equipment

PRODUCT	COMPANY
Nano Photometer	Implen (Munich, Germany)

2.2.3 Working Solutions

Bradford reagent (200 ml):

0.01 % Coomassie Brilliant Blue G 250	20 mg
1.6 M Phosphoric acid	20 ml
0.8 M Ethanol	9.4 ml
UHQ	ad 200ml

BSA – stock solution:

Stock solution BSA	1 mg/ml in diluted DIGE buffer

2.2.4 Protocol

The BSA – stock solution was diluted to concentrations of 10 µl/ml, 7 µl/ml, 4 µl/ml, 2 µl/ml and 1 µl/ml with the diluted DIGE buffer (100 µl each) for calibration. Also 100 µl blank was prepared (= 100 µl diluted DIGE buffer). Samples prepared according to 2.1.3 were diluted with UHQ in a ratio of 1:100. 100 µl of each sample (*Trichoderma atroviridae* and calibrants) were mixed with 900 µl fresh Bradford reagent (filtered through a filter paper from *Whatman® Schleicher &Schuell, Whatman*

Internatioinal, Maidstone, UK) giving a dilution factor of 1:1000 for each sample. Photometric measurements were carried out at 595 nm. Protein concentrations for the *Trichoderma atroviride* samples were determined using BSA for calibration. Usually a calibration curve with a correlation factor of 0.99 was achieved for the chosen concentration range.

2.3 Electrophoresis –SDS-PAGE

2.3.1 Chemicals

PRODUCT	COMPANY	QUALITY
Novex® 4 – 20 % TrisGlycin Gels 1.5 mm, 12 wells	Invitrogen (CA, USA)	no declaration (Lot Nr.: 12041653)*
Novex® TrisGlycin SDS Sample Buffer (2X)	Invitrogen (CA, USA)	no declaration
NuPAGE® Reducing Agent (10X)	Invitrogen (CA, USA)	no declaration (Lot Nr*.: 1035646)
Novex® TrisGlycin SDS Running Buffer (10X)	Invitrogen (CA, USA)	no declaration
Novex® Sharp Pre-stained Protein Standard	Invitrogen (CA, USA)	no declaration

* Lot Nr. is only mentioned for chemicals playing critical roles in the process (not mentioned for consumables).

2.3.2 Equipment

PRODUCT	COMPANY
Electrophoresis Power Supply EPS 301	Amersham Bioscience (Uppsala, Schweden)
Xcell*Surelock*® Mini Cell	Invitrogen (CA, USA)

2.3.3 Working Solutions

Running buffer (1X)

Novex® TrisGlycin SDS Running Buffer (10X)	100 ml
UHQ	900 ml

2.3.4 Protocol

For electrophoretic separation20 µl (referring to the determined protein concentration of approximately 8.14 µg/µl to achieve an average protein amount of 32 µg per gel lane) of the *Trichoderma atroviride* sample were mixed with 25 µl TrisGlycin SDS sample buffer (2X) and 5 µl of NuPAGE® reducing agent (10X). The samples were heated at 85 °C for two minutes. 20 µl of the prepared samples were loaded onto the gel, as well as 10 µl of the molecular weight marker. The upper chamber of the XCell*SureLock*® Mini-Cell was filled with 200 ml and the lower buffer chamber

with 600 ml of running buffer. Electrophoresis was carried out at a voltage of 125 V (constant) and an expected current of 35 mA (at the start of the electrophoresis), respectively 8-12 mA at the end for approximately 100 minutes.

2.4 Coomassie Brilliant Blue – MS compatible – Staining

2.4.1 Chemicals

PRODUCT	COMPANY	QUALITY
Ethanol	Merck(Darmstadt, Germany)	p.a.
Glacial acid	Merck(Darmstadt, Germany)	100 %
Coomassi Brilliant Blue R 250	Merck(Darmstadt, Germany)	for electrophoresis

2.4.2 Working Solutions

Fixing solution (100 ml):

50 % Ethanol	50 ml
10 % Glacial adic	10 ml
UHQ	ad 100 ml

Staining solution (100 ml)

Coomassie Brilliant Blue R 250	0.116 g
25 % Ethanol	25 ml
8 % Glacial adic	8 ml
UHQ	ad 100 ml

Destaining solution (100 ml):

35 % Ethanol	25 ml
8 % Glacial adic	8 ml
UHQ	ad 100 ml

2.4.3 Protocol

The gel was removed from the electrophoresis apparatus and washed shortly with UHQ to remove excessive buffer solution. Proteins were fixed by immersing the gel in the fixing solution for 30 minutes. After removal of the fixing solution the gel was stained in the staining solution for 10 minutes and destained over night with the destaining solution via mildly shaking at room temperature. Destaining solution was exchanged three times. Between every solvent exchange the gel was rinsed shortly with dH_2O.

2.5 Digestion

2.5.1 Chemicals

PRODUCT	COMPANY	QUALITY
Trypsin rec.	Roche (Mannheim, Deutschland)	proteomics grade (Lot Nr.: 12837723)*
HCl (Hydrochloric acid)	Merck (Darmstadt, Germany)	37 %
NH_4HCO_3	Fluka Chemie AG (Buchs, Switzerland)	≥99.5 %
NH_3	Merck (Darmstadt, Germany)	25 %
DTT (Dithiothreitol)	Sigma (St. Louise, MO, USA)	≥ 99.0 %
IAA (Iodoacetamic acid)	Sigma (St. Louise, MO, USA)	≥ 99.0 %
Acetonitrile (ACN)	Merck (Darmstadt, Germany)	p.a.
Formic acid	Acros (New Jersey, USA)	99 %
TFA (Trifluroacetic acid)	Riedel de Haen (Seelze, Germany)	99 %

* Lot Nr. is only mentioned for chemicals playing critical roles in the process (not mentioned for consumables).

2.5.2 Working Solutions

Trypsin reconstitution solution (10mM HCl):

1 M HCl	100 µl
UHQ	9.9 ml

Trypsin reconstitution:

Trypsin	25 µg
Trypsin reconstitution solution	250 µl
10 µl aliquots were stored at – 20 °C. Before use, 90 µl digestion buffer were added (trypsin concentration 10 ng/µl).	

100 mM NH_4HCO_3, pH = 8.5:

NH_4HCO_3	790.6 mg
UHQ	ad 100 ml
pH adjustment with NH_3 to 8.5	

Digestion buffer:

100 mM NH_4HCO_3	2.5 ml
Acetonitrile	500 µl
UHQ	7 ml

Reducing solution I (400 mM DTT)- for In-Solution Digestion:

DTT	61.0 mg
Digestion buffer	1 ml

Reducing solution II (10 mM DTT)- for In-Gel Digestion:

DTT	1.54 mg
Digestion buffer	1 ml

Alkylation solution I (800 mM IAA) – for In-Solution Digestion:

IAA	140.1 mg
NH_4HCO_3	1 ml

Alkylation solution II (54 mM IAA) – for In-Gel Digestion:

IAA	10 mg
NH_4HCO_3	1 ml

2.5.3 Protocols

2.5.3.1 Protocol for In-Solution Digestion

20 mg of protein were dissolved in 500 µl 100 mM NH_4HCO_3 and 500 µl double distilled UHQ. The alkylation was carried out with 50 µl reducing solution I for 60 minutes at 37 °C, followed by the reducing step with 50 µl alkylation solution I at room temperature for 30 minutes in the dark. Then again 50 µl alkylation solution I was added and incubated for 15 minutes at room temperature under mild agitation. The pH value was readjusted to pH 8.5 with NH_3. 100 µl 10 ng/µl trypsin solution was added and digested for 10 minutes in a domestic microwave (TCM microwave 230 V – 50 Hz, *Tchibo GmbH, Hamburg, Germany*) at approx. 170 W. Additional digestion was carried out at 37 °C over night. After digestion the pH was adjusted with formic acid to 3 and the solution was dried in the vacuum centrifuge. Dried peptides can be stored at this point at minus 20 °C. For MALDI-TOF-MS measurement the peptides were dissolved in 10 µl 0.1 % TFA and sonicated briefly.

2.5.3.2 Protocol for In-Gel Digestion

Every lane of the gel was divided into 14 parts. Gel sections varied according to the protein pattern. Gel sections were excised with a scalpel. The excised parts were further cut into 1 mm^3 pieces with a clean scalpel and transferred to a clean 0.5 ml sample tube. Simultaneously, a blank gel piece containing no protein was cut out and processed in the same way as all other gel pieces. The gel particles were washed with UHQ and UHQ/ACN 1:1 (v/v) – four changes per solvent and each incubation step lasts 15 min. The solvent volumes used in the washing steps should roughly equal the gel volume. All liquids were removed and enough acetonitrile was added to cover the gel particles. After the gel pieces shrunk and became milky and sticky, the ACN was removed and the gel pieces were rehydrated with 100 mM NH_4HCO_3 for 5 minutes followed by an addition of the same amount of ACN (to get a 1:1 mixture of NH_4HCO_3:ACN) and a 15 minute incubation. All liquids were removed and the gel pieces were dried in a vacuum centrifuge. For protein reduction the gel particles were swollen in reducing solution II and incubated for 45 minutes at 50-56°C under mild agitation. Sample

tubes were chilled to room temperature and the excess liquid was removed after centrifugation. Protein alkylation has to be carried out with freshly prepared alkylation solution at room temperature by adding enough alkylation solution II and incubation for 30 minutes in the dark. After removing the alkylation solution II, gel particles were washed with 100 mM NH_4HCO_3 (5 minutes incubation) and an equal volume of ACN to achieve a ratio of 1:1 NH_4HCO_3:ACN was added (15 minutes incubation). This last washing step was repeated until all the gel particles appeared completely transparent; the Coomassie stain should be removed at this time. Clear gel pieces were dried in the vacuum centrifuge. Gel particles can be stored at this point at -20 °C. Gel particles were rehydrated by adding 15 µl 10 ng/µl trypsin solution and incubated for 45 minutes at room temperature. 200 µl digestion buffer was added and the digestion was again carried out in a first step for 10 minutes in a domestic microwave at approx. 170 W and then at 37 °C over night. After overnight digestion a sufficient volume of 50 mM NH_4HCO_3 was added to cover the gel pieces and incubated for another 15 minutes for peptide extraction. An equal volume of ACN was added and the peptides were extracted again for 15 minutes. The supernatant, containing the peptides, was recovered in a new sample tube. The extraction of peptides from the gel particles was repeated two times with 1 % formic acid and ACN (1:1, v/v). All extracts were pooled. The combined supernatants were dried in the vacuum centrifuge. The peptides were dissolved in 10 µl 0.1 % TFA and sonicated briefly.

2.6 Desalting

2.6.1 Chemicals

PRODUCT	COMPANY	QUALITY
TFA (Trifluoroacetic acid)	Riedel de Haen (Seelze, Germany)	99 %
ACN (Acetonitrile)	Merck(Darmstadt, Germany)	p.a
Formic acid	Acros (New Jersey, USA)	99 %
ZipTip® C_{18}	Millipore (Hertfordshire, UK)	no declaration (Lot Nr.: R2CA9828, MKBL5757, R2H412629)*
HyperSep-96 C_{18} Plate	Thermo Scientific (Rockford, IL, USA)	no declaration (Lot Nr.: 60300-428)*
C_{18} Empore ™ Extraction Discs	Supelco(Bellefonte, USA)	no declaration (Lot Nr.:320465)*

* Lot Nr. is only mentioned for chemicals playing critical roles in the process (not mentioned for consumables).

2.6.2 Equipment

PRODUCT	COMPANY
Plate Prep Vacuum Manifold	Supelco (Bellefonte, USA)

2.6.3 Working Solutions

0.1 % TFA – solution (100 ml):

TFA	100 µl
UHQ	ad 100 ml

0.25 % TFA – solution (100 ml):

TFA	250 µl
UHQ	ad 100 ml

Elution solution for desalting withHyperSep-96 C_{18} Plate (100 ml):

ACN	80 ml
0.1 % TFA	20 ml

2.6.4 Protocols

2.6.4.1 Protocol for Desalting with ZipTip® C_{18}Tip

For ZipTip® purification, the ZipTip® pipette tip was wet three times with 100 % ACN and equilibrated with 0.1 % TFA (three cycles). The peptides were bound by sucking in the dissolved peptides three times. After washing the ZipTip® pipette three times with 0.1 % TFA the peptides were eluted with either 5 µl 0.1 % TFA/ACN (1:1) or directly on the MALDI – target with 2 µl matrix solution.

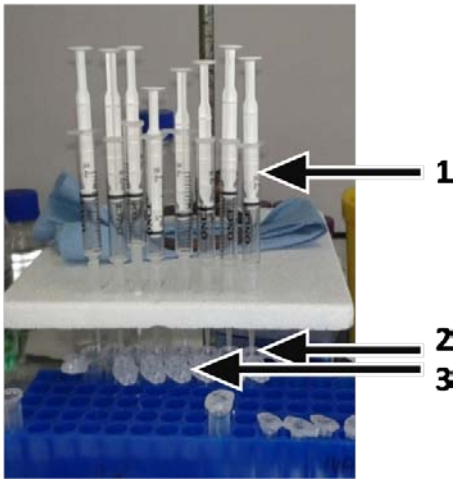
2.6.4.2 Protocol for Desalting with HyperSep-96 C_{18} Plate

For desalting with the HyperSep-96 C_{18} Plate the resin was washed with 1 ml ACN, followed by wetting the cartridge three times with 1 ml 0.25 % TFA (using depression). The peptides were loaded by flowing through the C_{18} resin with a flow rate of 1 ml/min (vacuum manifold, vacuum controlled via a manometer, pressure control set to – 20 kPa). After the washing step (four times with 0.25 % TFA) the peptides were eluted with 100 µl of elution buffer (using depression).

2.6.4.3 Protocol for Desalting with self-made Strata-X column

The Strata-X columns were custom-made by stacking four layers of C_{18} filter sheets in the top of a 0.5 µl – 20 µl Eppendorf® tip.

The desalting with the self-made Strata-X column is the same procedure like ZipTip® C_{18}desalting. First, the resin was wetted three times with 100 % ACN, and equilibrated three times with 0.1 % TFA. The peptides were bound by pressing 100 µl of the sample through the filter sheets. After washing



the columns three times with 0.1 % TFA the peptides were eluted with 20 µl 0.1 % TFA/ACN (1:1) into a new 0.5 µl sample tube.

Figure 2.3 Composition of the self made Strata-X tips
(1) disposable syringe, (2) four layers of C_{18}Empore ™ Extraction Discs in the top of an Eppendorf-tip (3) sample tubes for collecting the elution fraction

2.7 Enrichment

2.7.1 Chemicals

PRODUCT	COMPANY	QUALITY
Pierce ® *Magnetic Titanium Dioxide Phosphopeptide Enrichment Kit*	Thermo Scientific (Rockford, IL, USA)	no declaration (Lot Nr.: NI175935, NE172203)*
GE Healthcare *TiO2 Mag Sepharose*Kit	GE Healthcare(Buckinghamshire, UK)	no declaration (Lot Nr.: 380527A)*
Pierce® *Fe-NTA Phosphopeptide Enrichment Kit*	Thermo Scientific (Rockford, IL, USA)	no declaration (Lot Nr.: MI160304)*
TitansphereTiO 5µm	GL Sciences (Tokyo, Japan)	no declaration (Lot Nr.: ZQ5-3289-42)*
ACN (Acetonitrile)	Merck(Darmstadt, Germany)	p.a.
Glycolic acid	Alfa Aesar(Karlsruhe, Germany)	98 %
TFA (Trifluoroacetic acid)	Riedel de Haen(Seelze, Germany)	99 %
NH_3	Merck(Darmstadt, Germany)	25 %
Lactic acid	Sigma(St. Louise, MO, USA)	≥ 85 %
FA (Formic acid)	Acros(New Jersey, USA)	99 %

* Lot Nr. is only mentioned for chemicals playing critical roles in the process (not mentioned for consumables).

2.7.2 Protocol for *Pierce® Magnetic Titanium Dioxide Phosphopeptide Enrichment Kit*

2.7.2.1 Equipment

PRODUCT	COMPANY
MagnaBind™ Magnet for 96-Well Plate Separator	Thermo Scientific(Rockford, IL, USA)

2.7.2.2 Working Solutions

Binding Buffer:

The number of samples was multiplied by 1 590 µl to determine the total volume of binding buffer required. 5 vol% were added for excess. Equal volumes of ACN and *Binding Buffer*(stock)were mixed to obtain a homogenous solution.

Washing Buffer:

The number of samples was multiplied by 200 µl to determine the total volume of washing buffer required. 5 % were added for excess. Equal volumes of ACN and *Washing Buffer* (stock)were mixed to obtain a homogenous solution.

2.7.2.3 Protocol

Before use all plastic parts were rinsed three times with ACN to minimize contamination with polymers leaching from the plastics. The number of samples plus one was multiplied by 10 µl to determine the total volume of magnetic beads required. This calculated volume of *20x TiO_2 Magnetic Beads* was placed into a proper (i.e. 15 ml) polypropylene conical tube. To ensure homogeneity, the *20x TiO_2 Magnetic Beads* were mixed thoroughly before use by gentle vortexing. 190 µl of prepared binding buffer for every 10 µl of beads were added and again mixed thoroughly. Into each well of the 96-well plate, 200 µl of the bead suspension were pipetted and the 96-well PCR plate were placed onto the magnetic plate separator for one minute, this will collect the beads on the bottom, so that the supernatant can remove easier. The plate was removed from the magnet and 200 µl of prepared binding buffer were quickly added to the beads. This washing step was repeated twice. The plate was placed onto the magnetic plate separator for one minute and subsequently, the binding buffer was removed. 100 µl of the desalted sample were acidified with 2 µl of pure formic acid to get a formic acid concentration of 2% and added to the beads. The sample was aspirated three to four times to ensure homogeneity. The plate was placed on the magnetic separator for one minute and the supernatant was removed. For removing unbound components soluble in the binding buffer, 200 µl of the binding buffer were quickly added to resuspend the beads after removing the plate from the magnet. Incubation on the magnetic separator took place for one minute and the supernatant was again removed. This step was repeated three times. The plate was removed from the magnet and 200 µl of washing buffer were quickly added to again resuspend the beads. The plate was placed on the magnetic separator for one minute and the supernatant was completely removed. The plate was removed from the magnet and 30 µl of *Elution Buffer* were added and aspirated a few times to ensure complete coating of the beads with buffer. Incubation took place at room temperature for 10 minutes. The plate was placed on the magnetic separator for one minute and then the

supernatant containing eluted phosphopeptides was transferred into a fresh sample tube. The samples were dried in a vacuum centrifuge and suspended in 10 µl aqueous solution containing 5 % ACN and 1 % FA in the case of the relevant biological samples or in 10 µl 0.1 % TFA for the evaluation experiments. A desalting step with ZipTip® C_{18} Tips was followed before MALDI-TOF-MS analysis.

2.7.3 Protocol for *Pierce® Fe-NTA Phosphopeptide Enrichment Kit*

2.7.3.1 Equipment

PRODUCT	COMPANY
Centrifuge	Sigma (St. Louise, MO, USA)

2.7.3.2 Working Solutions

Wash Buffer A (per spin column):

Wash Buffer 2x Stock	150 µl
UHQ	150 µl

Wash Buffer B (per spin column):

Wash Buffer 2x Stock	150 µl
ACN	30 µl
UHQ	120 µl

2.7.3.3 Protocol

All plastic parts were rinsed three times with ACN to minimize contamination with polymers leaching from the plastics. The sample was dried in a vacuum centrifuge and solubilized in 200 µl *Binding Buffer*(including in the *Pierce® Fe-NTA Phosphopeptide Enrichment Kit*). The prepared sample was added to a Fe-NTA spin column and incubated for 20 minutes at room temperature under mild agitation. The bottom tab of the column was removed and the column was placed on top of a 2 ml microcentrifuge tube. Centrifugation was carried out at 1 000 x g for one minute (centrifuge conditions were the same for every washing step). The column was transferred to a new 2 ml sample tube. 100 µl wash buffer A were added to the spin column and the column material was gently mixed prior centrifugation. This washing step was repeated once with buffer A and after transferring to a new 2 ml sample tube, the same washing procedure was done with wash buffer B. 100 µl of UHQ were added and the affinity material was gently mixed prior centrifugation. The column was transferred to a new 2 ml collection tube and the elution was carried out by adding 50 µl of *Elution Buffer* to the resin and incubates the material for 3 – 5 minutes at room temperature. The column was placed on top of a 2 ml new sample tube and centrifuged at 1 000 x g for one minute. The

phosphopeptide eluate was retained for analysis. The elution step was repeated two additional times and the elution fractions were pooled. The enriched phosphopeptides were acidified by adding 200 µl of 2.5 % TFA. The samples were dried in a vacuum centrifuge and suspended in 10 µl 0.1 % TFA. A desalting step with ZipTip® C_{18} Tips was followed for MALDI analysis.

2.7.4 Protocol for *GE Healthcare TiO_2 Mag Sepharose*

2.7.4.1 Equipment

PRODUCT	COMPANY
Magnetic Particle Concentrator	Invitrogen (CA, USA)

2.7.4.2 Working Solutions

Binding Buffer (5 ml):

Glycolic acid	380.25 mg
ACN	4 ml
TFA	0.50 ml
UHQ	ad 5ml

Wash Buffer (5 ml):

ACN	4 ml
TFA	0.05 ml
UHQ	ad 5ml

Elution Buffer (5 ml):

NH_3	1 ml
UHQ	ad 5ml

2.7.4.3 Protocol

50 µl of medium slurry were added to a 1.5 ml sample tube. The sample tube was placed in the magnetic rack to collect magnetic beads at the bottom and after one minute the storage solution was removed. The equilibration was carried out with 500 µl binding buffer by manual agitation to resuspend the medium. The liquid was removed after one minute incubation on the magnetic rack. The dried sample was solubilized in 100 µl binding buffer and added to the beads. The following incubation took place at room temperature for 30 minutes in a mixer suitable for 1.5 ml sample tubes. For the removal of the liquid, the sample tube was placed in the magnetic rack for one minute. Then, three washing steps followed. Washing step one included the addition of 500 µl binding buffer, resuspending the medium by manual agitation a few times and removing the liquid after incubation(1 min in the magnetic rack). The other two washing steps were performed the same way,

but wash buffer was used instead of the binding buffer. Final elution of the phosphopeptides was performed by adding 50 µl elution buffer and incubation for 5 minutes in a mixer. After bead separation in the magnetic rack, the supernatant was collected and transferred in a 0.5 ml new sample tube. The elution step was repeated once. The samples were dried in a vacuum centrifuge and suspended in 10 µl 0.1 % TFA. A desalting step with ZipTip® C_{18} Tips was followed for MALDI analysis.

2.7.5 Protocol for *Non Magnetic TiO_2Phosphoenrichmnent*

2.7.5.1 Equipment

No additional equipment was needed for this enrichment method.

2.7.5.2 Working Solutions

Loading Buffer (2 ml):

ACN	1600 µl
TFA	100 µl
Lactic acid	211.96 µl
UHQ	88.04 µl

Wash Buffer 1 (2 ml):

ACN	1600 µl
TFA (1 %)	400 µl

Wash Buffer 2 (2 ml):

ACN	400 µl
TFA (0.1 %)	1600 µl

2.7.5.3 Protocol

After digestion and ZipTip® C_{18} Tips desalting as prepurification step the sample was dried in a vacuum centrifuge and solubilized in 100 µl 0.1 % TFA. After adding 200 µl loading buffer the content was mixed gently to ensure homogeneity. 10 mg TiO_2 beads were added and incubated at room temperature for 15 minutes prior centrifugation at 7 000 x g for 4 minutes (centrifugation conditions were the same for every centrifugation step). The supernatant was removed carefully. To minimize the bead loss, up to 10 µL of liquid were left in the sample tube. 100 µl of loading buffer were added, gently mixed and centrifuged. This was repeated two times. The beads were washed with 100 µl wash buffer 1 and centrifuged to remove the supernatant. The washing step was repeated once with

wash buffer 1 and twice with wash buffer 2. Then, the beads were dried in a vacuum centrifuge and 30 µl of NH_3 (pH = 11) were added to elute phosphopeptides. Incubation for 15 minutes and a centrifugation step followed. The supernatant was retained in a new collection tube and dried in a vacuum centrifuge. The dried enriched phosphopeptides were solubilized in 14 µl FA and 4 µl 0.1 % TFA. The samples were dried in a vacuum centrifuge again and suspended in 10 µl 0.1 % TFA. A desalting step with ZipTip® C_{18} Tips was followed for MALDI analysis.

2.8 Matrices

2.8.1 Chemicals

PRODUCT	COMPANY	QUALITY
CHCA (α-cyano-4-hydroxycinnamic acid)	Aldria(Steinheim, Germany)	97 % (Lot Nr.: 28166-41-8)*
DHB (2,5-dihydroxy-benzoic acid)	Fluka Chemie AG (Buchs, Switzerland)	99 % (Lot Nr.: 1294972)*
THAP (2´,4´,6´,-trihydroxy-acetophenon)	Fluka Chemie AG (Buchs, Switzerland)	≥ 99.5 % (Lot Nr.: BCB66917)
$(NH_4)_2HPO_4$(Di-ammonium hydrogen phosphate)	Fluka Chemie AG (Buchs, Switzerland)	≥ 99 %
$NH_4H_2PO_4$ (Ammonium di-hydrogen phosphate)	Alfa Aesar(Karlsruhe, Germany)	≥ 98 %
DHAC (di-Ammonium hydrogen citrate)	Fluka Chemie AG (Buchs, Switzerland)	≥ 99 %
H_3PO_4(Phosphoric acid)	Sigma(St. Louise, MO, USA)	≥ 85 %
ACN (Acetonitrile)	Merck(Darmstadt, Germany)	p.a.
TFA (Trifluoroacetic acid)	Riedel de Haen(Seelze, Germany)	99 %

* Lot Nr. is only mentioned for chemicals playing critical roles in the process (not mentioned for consumables).

2.8.2 Working Solutions

Table 2.1 List of the different matrices, matrix combination and the required solutions

	Matrix	Compound	Concentration	Solution
1	CHCA	α-cyano-4-hydroxycinnamic acid	3 mg/ml 5 mg/ml 10 mg/ml	50 % ACN, 0.1 % TFA
2	DHB	2,5-dihydroxybenzoic acid	5 mg/ml 10 mg/ml	50 % ACN, 1 % H_3PO_4
3	THAP	2´,4´,6´,-trihydroxy-acetophenon	5 mg/ml 10 mg/ml	DHAC: 50 % ACN + 50 mg/ml DHAC THAP/DHAC 9:1(v/v)

4	CHCA/DHB	CHCA / DHB 9:1 (v/v)	10 mg/ml CHCA and 10 mg/ml DHB	**CHCA**: 50 % ACN, 0.1 % TFA **DHB**: 50 % ACN, 1 % H_3PO_4
5	CHCA + Additiv 1*	CHCA / $(NH_4)_2HPO_4$ 1:1 (v/v)	5 mg/ml CHCA and 1 mM $(NH_4)_2HPO_4$	**CHCA**: 50% ACN, 0.1% TFA **$(NH_4)_2HPO_4$**: ACN/H_2O1:1 (v/v)
6	DHB + Additiv 2*	DHB / $(NH_4)_2HPO_4$ 1:1 (v/v)	7.5 mg/ml DHB and 10 mM $(NH_4)_2HPO_4$	**DHB**: 50% ACN, 1% H_3PO_4 **$(NH_4)_2HPO_4$**: ACN/H_2O 1:1(v/v)
7	DHB + Additiv 3*	DHB / $NH_4H_2PO_4$ 1:1 (v/v)	7.5 mg/ml DHB and 10 mM $NH_4H_2PO_4$	**DHB**: 50 % ACN, 1 % H_3PO_4 **$NH_4H_2PO_4$**: ACN/H_2O 1:1 (v/v)

*1 µl additiv was added on the dried droplet spot

2.8.3 Protocol

Four different matrices, including a combination of CHCA and DHB, with varying concentrations were tested with or without the addition of buffers (see Table 2.1). The different matrices were prepared, sonicated briefly and spotted either in the dried droplet technique [Kemptner et al., 2009] or used as elution solvent for ZipTip® C_{18}desalting.

2.9 Mass Spectrometry

2.9.1 Instrumentation

MS analyses were carried out on two different mass spectrometers. For the evaluation of a proper sample method, including testing the different desalting methods, enrichment strategies and matrices, an AXIMA – CFR$^+$ mass spectrometer (*Shimadzu Biotech Kratos Analytical, Manchester, UK*), operating with a pulsed nitrogen laser was used. The analyses of biological *Trichoderma atroviride* samples were carried out on an UltrafleXtreme (*BRUKER Daltonics, Bremen, Germany*), operating with a modified Nd:YAG (neodymium-doped yttrium aluminum garned) laser [Holle et al., 2006]. Data were processed with the software of the manufacturers. To calibrate the instrument an external calibration, with a mix of 10 standard peptides, was used. The different calibration peptides are listed in the Table 2.2.

Table 2.2 Calibration mix with 10 different standard peptides

Calibration Peptides	*m/z* of $[M+H]^+$ monoisotopic	*m/z* of $[M+H]^+$ average	[MH]+	Sequence
Bradykinin 1-5	573.310	573.665	C27H41N8O6	RPPGF
Bradykinin 1-7	757.400	757.858	C35H53N10O9	RPPGFSP

Angiotensin 2	1046.54	1047.189	C50H72N13O12	DRVYIHPF
Angiotensin 1	1296.69	1297.486	C62H90N17O14	DRVYIHPFHL
Glu – 1 – fibrinogen	1570.68	1571.583	C66H96N19O26	EGVNDNEEGFFSAR
N – acetyl – Renin	1800.94	1802.063	C87H126N21O21	AcDRVYIHPFHLLVYS
ACTH fragement 1-17	2093.09	2094.427	C95H146N29O23S	SYSMEHFRWGKPVGKKR
ACTH fragment 18-39	2465.19	2466.681	C112H166N27O36	RPVKVYPNGAEDESAEAFPLEF
ACTH fragment 7-38	3657.93	3660.131	C167H258N47O46	FRWGKPVGKKRRPVKVYPNGAEDES AEAFPLE

2.9.2 Protein Mass Fingerprint Analysis

2.9.2.1 PMF – Analysis for Method - Evaluation

For the PMF analyses for the evaluation methods on the AXIMA – CFR$^+$ the laser power was set between 58 and 72 depending on the matrix used. Mass spectra were acquired using the reflectron mode from 500 – 4000 Da with the delayed extraction set to 2000 Da. Approximately 2000 shots were acquired manually for each mass spectrum.

2.9.2.2 PMF – Analysis for *Trichoderma atroviride* Samples

The PMF analyses were carried out on an UltrafleXtreme with a laser power of 33 %. Mass spectra were acquired using the reflectron mode from 600 – 4000 Da with the delayed extraction set to 2000 Da. In sum, 4000 shot were added to acquire a mass spectrum.

2.9.3 Peptide Sequencing

2.9.3.1 Peptide Sequencing using PSD with the AXIMA – CFR$^+$

The PSD spectra were obtained using the reflectron mode and an increased laser power of 85 – 110. A 15 Da ion gate was set and up to 4500 unselected single profiles per spectra with a delayed extraction of 2000 Da were used. These spectra were smoothed with the Savitsky – Golay algorithm [Savitzky and Golay, 1964], (peak width was set to 25 and the smoothing filter width set to 15). Also a baseline subtraction with a baseline filter width of 60 was done.

2.9.3.2 Peptide Sequencing using LIFT-TOF/TOF with the UltrafleXtreme

All MS/MS spectra were measured in the LIFT-TOF/RTOF mode without the addition of extra gas. Up to 3600 selected single profiles per spectra (depending on the quality of the single spectrum; minimal conditions 5 peaks with an S/N ratio > 5), with an ion gate of ± 7 % of the parental ion´s *m/z* value, were added with a delayed extraction of 2000 Da. All MS^2 spectra were processed with the

preinstalled LIFT-method script (Smoothing: algorithm = Savitzky – Golay, width = 0.15 m/z, cycles = 4; Baseline subtraction: select algorithm = TopHat).

2.9.4 Data Analysis

Data of the MS analyses (PMF, PSD, LIFT-TOF/TOF) were searched either in MASCOT (http://matrixscience.com)[Koenig et al., 2008; Perkins et al., 1999] or with the free software program *mMass* (Version 5.3.0.0 ; www.mmass.org)[Strohalm et al., 2008].

Search parameters are listed in Table 2.3.

Table 2.3 Search parameters for data analysis

Category		Search parameter
Database		NCBInr
Taxonomy		Fungi
Enzyme		Trypsin
Partials		≤ 2
Global (fix) modification		Carbamindomethyl (C)
Variable modification		Gln -> pyro-Glu (N-term Q)
		Oxidation (M)
		Phospho (ST)
		Phospho (Y)
AXIMA – CFR^{+}	**Peptide tolerance PMF**	± 0.5 Da
	Mass type PMF	Monoisotopic
	Peptide tolerance PSD	± 0.8 Da
	Mass type PSD	Average
UltrafleXtreme	**Peptide tolerance PMF**	No database search*
	Mass type PMF	No database search*
	Peptide tolerance MS^{2}	± 0.8 Da
	Mass type MS^{2}	Monoisotopic

*no database search was done for PMF gaining from MALDI-LIFT-RTOF/TOF-MS, because the UltrafleXtreme was used to investigate the whole phosphoproteome (digested, desalted and phosphor enriched) from *Trichoderma atroviride* samples, not specific proteins. This approach makes the use of a database search for PMF senseless.

3 RESULTS AND DISCUSSION

3.1 Overview

Phosphorylations of proteins play an important and critical role in different control mechanisms, like activation or inactivation of mycoparasitism, a strategy of *Trichoderma atroviride* to antagonize phytopathogenic fungi [Trost et al., 2010]. The analysis and identification of phosphoproteins is a challenging task for any analytical method, due to their low relative abundance, low stoichometry and the dynamic regulation [Dunn et al., 2010; Mann et al., 2002]. These facts are the reason for evaluation of a proper sample preparation method before identification of the phospho - proteins of *T. atroviride*. For the sample preparation steps different matrices, desalting strategies and phosphopeptide enrichment methods were compared. Specific phosphopeptide enrichment is necessary and represents possibly the most widely used approach in phosphoproteomics [Tichy et al., 2011].

3.2 Evaluation of Sample Preparation Methods

The evaluations of proper sample preparation methods were performed on three different points of applications, evaluation of the MALDI matrix, the desalting method and the enrichment strategy.

α-Casein (from bovine milk, *Sigma Aldrich, Germany, Lot Nr.: 075K7425V*) was used to develop an adequate sample preparation strategy. Peptides were produced by using in-solution digestion with trypsin (see also chapter2.6). Table 3.1displays the methods, which were tested and the criteria for evaluation.

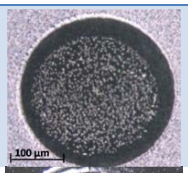
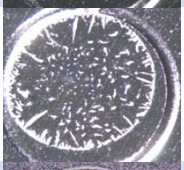
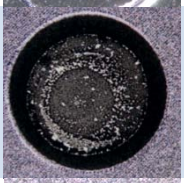
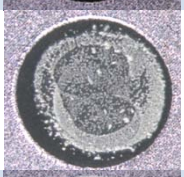
Table 3.1 Overview of the methods, that had to be evaluated and their desirable effects

MALDI – Matrix	Desalting method	Enrichment strategy
• Reaching a high sequence coverage for PMF • Avoiding the loss of phosphorylation during ionization	• Minimize loss of peptides • Eliminating interfering substances	• Achieving a highly selective enrichment of phosphopeptides • Removing non-phosphorylated peptides

3.2.1 MALDI – Matrix

As mentioned in chapter 1.6.4eight different matrices, including pure matrices as well as matrix combination and matrices with additives, were tested. A summary of all matrices used in this study is given inTable 3.2. In this table microscopic images (recording with a *Nikon SMZ 800 Microscop, Tokio, Japan*) of the matrix spots are included.

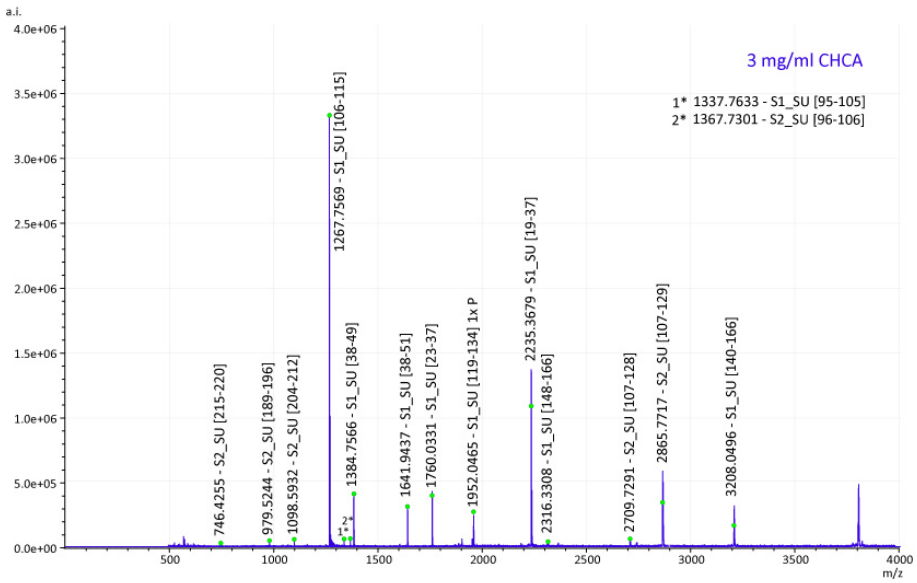
Table 3.2 List of the matrices used in this evaluation approach.

Matrix	Compound	Concentration	Picture of the matrix spot
CHCA	α-cyano-4-hydroxycinnamic acid	3 mg/ml* 5 mg/ml 10 mg/ml	
DHB	2,5-dihydroxybenzoic acid	10 mg/ml	
THAP	2´,4´,6´,-trihydroxy-acetophenon	5 mg/ml 10 mg/ml*	
DHAP	2´,6´,-dihydroxy-acetophenone	10 mg/ml	
CHCA/DHB	CHCA / DHB 9:1 (v/v)	10 mg/ml CHCA and 10 mg/ml DHB	
CHCA + Additive 1	CHCA / $(NH_4)_2HPO_4$ 1:1 (v/v)	5 mg/ml CHCA and 1 mM $(NH_4)_2HPO_4$	
DHB + Additive 2	DHB / $(NH_4)_2HPO_4$ 1:1 (v/v)	7.5 mg/ml DHB and 10 mM $(NH_4)_2HPO_4$	
DHB + Additive 3	DHB / $NH_4H_2PO_4$ 1:1 (v/v)	7.5 mg/ml DHB and 10 mM $NH_4H_2PO_4$	

* if different concentrations were tested, the concentration marked with a star is represented in the image

The different matrices were tested using α-casein, digested with trypsin, desalted with ZipTip® and spotted by direct elution with the matrix on the target. If additives were used, 1 µl of the additive

was added on the dried droplet. The different spectra were obtained by using the AXIMA – CFR^{+} *(Shimadzu Biotech Kratos Analytical*). In Figure 3.1 to Figure 3.11 the spectra of the different matrices are shown with focus on sequence coverage of α-casein, divided into the two subunits αS1 subunit and αS2 subunit. Unassigned peaks are related to matrix cluster, background peaks and trypsin related peaks. Getting a better overview of the sequence coverage, a table lists the sequence coverage of the different matrices (Table 3.3).



Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25386.1140	25401.5719	44.4 %	78.8 %

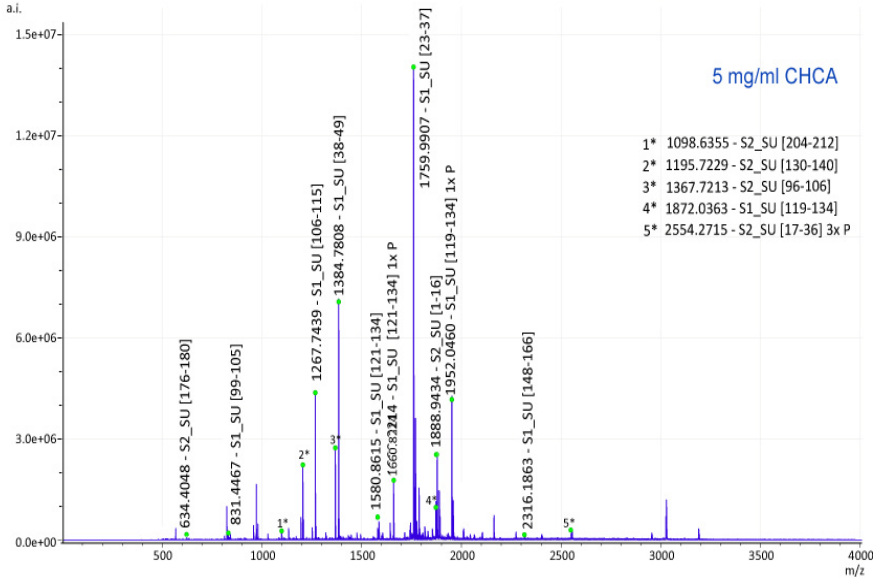
MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYE YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27212.9016	27229.3809	42.8 %	12.5 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVIMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.1 Positive ion reflector TOF MALDI - mass spectrum with 3 mg/ml CHCA matrix



Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25386.1140	25401.5719	36.9 %	73.9 %

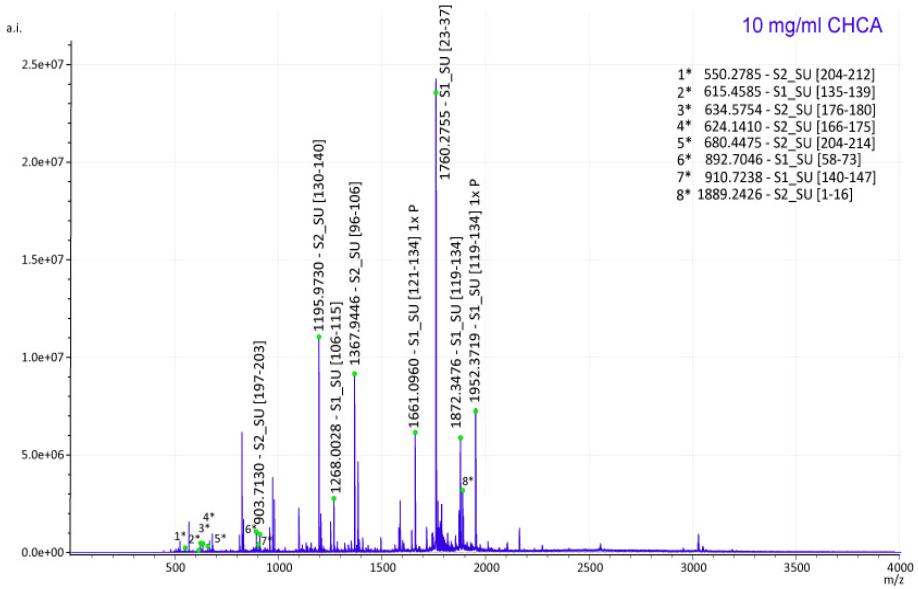
MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27212.9016	27229.3609	32.4 %	11.2 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVIMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.2 Positive ion reflector TOF MALDI - mass spectrum with 5 mg/ml CHCA matrix



Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25386.1140	25401.5719	35.5 %	34.3 %

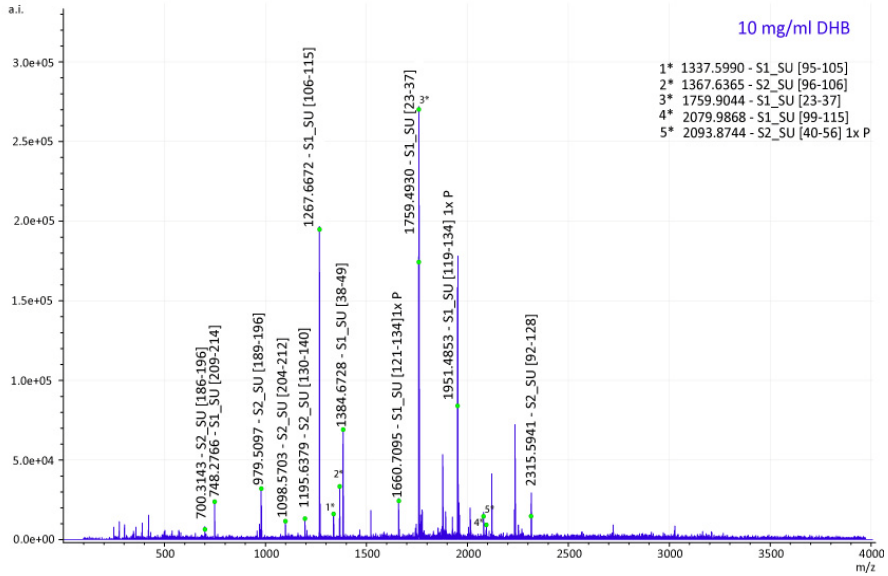
MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27244.8915	27261.3597	32.0 %	20.3 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVIMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.3 Positive ion reflector TOF MALDI - mass spectrum with 10 mg/ml CHCA matrix



Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25338.1375	25353.5908	32.7 %	68.6 %

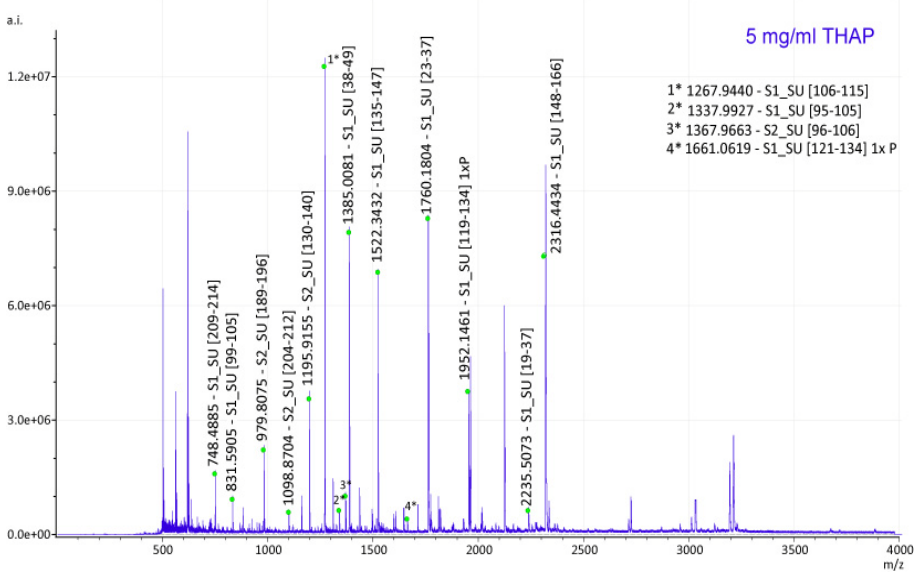
MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27244.8915	27261.3597	38.3 %	9.5 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVDMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.4 Positive ion reflector TOF MALDI - mass spectrum with 10 mg/ml DHB matrix



Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25418.1038	25433.5707	49.5 %	50.0 %

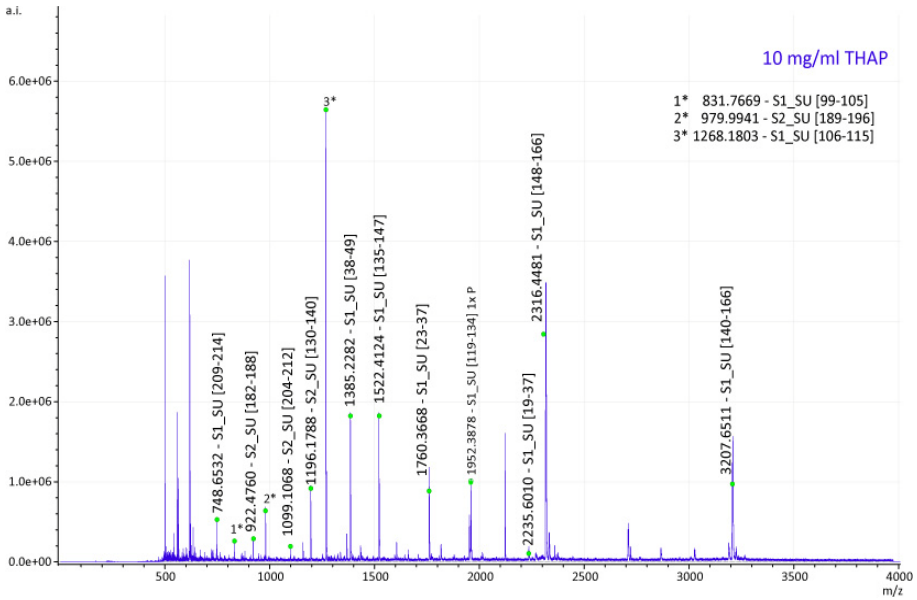
MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27244.8915	27261.3597	31.1 %	9.7 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVDMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.5 Positive ion reflector TOF MALDI - mass spectrum with 5 mg/ml THAP matrix



Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25418.1038	25433.5707	47.7 %	48.0 %

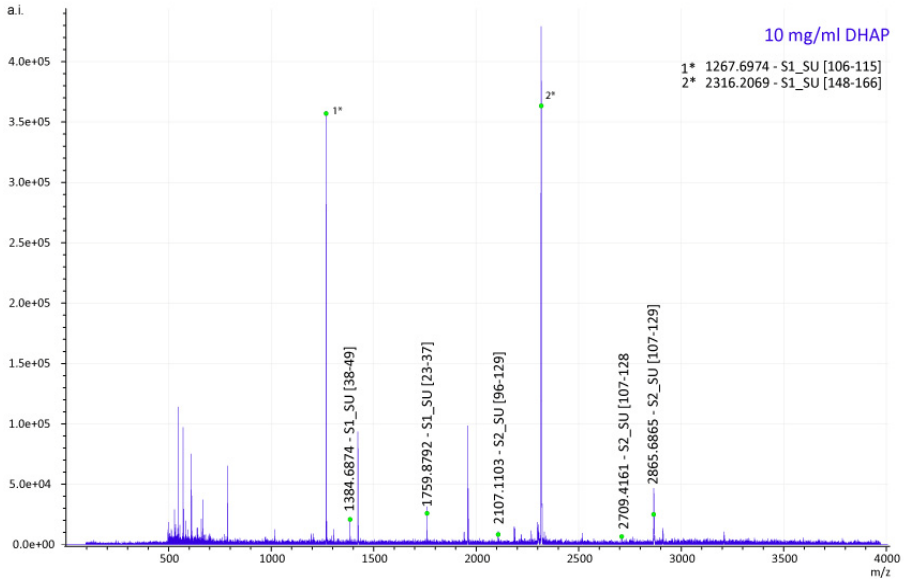
MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27244.8915	27261.3597	18.5 %	8.5 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVDMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.6 Positive ion reflector TOF MALDI - mass spectrum with 10 mg/ml THAP matrix



Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25418.1038	25433.5707	26.2 %	50.3 %

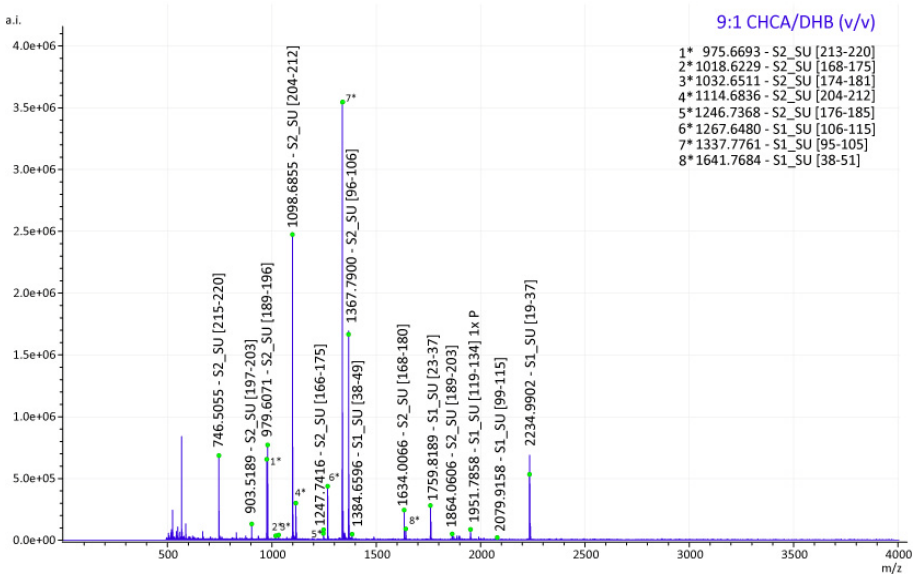
MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27244.8915	27261.3597	15.3 %	2.9 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVDMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.7 Positive ion reflector TOF MALDI - mass spectrum with 10 mg/ml DHAP matrix



Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25386.1140	25401.5719	32.7 %	35.9 %

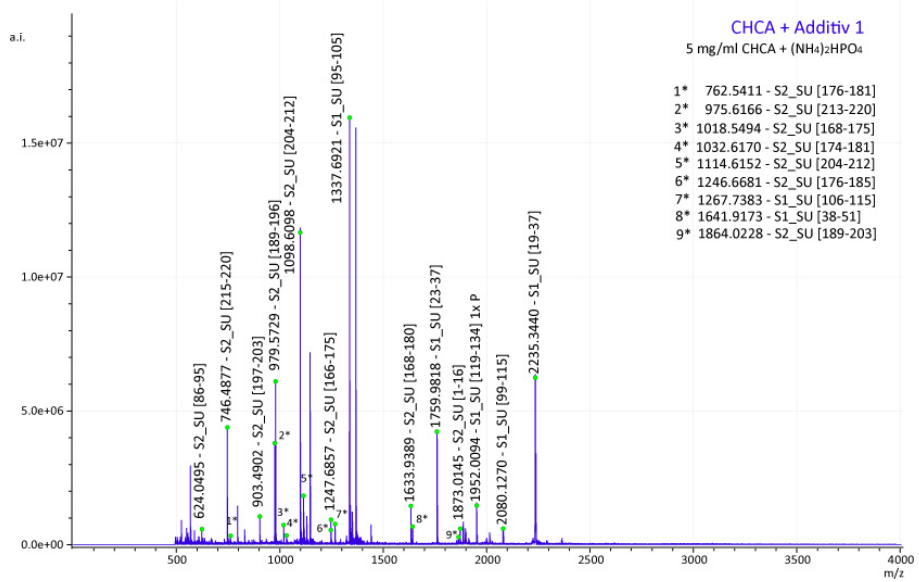
MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27212.9016	27229.3609	28.4 %	51.9 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVDMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.8 Positive ion reflector TOF MALDI - mass spectrum with CHCA/DHB (9/1) matrix



Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25386.1140	25401.5719	32.7 %	30.2 %

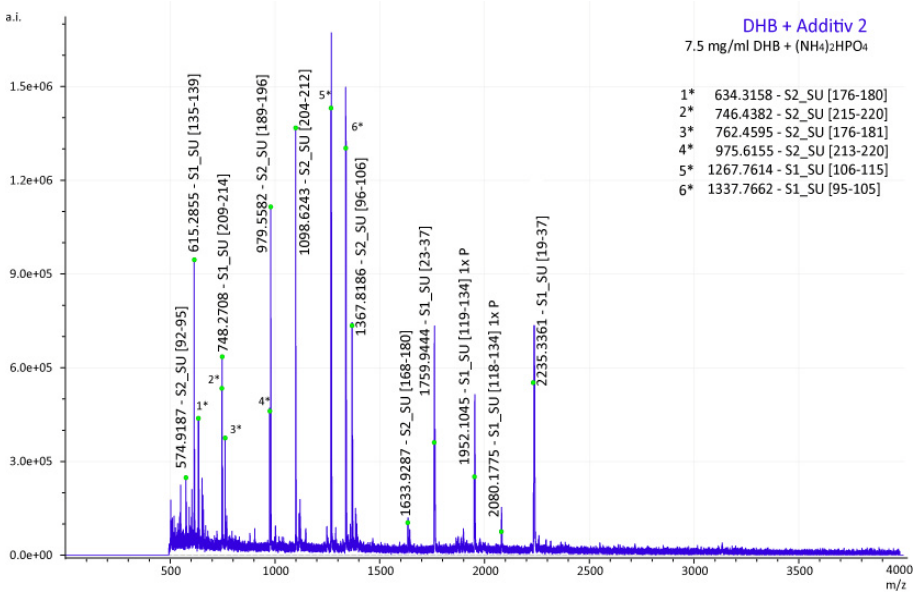
MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

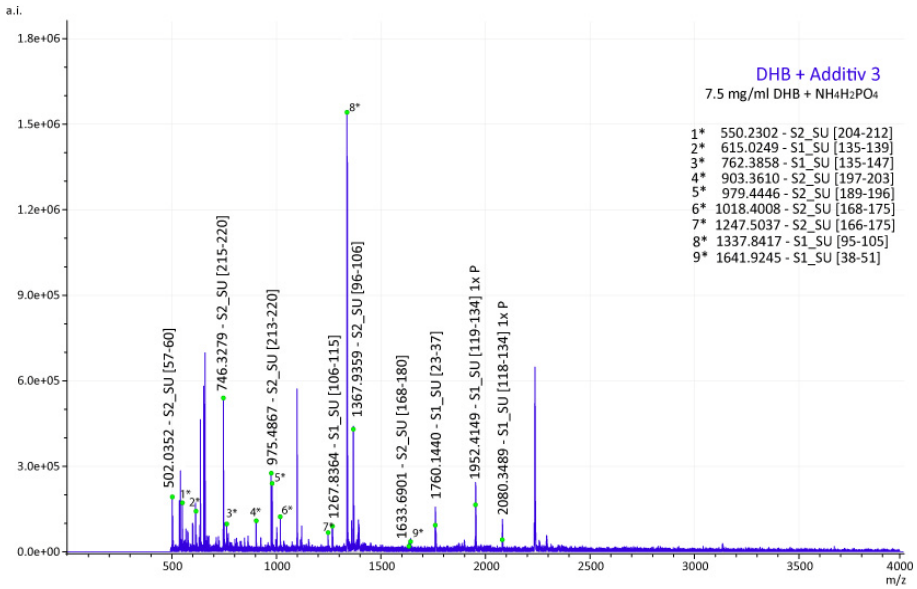
Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27212.9016	27229.3609	35.1 %	34.5 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVDMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.9 Positive ion reflector TOF MALDI - mass spectrum with 5 mg/ml CHCA matrix + Additive $(NH_4)_2HPO_4$





Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25418.1038	25433.5707	31.8 %	45.7 %

MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27244.8915	27261.3597	24.3 %	44.9 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVDMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.10 Positive ion reflector TOF MALDI - mass spectrum with 7.5 mg/ml DHB matrix + Additive $(NH_4)_2HPO_4$

Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25418.1038	25433.5707	37.4 %	29.1 %

MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27137.0347	27153.5348	27.9 %	28.3 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVDMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.11 Positive ion reflector TOF MALDI - mass spectrum with 7.5 mg/ml DHB matrix + Additive $NH_4H_2PO_4$

The following table gives an overview of the different sequence coverage, divided in the two subunits. Also the calculated sequence coverage of the total protein is given.

Table 3.3 Sequence coverage of the different matrices used for the sample preparation evaluation.

Matrix	Sequence coverage -αS1 [%]	Sequence coverage - αS2 [%]	Sequence coverage – Total Protein [%]
CHCA 3 mg/ml	44.4	42.8	**87.2**
CHCA 5 mg/ml	36.9	32.4	66.3
CHCA 10 mg/ml	35.5	32.0	67.5
DHB 10 mg/ml	32.7	38.3	71.0
THAP 5 mg/ml	49.5	31.3	80.8
THAP 10 mg/ml	47.7	18.5	66.2
DHAP 10 mg/ml	26.2	15.3	41.5
CHCA/DHB 9:1	32.7	28.4	61.1
CHCA + Additive 1*	32.7	35.1	67.8
DHB + Additive 2*	31.8	24.3	56.1
DHB + Additive 3*	37.4	27.9	65.3

MALDI-MS measurements are not easy for all of the tested matrices, because of different crystal structures. THAP and DHB produce large crystals, decreasing the homogeneity of the sample distribution in the matrix. Moreover, it was observed that larger crystals need more laser energy for the ionization. As a consequence, mass resolution decreases which makes the assignment of monoisotpic peaks more difficult. Thus protein identification his hampered.

The best performing matrix is 3 mg/ml CHCA (highlighted in red). The total protein sequence coverage is 87.2 %, followed by 5 mg/ml THAP (80.8 %). However, the use of the THAP matrix is not recommended, due to the higher laser energy required for the ionization and the resulting high abundant matrix (=background) peaks occurring in the spectra. The same experience was made with DHB. DHB crystallizes in the similar to THAP. Large crystals are formed, that hampers the homogeneity of the matrix sample mixture. Even at an *m/z* ratio of 1200 Da the iosotopic pattern deteriorates. Due to this, the assignments of the monoisotopic peaks were hindered.

The combined CHCA/DHB matrix, suggested in literature [Lau et al., 2012], turned out to be not the matrix of choice for this approach; the sequence coverage is only 61.1 %. In our experience, the use of additives is not favorable. By the addition of additives to both matrices, CHCA and DHB, the abundance of undefined background peaks increased. This leads to suppression of the phosphopeptide peaks, which are hardly detected anyway and would explain the low sequence coverage between 56.1 % and 67.8 %.

DHAP matrix performed worst, giving sequence coverage of less than the half of the best results (41.5 %).

As mentioned in chapter 1.7.4 sequence specific fragments that are specific for a defined type of modification are produced during fragmentation. In case of phosphorylated peptides, the mass differences of Δ - 80 Da and Δ - 98 Da indicate the loss of either HPO_3 or H_3PO_4. These differences are evidence for the presence of phosphopeptides. pSer and pThr tend to lose phosphoric acid (- H_3PO_4), pTyr residues are more stable and tend to lose - HPO_3. In casein only serine residues are phosphorylated, therefore the theoretical loss of Δ - 98 Da and detected corresponding m/z ratios are opposed in Table 3.4.

Table 3.4Indication of phosphorylation of peptides by means of loss of H_3PO_4

Matrix	Concentration	m/z of pSer	Number of detected pSer	- H3PO4 (theoretical)	- H3PO4 (measured)
				-98 Da	-98 Da
CHCA	3 mg/ml	1952.047	1	1854.047	**1854.116**
		1660.822	1	1562.822	**1562.835**
	5 mg/ml	1952.046	1	1854.046	**1854.059**
		2554.272	3	2456.272	n. d.
				2358.272	n. d.
				2260.272	n. d.
	10 mg/ml	1661.096	1	1563.096	**1563.155**
		1952.372	1	1854.372	**1854.287**
DHB	10 mg/ml	1660.710	1	1562.710	n. d.
		1951.465	1	1853.465	n. d.
		2093.874	1	1995.874	n. d.
THAP	5 mg/ml	1952.146	1	1854.146	n. d.
		1661.062	1	1563.062	n. d.
	10 mg/ml	/	0	/	/
DHAP	10 mg/ml	/	0	/	/
CHCA/DHB	10 mg/ml + 10 mg/ml (9:1)	1951.786	1	1853.786	n. d.
CHCA + Additive 1	10 mg/ml	1952.008	1	1854.008	**1854.023**
DHB + Additive 2	7.5 mg/ml	1952.105	1	1854.105	n. d.
		2080.178	1	1982.178	n. d.
DHB + Additive 3	7.5 mg/ml	1952.105	1	1854.105	n. d.
		2080.178	1	1982.178	n. d.

n.d. … no peak detected; / no phosphorylated peptide detected

First, the absence of detected phosphorylated serine residues by using 10 mg/ml THAP or DHAP residues is noticeable. This is a further indication that these matrices are not recommended for this approach because the prime goal for matrix evaluation is the avoidance of the loss of phosphorylation during ionization. Peaks, corresponding to the loss of the phosphoric acid (- 98 Da) were only measured using the CHCA matrix (independent of matrix concentration or the use of additive). As an example, the positive ion reflectron MALDI – TOF mass spectrum with 5 mg/ml CHCA is given in Figure 3.12. However, no peak related to the loss of one, two or all three phoshpo-residues were detected to confirm the triple phosphorylated serine using the 5 mg/ml CHCA. Due to the highest sequence coverage gaining with 3 mg/ml CHCA and the indication of pSer by the detection of the loss of phosphoric acid, this matrix was chosen for further analyses.

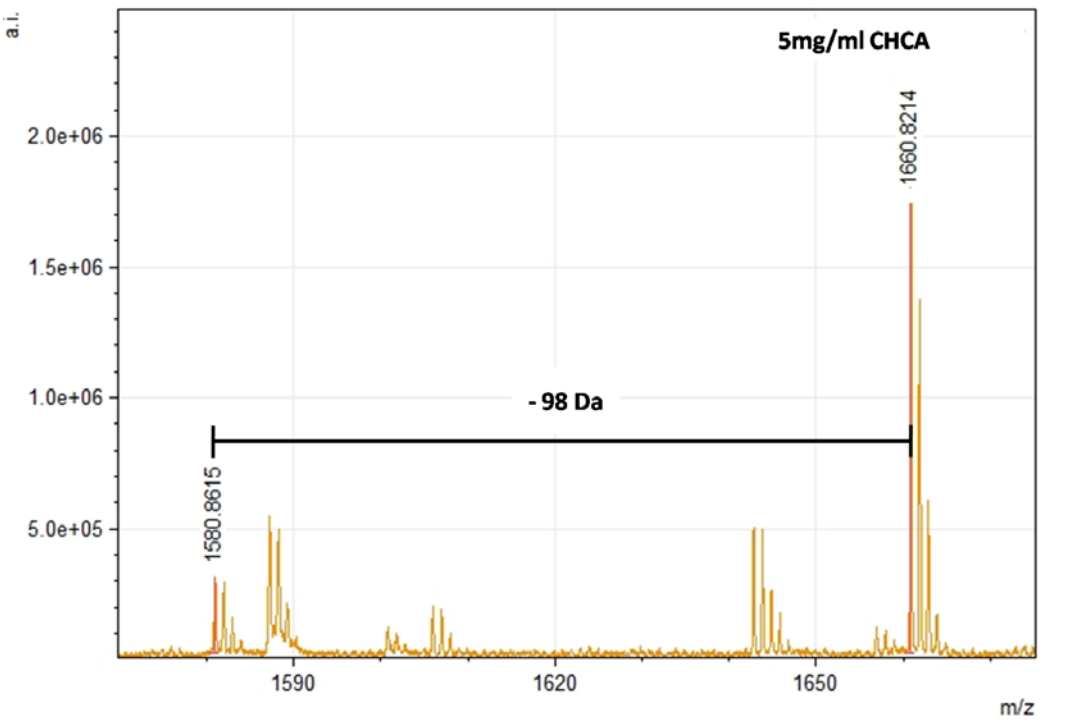


Figure 3.12 Positive ion reflectron MALDI - TOF mass spectrum with 5 mg/ml CHCA showing the typical loss of phosphoric acid (Δ-98 Da) of a phophorylated peptide of casein

3.2.2 Desalting Methods

Evaluation of a proper desalting method is important to eliminate interfering substances which hinder mass analyses by suppression effects. The main focus is on minimizing the loss of the peptides during salt removal and hence to gain high sequence coverage.

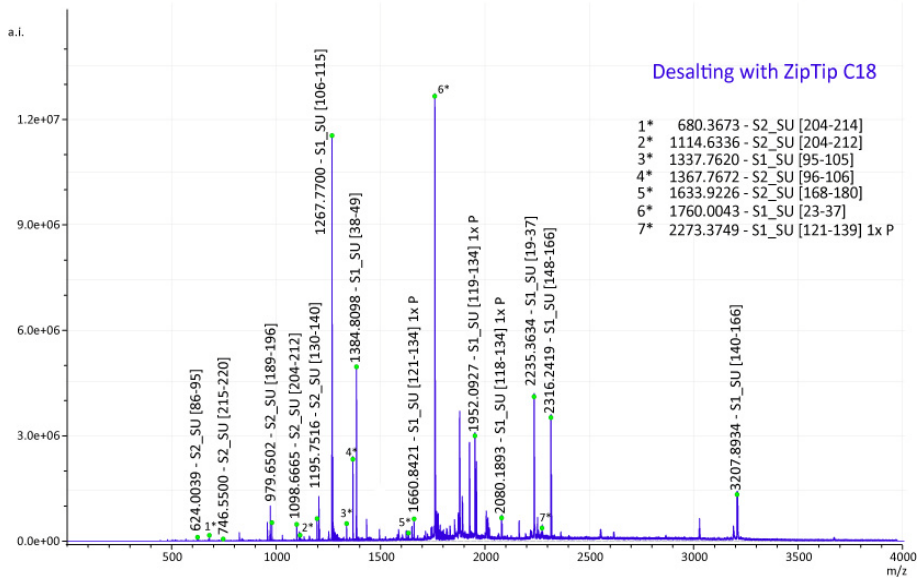
The experiments were carried out using trypsin digested α-casein samples that were desalted with three different methods and spotted on the MALDI target with 3 mg/ml CHCA, the matrix that

obtained the best results in the prior evaluation step. Samples were measured on the AXIMA – CFR^{+} (*Shimadzu Biotech Kratos Analytical*).

The three different desalting methods were:

- ZipTip® C_{18} tips(Millipore)
- HyperSep – 96 C_{18} Plate (Thermo Scientific)
- Self made Strata-X column

The detailed composition and the assembly of the self made Strata-X column as well as the desalting procedure itself are described in chapter 2.6 on page 42. The following figures show the resulting MALDI mass spectra. The unassigned peaks are related to matrix cluster, background peaks and trypsin related peaks.



Sequence coverage for α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25418.1038	25433.5707	47.2 %	65.8 %

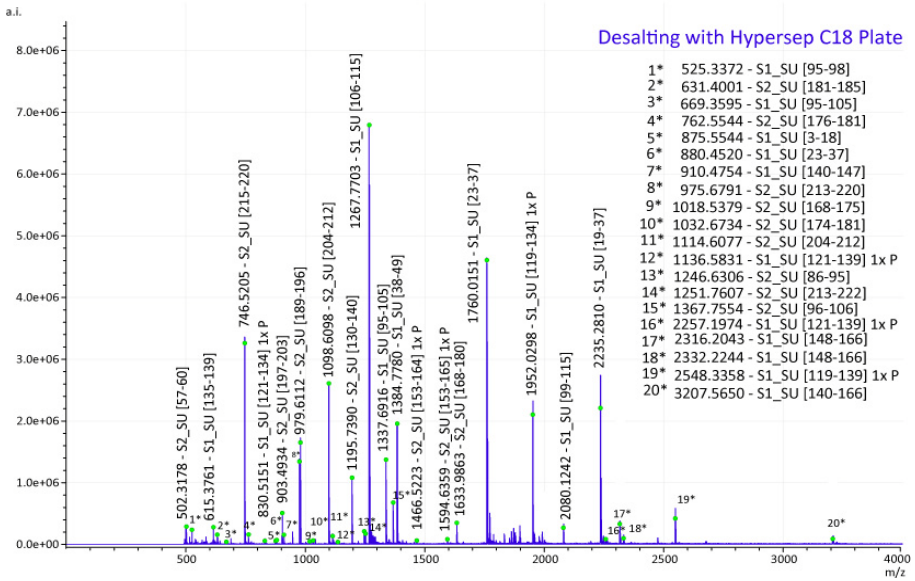
MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

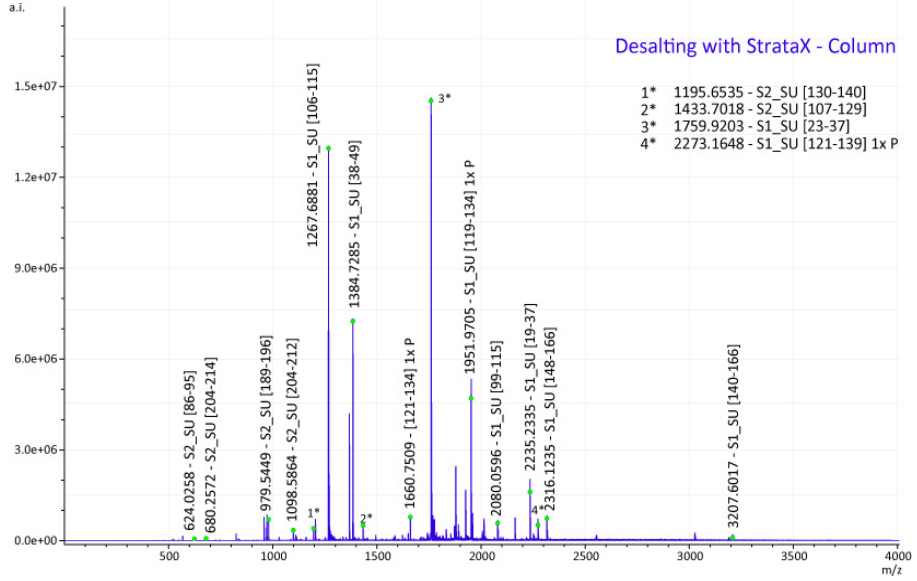
Sequence coverage for α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27244.8915	27261.3597	31.5 %	7.1 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVDMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.13 Positive ion reflectron MALDI TOF - mass spectrum with 3 mg/ml CHCA desalted with ZipTip®





Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25418.1038	25433.5707	54.2 %	61.2 %

MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27244.8915	27261.3597	45.5 %	29.5 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVDMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.14 Positive ion reflectron MALDI TOF - mass spectrum with 3 mg/ml CHCA desalted with HyperSep C18 Plate

Sequence coverage α S1:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	214	25338.1375	25353.5908	44.9 %	79.8 %

MKLLILTCLV AVALARPKHP IKHQGLPQEV LNENLLRFFV APFPEVFGKE KVNELSKDIG SESTEDQAME DIKQMEAESI SSSEEIVPNS VEQKHIQKED
VPSERYLGYL EQLLRLKKYK VPQLEIVPNS AEERLHSMKE GIHAQQKEPM IGVNQELAYF YPELFRQFYQ LDAYPSGAWY YVPLGTQYTD APSFSDIPNP
IGSENSEKTT MPLW

Sequence coverage α S2:

Accession	Length	Mo. Mass	Av. Mass	Coverage	Matched Int.
	222	27244.8915	27261.3597	33.3 %	5.1 %

MKFFIFTCLL AVALAKNTME HVSSSEESII SQETYKQEKN MAINPSKENL CSTFCKEVVR NANEEEYSIG SSSEESAEVA TEEVKITVDD KHYQKALNEI
NQFYQKFPQY LQYLYQGPIV LNPWDQVKRN AVPITPTLNR EQLSTSEENS KKTVDMESTE VFTKKTKLTE EEKNRLNFLK KISQRYQKFA LPQYLKTVYQ
HQKAMKPWIQ PKTKVIPYVR YL

Figure 3.15 Positive ion reflectron MALDI TOF - mass spectrum with 3 mg/ml CHCA desalted with self made Strata-X column

Gaining a better overview of the results (Figure 3.13 to Figure 3.15 represents the spectra) the sequence coverage is summarized in the table below (Table 3.5). This table shows the single sequence coverage for the two subunits (αS1 and αS2) as well as the calculated average.

Table 3.5 Sequence coverage of the different desalting methods

Desalting method	Sequence coverage α S1 [%]	Sequence coverage α S2 [%]	Sequence coverage Total Protein [%]
ZipTip® C_{18}	47.2	31.5	78.7
HyperSep C_{18} well plate	54.2	45.5	**99.7**
Self made Strata-X column	44.9	33.3	78.2

Although the principle of the different desalting methods is the same, reversed phase chromatography on C_{18}medium, disparities in the results could be observed. Desalting with HyperSep 96 C_{18} well plate (from *Thermo Scientific, Rockford, IL, USA*) shows clearly the best result as the highest sequence coverage for the protein could be achieved (highlighted in red). The main advantage, beneath the highest sequence coverage, is the possibility for high throughput analyses by using 96-well plates. The sequence coverage for the other two methods is almost the same. However, desalting with the self made Strata-X column is highly time-consuming and tedious, due to the laborious production of these columns, the low throughput as also the desalting procedure itself is time consuming. Keeping sequence coverage for successful protein identification in focus, desalting with the HyperSep 96 C_{18} well plate was the method of choice for further analyses of *Trichoderma atroviride* samples.

3.2.3 Enrichment Strategies

The important factor for phosphoproteomics is the specific enrichment of phosphoproteins or – peptides. Therefore, as mentioned in the chapter 1.6.3 on page 24, different strategies were developed. In this study three different commercially available phosphopeptide enrichment kits and one non-magnetic titanium dioxide method were tested. The kits used in this study were the Pierce® *Fe-NTA Phosphopeptide Enrichment Kit*, the Pierce® *Magnetic Titanium Dioxide Phosphopeptide Enrichment Kit*, and the *TiO_2 Mag Sepharose* from GE Healthcare. The non-magnetic enrichment procedure was performed with *TiO_2 beads* from GL Science. To test the efficiency of the different enrichment strategies α-casein digested with trypsin was used. The digest was desalted withHyperSep C_{18}well plates and measured in the AXIMA – CFR$^+$ (*Shimadzu Biotech Kratos Analytical*) using 3 mg/ml CHCA as matrix. In Figure 3.16the result of all tested strategies are displayed. Only phosphorylated peptides are annotated. Non-phosphorylated peptides, matrix cluster, background peaks and trypsin related peaks are not taken labeled.

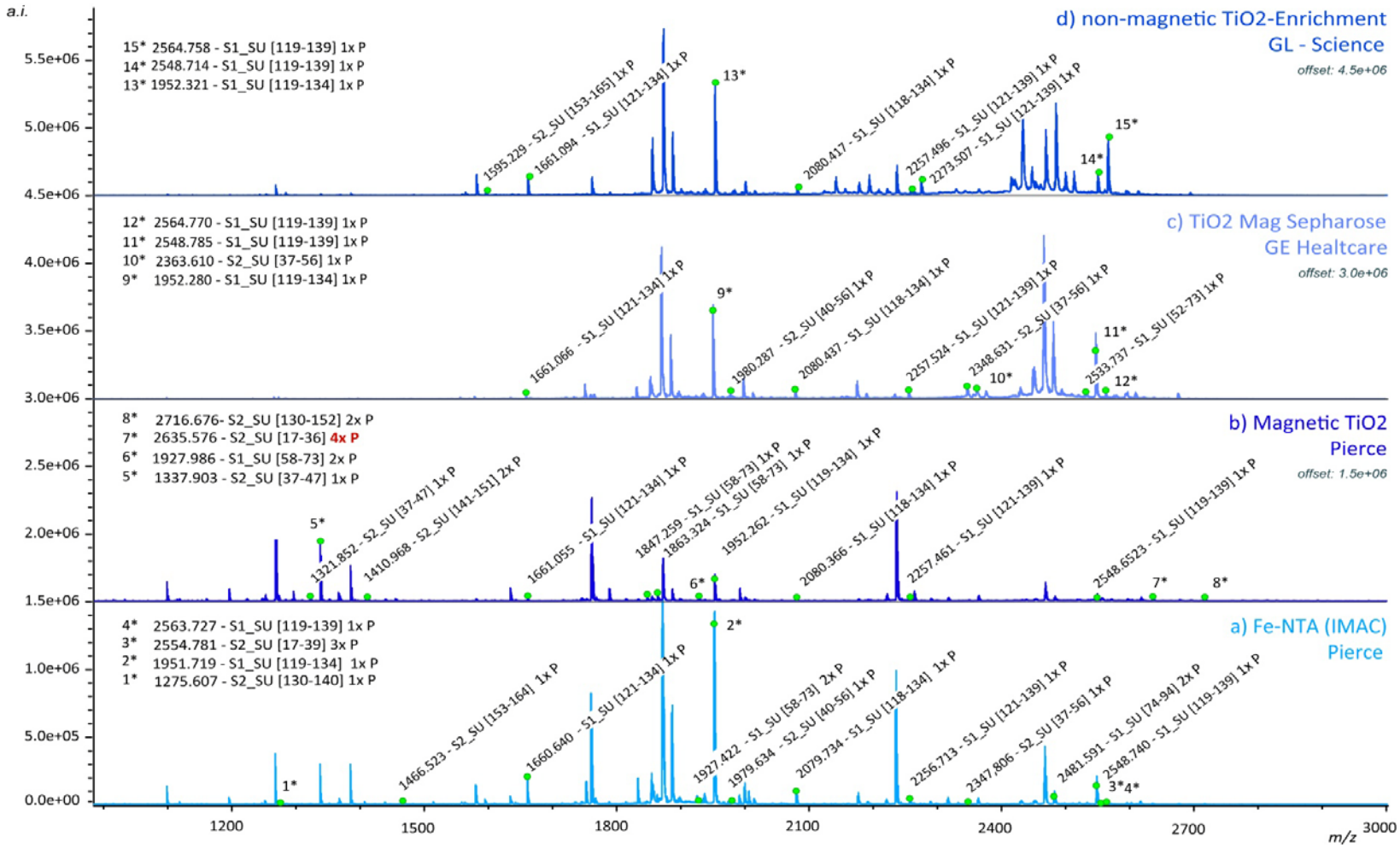


Figure 3.16 Positive ion reflectron MALDI TOF - mass spectra of enriched α-Casein using four different enrichment methods.

Methods: a) Pierce ® *Fe-NTA Phosphopeptide Enrichment Kit*, b) Pierce ® *Magnetic Titanium Dioxide Enrichment Kit*, c) GE Healthcare *MagnSepharose Kit* and d) *non – magnetic* TiO_2phophopeptide einrichment strategy

The goal of the enrichment step was to achieve a highly selective enrichment of phosphopeptides and to remove non-phosphorylated peptides. The tryptic digestion can lead to multiple identifications of peptides, with or without phospho sites due to missed cleavage. The following table summarizes the results including the total number of detected peaks resulting from the α-Casein sample using 3mg/ml CHCA (matrix, background, trypsin related peaks not taken into account), the identified phosphorylated peptides, the number of phosphorylated serine and peptides with non-phosphorylated sites. In consideration of these factors, as well as handling and overall time-consumption for a sample a ranking was assessed.

Table 3.6 Summary of the different enrichment strategies

	Pierce® Fe-NTA Phoshpopeptide Enrichment Kit	Pierce® Magnetic Titanium Dioxide Phosphopeptide Enrichment Kit	TiO_2 Mag Sepharose Kit from GE Healthcare	Non magnetic enrichment strategy with TiO_2 Beads from GL Science
Total number of assigned peaks	78	71	40	42
Number of identified pSer	13	13	10	8
Number of identified unique pSer*	11	11	3	2
Number ofpeptides related to casein without phosphorylation	24	26	14	18
Rank	**2**	**1**	**3**	**4**

*...only phosphoserine are annotated because in casein contains phosphorylations only on serine residues. Every phosphorylated serine, which could be identified in one sample, is taken only one time in account.

The Pierce® Fe-NTA Phoshpopeptide Enrichment Kit and the Pierce® Magnetic Titanium Dioxide Phosphopeptide Enrichment Kit performed both very good. Both methods enabled the identification of 13 peaks correlated to phosphorylated peptides. As you can see, only 11 pSer could be detected although 13 phosphorylated serine were identified. This experience can be explained by missed cleavages. Trypsin cuts the casein´s amino acid sequence after lysine or arginine. If trypsin missed such cleavage site, two peaks with the same phosphorylated serine residues are detectable, only the length of the peptide is different. As an example, a part of the amino acid sequence of the S1 subunit (119-140) is YKVPQLEIVPNSAEERLHSMKL (written in red are the cleavage sites, written in green pSer). So there are two possibilities to detect the pSer (130), provided that K (120) is cleaved anyway:

1) Tryspin cleaved at position R (134), resulting in VPQLEIVPNSAEER with an m/z ratio of 1788,889 Da.
2) Trypsin missed the cleavage site (R134) and cut the sequence after K (139) resulting in VPQLEIVPNSAEERLHSMKwith an m/z ratio of 2385,200 Da.

The main difference for these two enrichment strategies, and also the reason for the different ranking, is the fact that a tetra-phosphorylated peptide of casein (assigned in Figure 3.16 in red) could be detected after Magnetic Titanium Dioxide Enrichment. Furthermore, with phosphopeptide enrichment with this kit showed less unassigned peaks than the enrichment with the *Pierce® Fe-NTA Phoshpopeptide Enrichment Kit* (more precisely 32 peaks were unassigned using the Magnetic Titanium Dioxide Enrichment and 42 peaks with the Fe-NTA Phoshpopeptide Enrichment Kit). All these facts and the time-requirement factor argue for this enrichment method for further analyses.

3.2.4 Summary of the Evaluation Steps

Keeping the main functions and goals of the different sample preparation methods in mind (Table 3.1 page53) it can be said, that proper sample preparation techniques were evaluated. The best MALDI – Matrix for the detection of phosphopeptides is CHCA with a concentration of 3 mg/ml. Desalting with the HyperSep C_{18} well plate from Thermo Scientific turned out to be the most appropriate method to eliminate interfering substances. The most critical point in phosphoproteomics is the selective enrichment of phosphorylated peptides. Therefore, the enrichment with the *Pierce® Magnetic Titanium Dioxide Phosphopeptide Enrichment Kit* performed best for our approach. After digestion the biological protein, the final sample preparation procedure starts with desalting with the HyperSep C_{18} well plate, followed by the phosphopeptide enrichment by means of the *Pierce® Magnetic Titanium Dioxide Phosphopeptide Enrichment Kit*. MALDI – MS analysis is then carried out using 3 mg/ml CHCA.

3.3 Identification of Phosphoproteins expressed in *Trichoderma atroviride*

After evaluation of every analytical step for sample preparation, a method appropriate for the analyses of the phosphoproteome of *Trichoderma atroviride* was established. First, the whole lysate was under investigation. You will see in chapter 3.3.2 that this strategy does not lead to the desired results, because of the low number of identified phosphorylated peptides after phosphopeptide -

enrichment. So the workflow had to be adapted and a protein separation step was included after cell lysis. The complete workflow is displayed in the figure below (Figure 3.17).

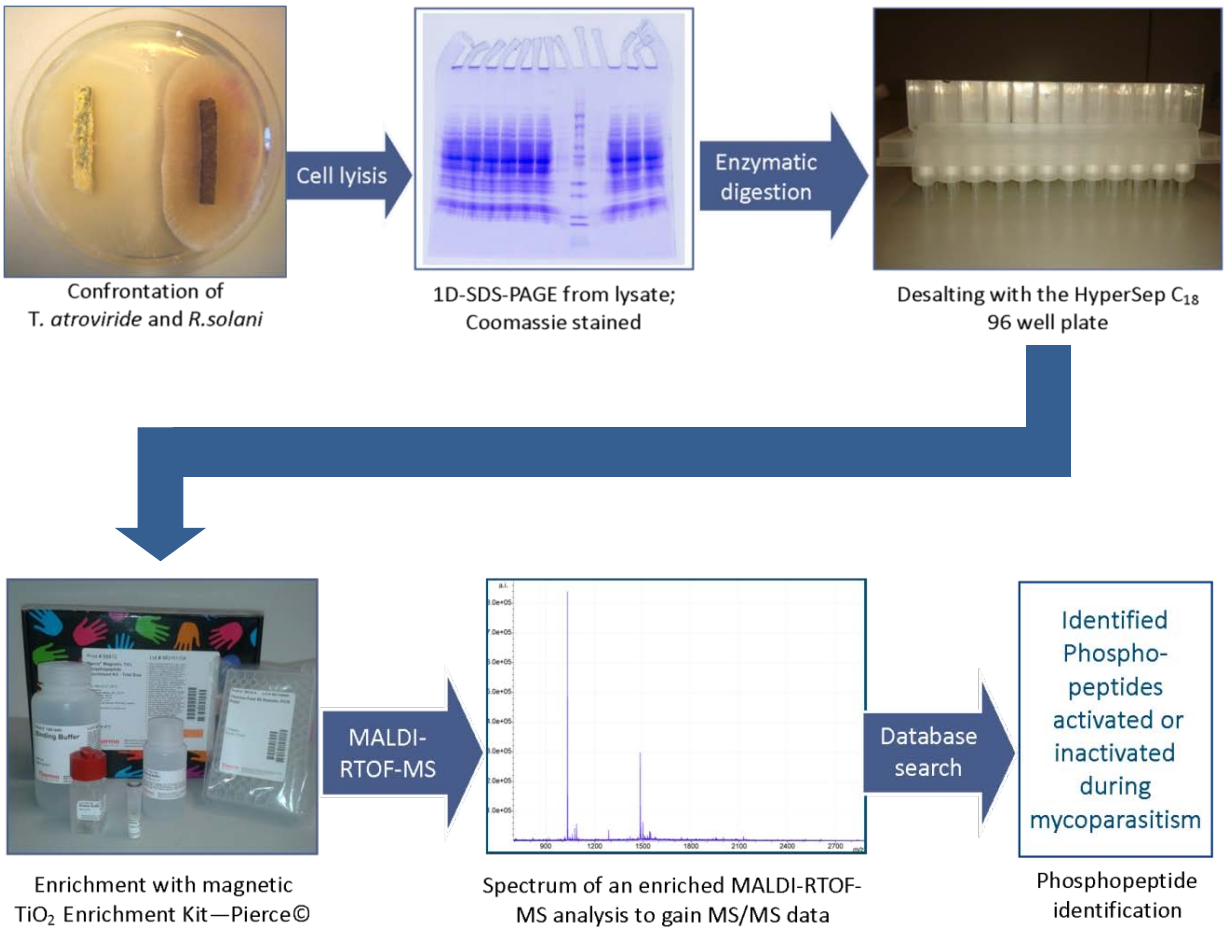


Figure 3.17 Workflow for the identification of phosphoproteins in *Trichoderma atroviride*

The biological material was provided by the Institute for Chemical Engineering, Vienna University of Technology. As described in chapter 2.1 on page 35, the *Trichoderma atroviride* sample was taken from the confrontation area, lysed by sonication and subsequently proteins were precipitated with TCA. In case of in solution digestion of the whole lysate without any separation, a protein solution containing 700 µg protein/ml (in digestion buffer NH_4HCO_3, pH 8.5) was used for further analysis. Additionally a method was developed including a SDS – PAGE separation after lysis. For this, after SDS-PAGE separation every sample lane was divided into 14 fractions, according to protein band pattern, and followed by an in-gel digestion. After that desalting and phosphopeptide enrichment was carried out. For all of these experiments the MALDI – MS measurements were carried out on a MALDI – TOF/TOF instrument (*UltraflXtreme, BRUCKER Daltonics, Germany*) and the amino acid sequences were achieved by PSD analyses [Spengler, 1997; Thiede et al., 2005]. After peak annotation the peak list was submitted to the latest NCBI database (August – October 2012) using Mascot (Matrix Science) [Perkins et al., 1999].

3.3.1 Protein Concentration Determination via Bradford Assay

For detailed information about the protocol of the Bradford assay see chapter 2.2. First, a calibration curve using BSA was established (Figure 3.18) to determine the protein concentrations of the *T. atroviride* samples. Table 3.7 displays the measured absorbance of the standards and the average of to get a linear regression.

Table 3.7 The determined absorbance of the BSA - standards

Standard conc. [µl/ml]	1st Abs.	2nd Abs	Absorbance (average)
1.00	0.0700	0.075	**0.073**
2.00	0.109	0.126	**0.118**
4.00	0.202	0.202	**0.202**
7.00	0.319	0.319	**0.319**
10.00	0.420	0.431	**0.426**

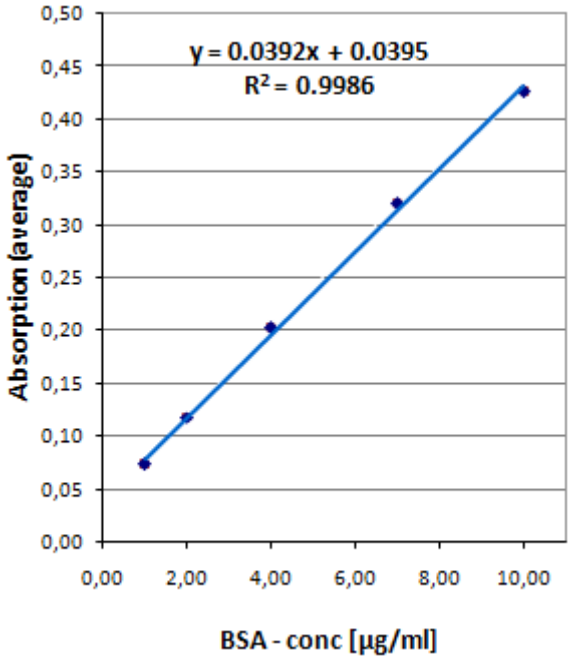


Figure 3.18 Regression line for the determination of the protein concentration using BSA.

In Table 3.8 the absorbance measured in a triplet and the resulting protein concentrations for three different samples (*Trichoderma atroviride* $_{wt}$ vs. Trichoderma atroviride $_{wt}$, un-induced mycoparasitism; *Trichoderma atroviride* $_{wt}$ vs. *Rhizoctonia solani*, induced mycoparasitism and *Trichoderma atroviride* $_{tmk1}$ vs. *Rhizoctonia solani*, reduced mycoparasitism) are given.

Table 3.8 Calculation of the protein concentration of the *Trichoderma atroviride* samples

Sample	Absorbance			Concentration	
	1st measurement	2nd measurement	3rd measurement	[µg/ml]	[mg/ml]
T. atroviride $_{wt}$ **vs.** ***T. atroviride*** $_{wt}$	0.372	0.370	0.371	8.457	**8.457**
T. atroviride $_{wt}$**vs.** ***R. solani***	0.395	0.,373	0.384	8.788	**8.788**
T. atroviride $_{tmk1}$**vs.** ***R. solani***	0.322	0.321	0.,322	7.194	**7.194**

3.3.2 Analyzing the Cell Lysate without prior Separation

After the lysis, 500 µl of the 700 µl/ml solution per *Trichoderma atroviride* sample were digested with trypsin. The efficiency of the digestion was controlled by PMF analyses of without a phosphopeptide enrichment step. The PMF spectra are shown in Figure 3.19. Due to low abundance and low stoichiometry of phosphoproteins it is unlikely that phosphorylated peptides occur as intense peaks. Additionally non-phosphorylated peptides will overlap them. Several peaks were chosen for PSD analyses to determine the amino acid sequence and to subsequently identify the protein (see chapter1.7). In Table 3.9, the results of the PSD – analyses are summarized and the identified peptide sequences are given as well as the protein and the organism they belong to. The PSD – spectra of the identified *Trichoderma atroviride* proteins are shown in chapter 6, Appendix.

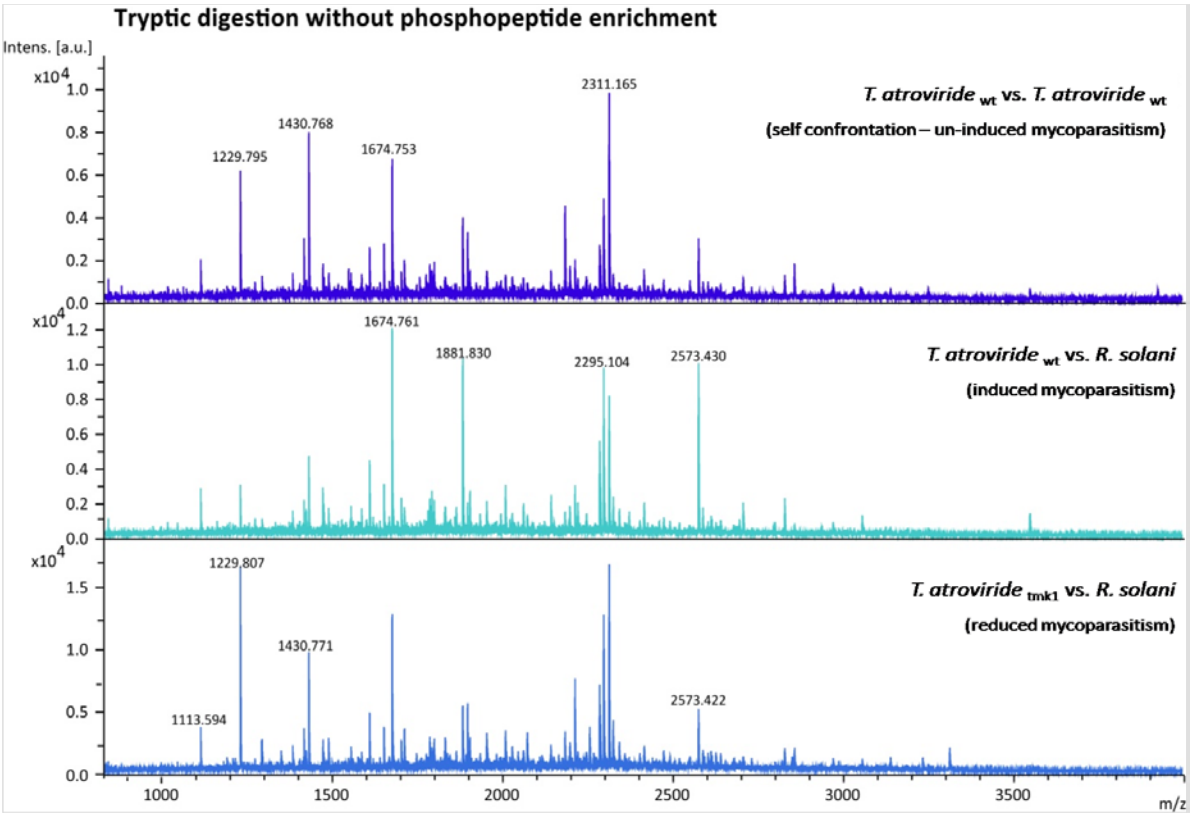


Figure 3.19 Positive ion reflectron MALDI TOF - mass spectra of the three *T. atroviride* samples after tryptic digestion without phosphopeptide enrichment
Only the peaks chosen for PSD analyses are annotated.

Table 3.9 Overview of the identified peptides of the picked out peaks from the unseparated *Trichoderma atroviride* samples

	m/z - value	NCBI - DB	Score	TH 0.05	Peptide	Database-Name	Function
un-induced Mycoparasitism *T.atroviride* $_{wt}$ vs. *T. atriviride* $_{wt}$	1229.795	gi|299752451	21	55	R.APAMNGG**S**ESGR.G + Oxidation (M); Phospho (ST)	hypothetical protein CC1G_02386 [Coprinopsis cinerea okayama7#130]	hypotetical protein
	1430.768	gi|358393698	34	55	**K.DIQEVILVGGMTR.M**	**hypothetical protein TRIATDRAFT_149341 [Trichoderma atroviride IMI 206040]**	**Hsp70 family protein**
	1674.753	gi|358399668	**55**	55	**K.LVSWYDNEWGYSR.R**	**hypothetical protein TRIATDRAFT_297741 [Trichoderma atroviride IMI 206040]**	**Glyceraldehyde-3-phosphate dehydrogenase**
	2311.165	gi|358393376	38	56	**K.MVPSKPMCVEAFTDYPPLGR.F + Oxidation (M)**	**hypothetical protein TRIATDRAFT_300828 [Trichoderma atroviride IMI 206040]**	**Tranlation elongatioin factor 1 alpha**
indcuded Mycoparasitism *T.atroviride* $_{wt}$ vs. *R. solani*	1674.761	gi|358399668	**64**	54	**K.LVSWYDNEWGYSR.R**	**hypothetical protein TRIATDRAFT_297741 [Trichoderma atroviride IMI 206040]**	**Glyceraldehyde-3-phosphate dehydrogenase**
	1881.830	gi|358397245	**104**	55	**R.TINECNDPDLFWAMR.G**	**hypothetical protein TRIATDRAFT_299189 [Trichoderma atroviride IMI 206040]**	**FAD/FMN-containing dehydrogenases**
	2295.104	gi|358393376	**58**	56	**K.MVPSKPMCVEAFTDYPPLGR.F**	**hypothetical protein TRIATDRAFT_300828 [Trichoderma atroviride IMI 206040]**	**Tranlation elongatioin factor 1 alpha**
	2573.430	gi|289657846	28	58	R.VETGVIK**S**GMVVTFAPSNVTTEVK.S + Phospho (ST)	translation elongation factor-1 alpha, partial [Byssolophis sphaerioides]	Translation elongation factor-1 alpha
reduced Mycoparasitism *T.atroviride* $_{tmk1}$ vs. *R. solani*	1113.594	gi|320588617	21	53	K.FSVTVDIPR.Q + Phospho (ST)	RNA-binding effector protein [Grosmannia clavigera kw1407]	RNA-binding effector protein
	1229.807	gi|83767589	30	55	R.ANISSSSAPR.T + 3 Phospho (ST)	unnamed protein product [Aspergillus oryzae RIB40]	Fungal specific transcription factor (C6)
	1430.771	gi|358393698	37	55	**K.DIQEVILVGGMTR.M**	**hypothetical protein TRIATDRAFT_149341 [Trichoderma atroviride IMI 206040]**	**Hsp70 family protein**
	2283.165	gi|358393759	13	56	K.AATLELSHLLTVATYVQHR.L + 2 Phospho (ST)	hypothetical protein TRIATDRAFT_247392 [Trichoderma atroviride IMI 206040]	Transcription-associated recombination protein
	2573.422	gi|289657846	20	52	R.VETGVIKSGMVVTFAPSNVTTEVK.S + Phospho (ST)	translation elongation factor-1 alpha, partial [Byssolophis sphaerioides]	Translation elongation factor-1 alpha

The peptides written in bold are related to *Trichoderma atroviride*, and the scores highlighted in blue are significant identified peptides (with a threshold of 0.05)

It can be said, that the *Trichoderma* samples were successfully digested, due to the obtained spectra and the identified peptides, which are related to proteins of *T. atroviride*. However, none of the identified peptides carried a phosphogroup. This is due to the fact, that proteins/peptides without post transcriptional modifications are usually easier to ionize suppressing therefore signals from phosphopeptides. Another observation is the similarity of the three spectra. This experience suggests that the identified proteins represent so called housekeeping proteins/peptides, which are highly abundant. Proteins playing a regulative role are relatively low concentrated and therefore hard to detect in the presence of high abundant proteins/peptides. Due to the minimal information about regulating proteins/peptides, no conclusion about the changes of the phosphoproteome caused by activating the mycoparasitic response can be drawn.

The ratio of phosphorylated to non-phosphorylated proteins present in cells is an important factor, some residues are permanently phosphorylated and others may only be transiently phosphorylated. For proteins playing a key role in signaling pathways phosphorylation rates are very low, only 1-2%. Therefore, proteins/peptides important for regulation do not appear in high abundances in their respective phosphorylated forms. Usually housekeeping proteins are present in a significant amount and their peptides are covering therefore low abundance phospho - peptides. So, peptides carrying phosphorylations could not be detected at all. This leads to the conclusion that a phosphor enrichment step is essential.

Therefore, the digested *Trichoderma* lysates were treated with the evaluated enrichment technique (*Pierce® Magnetic Titanium Dioxide Phosphopeptide Enrichment Kit*) and measured by MALDI – MS. The PMF spectra are given in Figure 3.20.

Despite TiO2 enrichment and desalting, no significant differences between the three spectra are observable. All spectra look very similar and show a surprisingly low number of signals. This is contrary to the expected result. It was assumed that the digestion of the whole lysate and a subsequent phosphopeptide enrichment leads to the detection of a significant number of phosphopeptides. To clarify the occurrence of phosphorylated peptides, four peaks were chosen for PSD analyses. In the following table (Table 3.10) the results are displayed.

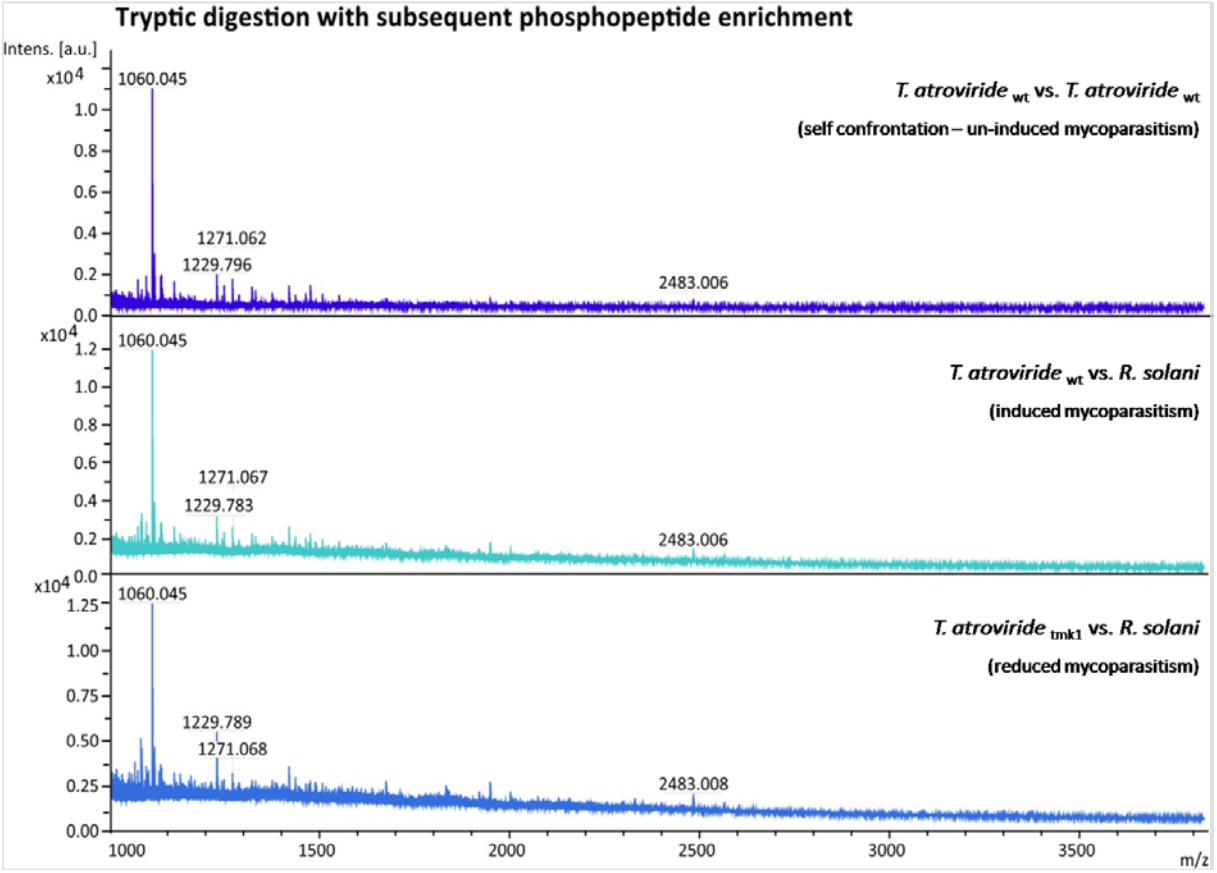


Figure 3.20 Positive ion reflectron MALDI TOF - mass spectra of the three *T. atroviride* samples after tryptic digestion with phosphopeptide enrichment. Only peaks chosen for PSD analyses are annotated

Table 3.10 Overview of the identified peptides of the picked out peaks from the unseparated and enriched *Trichoderma atroviride* samples

m/z-value	1.060.045	1.229.796	1.271.062	2.483.993
NCBI - DB	gi|145241472	gi|70998851	gi|358401110	gi|331213311
Score	13	19	9	13
TH 0,05*	56	55	56	56
Peptide	R.TS**S**PGMDLR.D + Oxidation (M); Phospho (ST)	R.EKMVEAV**T**AR.E + Oxidation (M); Phospho (ST)	**R.SSANL<u>S</u>VGPFGR.E + Phospho (ST)**	R.TL**Y**LKIVEAVSQEDDYFIQK.R + Phospho (Y)
Database-Name	Zn2Cys6 transcription factor [Aspergillus niger CBS 513.88]	pentafunctional AROM polypeptide [Aspergillus fumigatus Af293]	**hypothetical protein TRIATDRAFT_289166 [Trichoderma atroviride IMI 206040]**	terpenoid cylase/protein prenyltransferase alpha-alpha toroid [Puccinia graminis f. sp. tritici CRL 75-36-700-3]
Function	Zn2Cys6 transcription factor	pentafunctional AROM polypeptide	**Uncharacterized conserved protein [Function unknown)**	terpenoid cylase/protein prenyltransferase alpha-alpha toroid

*TH = Threshold, 0.05 = scores higher than this threshold have a 5% probability that the observed match is a random event. The peptides written in bold are related to Trichoderma atroviride, and the peptides highlighted in red are phosphorylated peptides

Due to the similarity of these spectra, it was decided to analyze the four peaks, which were represented in all three spectra by means of PSD. Every PSD spectrum submitted to Mascot pointed out the presence of a potential phosphogroup. However, only one peptide could be identified to be related to *Trichoderma atroviride*, however this identification was below the statistical threshold of 0,05. This means, that this match could be a random event with more than 5 % possibility. The respective PSD – spectrum is given in the chapter 6 Appendix.

The problem of the lacking number of occurring peaks could be possibly explained by the capacity limit of the adsorption phase. The high number of peptides in the total cell lysate after digestion may mask the active binding sites of the enrichment material resulting therefore in an inefficient enrichment.
Another possible reason is an inefficient desalting or digestion step. However, both explanations are less likely, because the measurements of the whole lysate without subsequent enrichment showed reasonable results. Significantly identified peptides did indeed relate to *Trichoderma atroviride*.

It was decided to include a simple separation step before digestion. Single bands of SDS PAGE separated samples were digested, desalted and phosphopeptides were further enriched.

3.3.3 Analyzing the Phosphoproteome of *Trichoderma atroviride* including a Separation via 1D–SDS–PAGE

As mentioned above a separation by 1D – SDS – PAGE was included into the workflow to increase protein identification rate and phosphoprotein recovery.

Prior discussing the results in detail, some difficulties of this approach have to be pointed out. The results are no strict statements on the samples, only general tendencies can be pointed out. This means that up- and down regulations cannot be determined with this approach, only the presence or absence of proteins with or without phosphorylated residues is under investigation. Proteins are up- and down regulated by means of different environmental conditions that influence the expression rate of proteins and therefore the results. Changes in the environmental conditions include i.e. the nutrition availability during growth or the presence of a phytopathogenic fungus. Up- and down regulation of proteins influence the detectability in consequence of different concentrations. As a conclusion, the detection of a protein in only one sample, does not strictly exclude its presence in another sample. By up-regulation of a protein, the concentration in the sample increases and therefore the efficiency of the digestion improves and the binding affinity to the stationary phase increases. This has a positive effect on the identification on up regulated proteins. The other way around, a down regulated protein is difficult to detect and identify due to the lower concentration.

But again, only because of the miss of a significant identification for a peptide/protein it does not mean this protein is not present. To estimate the *Trichoderma atroviride´*s phosphoproteome, a sample, where *Trichoderma atroviride* $_{wt}$ grown against itself, was analyzed. With this approach proteins, expressed during un-induced mycoparasitism but with competition for nutrients between the two fungal colonies, were under investigation.

As mentioned in chapter 1.3 analyzing PTM is a big issue. Phosphorylated proteins are relatively low abundant proteins and the phosphogroup can be easily lost during the analyzing procedure, which makes the analysis of the phosphoproteom difficult, anyway. Hence, also methodical challenges are present. One critical point is the identification using databases, like NCBI. By submitting a peak list to a database using e.g. Mascot, the program always generates a list of matches, even if the matches are nonsense. Therefore, a threshold was set to $p<0.05$. That means, that if a threshold of $p<0.05$ is exceeded, only a 5 % possibility for random matches exists. In the following discussion, peptides are annotated with the achieved score and the threshold (score/threshold, $p<0.05$). If the score exceeded the threshold, a peptide is significantly identified and is described as “identified” otherwise it is not identified (declared as “detected”). A major technical problem is also the fragmentation behavior of a peptide which highly depends on the amino acids present in the respective amino acid sequence of the peptide. Thus, the identification based on sequence tags is not possible for scarcely fragmented peptides. Furthermore the concentration of the peptide on the sample on the MALDI target plays an important role. The less peptide is available for the PSD - measurement, the higher the difficulties to gain an adequate spectrum (PSD analysis were carried out from peaks with S/N ratios ≥ 5, an adequate spectrum includes a significant number of generated fragments; significant ≥ 6) for identification.

Also the electrophoretic separation technique is problematic. Due to the one dimensional separation, multiple proteins occur in one excised gel piece which is submitted to in-gel digestion, peptide desalting and enrichment. This is the reason why identification of proteins by means of PMF after SDS-PAGE of complex samples is not possible in this approach. High concentrated proteins are preferably identified, as already explained above. Proteins, respectively peptides after digestion, occurring in lower concentration can only bind with less efficiency to the adsorption phase because of the capacity of the stationary phase (most available positions are occupied with the higher concentrated peptides). In the detailed discussion of the determined peptides and the respective proteins, the theoretical molecular mass of the protein is given, as well as the gel piece they were located in. The comparison of the molecular weights (MW) gives the opportunity to draw some conclusions about the plausibility of the identified protein. If the theoretical MW does not match to the MW area of the excised gel part, there are two possibilities. The theoretical MW is higher or

lower than the MW depicted from the SDS-PAGE. The first possibility is more likely than the other and can be explained by the potential existence of different subunits within the protein, which were separated by means of the reducing agent using in the SDS-PAGE. Also a partial degradation of proteins is possible. A further explanation for the higher theoretical MW is the fact that the database entry very often includes the protein's signal sequence, which is cleaved prior the protein, is activated. The MW of such signal sequence of proteins is approximately 10 kDa. If the theoretical MW is lower than the MW depicted from the gel, then a potential protein aggregation has to be considered and SDS was not able to prevent the non-covalent binding.

These are essential limitations of this approach, which can be shown simply by repeating the analysis (duplicate analysis of all samples). For this, approximately 30 µg protein was loaded per SDS-PAGE lane. For detailed information about the electrophoretic protocol and staining method see chapter2.3 and 2.4In Figure 3.21 the gels are displayed after Coomassie staining.

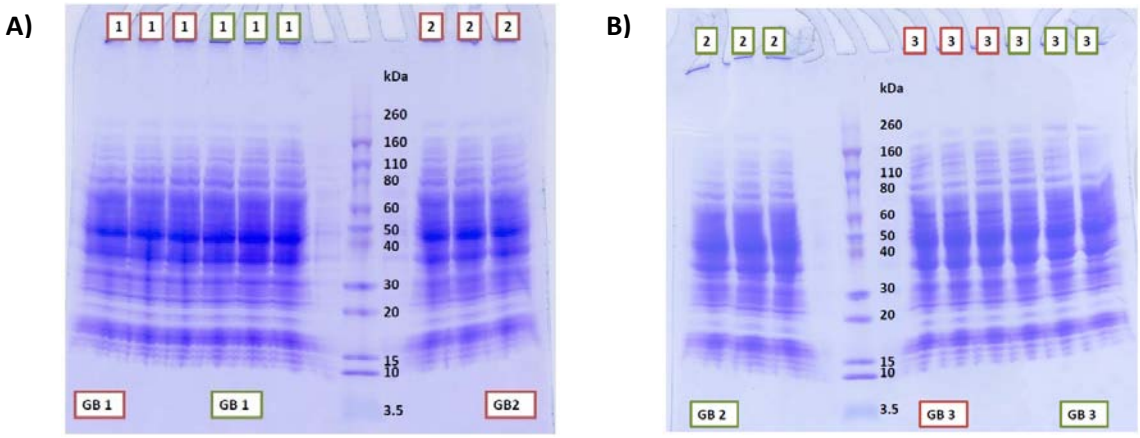


Figure 3.21 SDS – PAGE of *Trichoderma atroviride* samples, with Coomassie staining. Samples: (1) *T. atroviride*$_{WT}$ vs. *T. atroviride* $_{WT}$ (self-confrontation, un-induced mycoparasitism) (2) *T. atroviride*$_{WT}$ vs. *R. solani* (induced mycoparasitism) and (3) *T. atroviride* $_{tmk1}$ vs. *R. solani* (reduced mycoparasitism). The red and green borders show the sample lanes which were pooled for the analyses. GB indicates the region of the gel blanks

Each lane was divided into 14 pieces, orientated on the gel pattern. Figure 3.22 represents an example for the protein pattern achieved for the self-confrontation of *T. atroviride* $_{WT}$ vs. *T. atroviride* $_{WT}$ (un-induced mycoparasitism) and the respective 14 gel pieces. It can be assumed that the more intensive the staining of a gel band is the more protein is present at this position. Based on this assumption it was decided to cut out gel pieces with approximately the same amount of protein. If there is a dark blue staining area, a smaller gel piece was cut out than by light blue staining, to avoid a possible saturation due to the capacity limit of the adsorption phase.

After cutting out the gel pieces, an in-gel digestion according to the protocol given in chapter 2.5.3.2was carried out. The resulting peptides were desalted using the HyperSep C_{18}well plate from Thermo Scientific and enriched using the *Pierce® Magnetic Titanium Dioxide Phosphopeptide Enrichment Kit* before they were measured by MALDI – MS. Selected peptides were fragmented using PSD and spectra were submitted to the latest NCBI database (August – October 2012) using Mascot (Matrix Science) [Perkins et al., 1999] for protein identification. The single PMF - spectra are given in the appendix, chapter 6. The mass lists of the PSD - analyses and the relationship to *Trichoderma atroviride* are listed below the spectrum. If a peak is not related to *Trichoderma atroviride*, it could not be identified, neither as another fungus.

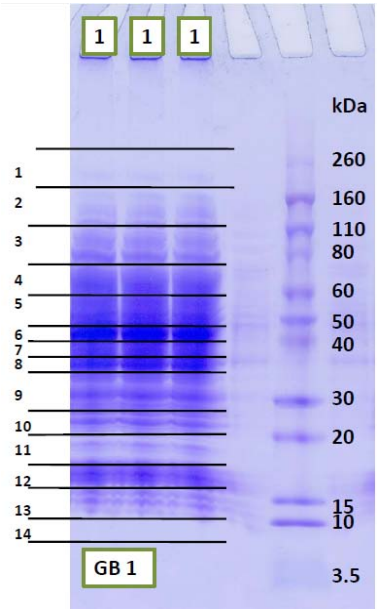


Figure 3.22 Coomassie stained SDS-PAGE. The numbered lines represent the cutting positions for the gel pieces which were further subjected to in-gel digestion and MS analysis. The numbering is related to the gel pieces, which were cut out for digestion, desalting and enrichment to gain MALDI – MS spectra for peptide/protein identification.

Having a look on the results of e.g. the sample with induced mycoparasitism (*Trichoderma atroviride*$_{wt.}$ vs. *Rhizoctonia solani*) the limitation of this method is obvious. The numbers of determined peptides are almost the same (29 peptides in the first analysis and 30 peptides in the replicate). But, only 15 peptides of them were determined in both samples.

In Table 3.11 the determined proteins are summarized. Detailed information about identifications and statistics are given in the appendix.

Table 3.11 Summary of the peptides detected in *Trichoderma atroviride* samples

Protein and the NCBI DB Name*		*T. atroviride* $_{wt}$ vs. *T. atroviride* $_{wt}$				*T. atroviride* vs. *R. solani*				*T. atroviride*$_{tmk1}$ vs. *R. solani*			
		1st measurement		2nd measurement		1st measurement		2nd measurement		1st measurement		2nd measurement	
		significant ID** (total)***	significant ID + $PO4_4$ (total) + $PO4_4$	significant ID (total)	significant ID + $PO4_4$ (total) + $PO4_4$	significant ID (total)	significant ID + $PO4_4$ (total) + $PO4_4$	significant ID (total)	significant ID + $PO4_4$ (total) + $PO4_4$	significant ID (total)	significant ID + $PO4_4$ (total) + $PO4_4$	significant ID (total)	significant ID + $PO4_4$ (total) + $PO4_4$
14-3-3-like protein	gi|358395807			1 (1)	0 (0)			0 (1)	0 (0)				
40S ribosomal protein S3	gi|358397895	0 (1)	0 (1)			1 (1)	0 (0)						
40S ribosomal protein S10	gi|358399687			1 (1)	0 (0)								
40S ribosomal protein S12	gi|358398659			0 (1)	0 (0)							0 (1)	0 (0)
40S ribosomal protein S15	gi|358398658							0 (1)	0 (0)			0 (1)	0 (0)
40S ribosomal protein S19	gi|358399317					0 (1)	0 (1)						
60S acidic ribosomal protein	gi|358391458			1 (1)	0 (0)							1 (1)	0 (0)
60S ribosomal protein L5	gi|358395995											0 (1)	0 (0)
60S ribosomal protein L16	gi|358399725									0 (1)	0 (0)		
Acetolactate synthase	gi|358399702							0 (1)	0 (1)			0 (1)	0 (0)
Ankyrin repeat containing protein	gi|358401578 gi|358392604					0 (1)	0 (1)	0 (1)	0 (1)				
Ca^{2+} dependent lipid-binding protein (containing C2 domain)	gi|358391401									0 (1)	0 (1)		
Calcium dependent mitochondrial carrier protein	gi|358396221			0 (1)	0 (1)								
cAMP regulated phosphoprotein family protein Igo1	gi|358401857					0 (1)	0 (1)						
Carboxypeptidase A	gi|358391622							0 (1)	0 (0)				
Cinnamyl-alcohol dehydrogenase family protein	gi|358397016	1 (1)	0 (0)									0 (1)	0 (0)
copper/zinc superoxid dismutase	gi|358398082			1 (1)	0 (0)	1 (1)	0 (0)	1 (1)	0 (0)			1 (1)	0 (0)
CorA-like Mg^{2+} transporter protein	gi|358394226			0 (1)	0 (1)								
Cyclophilin	gi|358390495	0 (1)	0 (1)	1 (1)	0 (1)			1 (1)	0 (0)			0 (1)	0 (0)

Cytochrom P450	gi|358400514					0 (1)	0 (1)						
DEAD-like helicases containing protein	gi|358396599					0 (1)	0 (0)						
Dihydrolipoamide acetyltransferase component	gi|358399676			1 (1)	0 (0)	1 (1)	0 (0)	0 (1)	0 (0)	1 (2)	0 (0)	2 (2)	0 (0)
Dihydrolipoamide succinyltransferase	gi|358399676											0 (1)	0 (0)
Elastinolytic metalloprotease	gi|358395328					0 (1)	0 (1)						
Elicitor Protein	gi|358392014			1 (1)	1 (1)	0 (2)	0 (2)	0 (2)	0 (2)	0 (1)	0 (1)	2 (2)	1 (1)
Elongation factor 1 beta (EF1B)	gi|358397747			3 (3)	3 (3)	2 (2)	2 (2)	3 (4)	3 (3)	1 (1)	1 (1)	2 (2)	2 (2)
Elongation factor 3 (EF-3)	gi|358399771	2 (2)	2 (2)	0 (1)	0 (0)	3 (4)	3 (3)	3 (4)	2 (2)	0 (2)	0 (2)	2 (4)	2 (2)
Enolase	gi|358400765											0 (1)	0 (0)
F-actin capping protein, beta subunit	**gi|358395844**					**2 (2)**	0 (0)	**1 (1)**	0 (0)				
FAD/FMN-containing dehydrogenases	gi|358394309	3 (7)	0 (0)	2 (5)	0 (0)	1 (3)	0 (0)	1 (4)	0 (0)	3 (6)	0 (0)	1 (3)	0 (0)
Fructose bisphosphate aldolase, class II	gi|358395434											0 (1)	0 (0)
Fungal specific transcription factor domain containing protein	gi|358390064					0 (1)	0 (1)						
Geranylgeranyl reductase family protein	gi|358389969											0 (1)	0 (0)
Glutamate-ammonia ligase	**gi|358397635**											**1 (1)**	0 (0)
Glycogen synthase kinase 3	gi|358401397	1 (1)	1 (1)	1 (1)	1 (1)	1 (1)	1 (1)	1 (1)	1 (1)	0 (1)	0 (1)	1 (1)	1 (1)
Heat shock 70 kDa protein	gi|358396940					0 (2)	0 (0)	2 (2)	0 (0)			1 (1)	0 (0)
Heme (Ascorbat and Cytochrome C) peroxidase region containing protein	gi|358395813			1 (2)	0 (0)	1 (1)	0 (0)	1 (1)	0 (0)	0 (1)	0 (0)	1 (1)	0 (0)
HMG box protein	gi|358391632			2 (2)	1 (1)	1 (2)	1 (2)	1 (2)	1 (2)	1 (1)	1 (1)	1 (1)	1 (1)
Kinesin motor domain containing protein	gi|358400646					0 (1)	0 (1)						
Malic enzyme	gi|358401365							0 (1)	0 (1)				
Mannosyl oligosaccharide glucosidase	gi|358396907					0 (1)	0 (1)						
MedA like protein	gi|358395489					0 (1)	0 (0)						
Molecular chaperone bip1	**gi|358398848**											**1 (1)**	0 (0)
NAC domain containing protein	gi|358393615							0 (1)	0 (0)				
Necrosis inducing protein	gi|358390537											0 (1)	0 (0)

Nuclear pore complex protein	gi|358398125			0 (1)	0 (1)								
p23 – hB – ind1 like protein	**gi|358396009**							**1 (2)**	0 (0)				
Pentatricopeptide repeat domain-containing protein	gi|358400387					0 (1)	0 (0)						
Phosphatidylinositol transfer protein	gi|358393449											0 (1)	0 (0)
Phospholipid - translocating P-type ATPase region containing protein	gi|358392421	0 (1)	0 (1)										
Plasma membrane H^+ - ATPase	gi|358397348											0 (1)	0 (1)
Plectin/S10 domain containing protein	gi|358399687	0 (1)	0 (1)			1 (1)	0 (0)	1 (1)	0 (0)			0 (1)	0 (0)
Poly (ADP-ribose) polymerase region containing protein	gi|358392615			0 (1)	0 (1)								
Protein kinase C-related kinase homology region 1	gi|358399396	0 (1)	0 (1)										
Protein phosphatase PTC2	gi|358390255											0 (1)	0 (0)
Putative aminotransferase	gi|358399612	0 (1)	0 (1)										
Ran-binding domain containing protein	gi|358397190			0 (1)	0 (0)			1 (1)	0 (0)	0 (1)	0 (0)	0 (2)	0 (0)
Ribosomal RNA-processing protein 7	gi|358391305									0 (1)	0 (0)		
Ribosome-associated chaperone zuotin	gi|358393305	1 (2)	1 (1)	0 (1)	0 (1)			2 (3)	2 (2)			1 (3)	0 (1)
RNA polymerase II subunit	gi|164449294					0 (1)	0 (1)						
Rossmann-fold $NAD(P)^+$-binding proteins (FAD-binding domain containing protein; FAD monooxygenase)	gi358389969			1 (1)	0 (0)			1 (1)	0 (0)	0 (1)	0 (0)	1 (1)	0 (0)
Rossmann-fold NAD(P)+-binding proteins (GDP dissociation inhibitor)	gi|35839368							0 (1)	0 (0)				
Rossmann-fold NAD(P)+-binding proteins (NADP binding domain containing protein; 6-phosphogluconate dehydrogenase)	gi|358391181			1 (1)	0 (0)			0 (2)	0 (0)			0 (2)	0 (0)
S-adenosylmehtionine synthase	gi|358391672							1 (1)	0 (0)			1 (1)	0 (0)
Short chain dehydrogenase/reductase family protein	gi|358398417					0 (1)	0 (1)						

Tetratricopeptide repeat domain contraining protein	gi|367020690		0 (1)	0 (0)			0 (1)	0 (1)		
Transaldolase like protein	gi|358398084		0 (2)	0 (0)	1 (2)	0 (0)	1 (2)	0 (0)	2 (3)	0 (0)
Translation initiation factor eIF3	gi|358401753		1 (1)	1 (1)					1 (1)	1 (1)
Type a willebrand factor domain-containing protein	gi|358394952		0 (1)	0 (0)						
WD 40 domain containing protein	gi|358392256 gi|358397996						0 (2)	0 (2)		

Color code: one significant hit; two significant hits; three significant hits of peptides for a protein;

Written in grey: proteins detected in the self confrontation sample;
Written in red: significant identified proteins
Bold framed numbers: only detected either at induced or at reduced mycoparasitism

*NCBI Database Name
**ID…Identification
***Total number of peptides

With the developed sample preparation strategy it was possible to determine 69 different proteins in a duplicate, 31 proteins in the sample with un-induced mycoparasitism, 45 in the sample with induced and 39 in the sample with reduced mycoparasitism. To again show the impact of the methodological and biological problems the numbers of proteins determined in both measurements are given. Only 5 proteins were determined in the first and second measurement in the sample with un-induced mycoparasitism, 17 in the sample with induced mycoparasitism and 10 in the sample with reduced mycoparasitism.

The *Trichoderma atroviride* $_{wt}$ vs. *Trichoderma atroviride* $_{wt}$ sample was under investigation to analyze the proteome of the wild type without inducing a mycoparasitic activity and to estimate which proteins were expressed during growth in the presence of another fungus, even if the other fungus represents the same species as the competition for e.g. nutrients may initiate some stress reactions. With the analyzed proteins of the sample with un-induced mycoparasitism, the standard proteome could be estimated. However, up and down regulations cannot be determined with this approach and therefore, the proteins occurring in the self confrontation sample are assumed to have no relevance in the activation of the mycoparasitic cascade and were excluded from further discussions and are written in grey in the table.

Taking these 31 proteins not into consideration, 25 proteins were determined only in the sample with induced mycoparasitism (*Trichoderma atroviride* $_{wt}$ vs. *Rhizoctonia solani*; three of them were determined in both measurements) and 17 only at reduced mycoparasitism (*Trichoderma atroviride* $_{tmk1}$ vs. *Rhizoctonia solani;* none of them were determined in both measurements).

Four of the 25, respectively 17 proteins, were determined in both samples (with induced and reduced mycoparasitism). These four proteins are 40S ribosomal protein S15 (35/56; respectively 43/55; the first score(s) is/are related to the sample with induced mycoparasitism and the last one is the result of the sample with reduced mycoparasitism; the values are separated by the word “respectively") acetolactate synthase (55/57; respectively 29/56), heat shock 70 kDa protein (51/54 and 46/54; respectively 57/55) and S-adenosylmethionine synthase (75/54; respectively 76/55).

A possible explanation for the presence in both samples, the wild type and the mutant, could be the fact that these proteins are expressed by *R. solani*. The proteome of *R. solani* was not determined in this approach. But, this could only be possible if the *Trichoderma atroviride* samples were contaminated with *R. solani* mycelia. However, it is assumed that the recognition of *R. solani* changed the proteome anyway, even if no mycoparasitic cascade was activated. Both, the wild type and the mutant recognized a different nutrition competitor and therefore activated some defense mechanism in early states of growth and some proteins are up- and some are down-regulated. Again,

no quantitative conclusions can be drawn, only the appearances or the absences of proteins are under investigations. Only when *Trichoderma atroviride* realized that the competitor is a phytophatogenic fungus, the mycoparasitic abatement is activated.

In the Table 3.11 the bold framed numbers marked the proteins, appearing only at induced (*Trichoderma atroviride* $_{wt}$ vs. *Rhizoctonia solani*) or reduced (*Trichoderma atroviride* $_{tmk1}$ vs. *Rhizoctonia solani*) mycoparasitism. As investigations revealed that the MAPK plays a key role in activating the mycoparasitic response [Reithner et al., 2007], the focus is on the identification of phosphorylated proteins. Keeping this goal in mind, only the proteins determined with phosphogroups are summarized in the table below (Table 3.12).

Table 3.12 Detected phosphorylated proteins either in the Trichoderma atroviride wild type or in the mutant

***T. atroviride*$_{wt}$ vs. *R. solani* (induced Mycoparasitism)**					
(Score/TH*)	NCBI DB**	Protein	Gel piece	theoretical MW [kDa]	MW area on the gel [kDa]
46/56	gi|358399317	40S ribosomal protein S19	12	16.523	16-18
19/56 18/55	gi|358401578 gi|358392604	Ankyrin repeat containing protein (!)	5 12	131.891 9.723	50-60 16-18
21/53	gi|358401857	cAMP regulated phosphoprotein family protein IgO1	4	13.982	60-75
16/54	gi|358394226	CorA-like Mg^{2+} transporter protein	9	60.864	30-40
14/55	gi|358400514	Cytochrom P450	3	59.067	75-110
51/57	gi|358395328	Elastinolytic metalloprotease	7	69.386	30-40
11/554	gi|358390064	Fungal specific transcription factor	11	59.760	18-20
19/55	gi|358400646	Kinesin motor domain containing protein	4	98.756	60-75
13/56	gi|358401365	Malic enzyme	6	73.992	40-50
26/55	gi|358396907	Mannosyl oligosaccharide glucosidase	3	120.275	75-110
24/55	gi|164449294	RNA polymerase II, subunit	6	38.140	40-50
18/57	gi|358398417	Short chain dehydrogenase/reductase family protein	4	29.927	60-75
37/57 13/53	gi|358392256 gi|358397996	WD 40 domain containing protein (!)	9 11	99.674 49.512	30-40 18-20

T. atroviride$_{tmk1}$ vs. *R. solani* (reduced Mycoparasitism)					
(Score/TH)	NCBI DB	Protein	Gel piece	theoretical MW [kDa]	MW area on the gel [kDa]
21/58	gi|358391401	Ca^{2+} dependent lipid-binding protein	8	166.309	30-40
45/54	gi|358397348	Plasma membrane H^+ - ATPase	1	111.508	160-260

*TH…Threshold <0.05 **NCBI DB…NCBI Database Name
(!) was detected two times in two different gel pieces

At a glance, it can be assumed that a higher number of phosphorylated peptides were determined in the *Trichoderma atroviride* $_{wt}$ than in the *Trichoderma atroviride*$_{tmk1}$sample. In the wild type strain of *Trichoderma atroviride*, 13 phosphoproteins and in the mutant only two were detected. One can assume that the mutant missing the Tmk1 MAPK is not able to phosphorylate certain proteins and subsequently is not able to activate proteins necessary for mycoparasitic response. Unfortunately, none of the respective peptides were identified within the requested significance (threshold $p< 0.05$).

Two proteins have to be mentioned explicitly: WD 40 domain containing protein and Ankyrin repeat containing protein. These proteins were detected by the sequence of two peptides in two different gel pieces. Due to the possibility of degradation or cleavage of subunits, it has to be clarified whether they originate from the same protein. However, the different database entries allude that these proteins are not the same. If it turns out that peptides are related to the same protein, the score can increase and it is possible that the resulting score can be higher than the threshold of <0.05 and the proteins are identified significantly. BLAST (Basic Local Alignment Search Tool) provides a tool to align two or more sequences to identify similarities. Aligning the two detected sequences for WD 40 domain containing protein, **SLSMRIFTLKWSSEGDSIEASLVR** and **QSGSFSSMLR**, do not lead to significant similarities (see Figure 3.23). The comparison of the whole proteins´ amino acid sequences shows only the appearance of this WD 40 domain in both proteins (see Figure 3.24) but only with total protein sequence coverage of 4 %. The amino acid sequences of both peptides, they were related to, are listed below.

Blast 2 sequences

Protein Sequence (24 letters)

Query ID	lcl|2821	**Subject ID**	lcl|2823
Description	None	**Description**	None
Molecule type	amino acid	**Molecule type**	amino acid
Query Length	24	**Subject Length**	10
		Program	BLASTP 2.2.28+

No significant similarity found. For reasons why,click here

Figure 3.23 BLAST result for the alignment of the two sequences for WD 40 domain containing protein

Blast 2 sequences

gi|358392256 (128 letters)

Query ID	gi|358392256|gb|EHK41660.1|	**Subject ID**	gi|358397996|gb|EHK47354.1|
Description	hypothetical protein TRIATDRAFT_302116 [Trichoderma atroviride IMI 206040]	**Description**	hypothetical protein TRIATDRAFT_129734 [Trichoderma atroviride IMI 206040]
Molecule type	amino acid	**Molecule type**	amino acid
Query Length	128	**Subject Length**	458
		Program	BLASTP 2.2.28+ ▸Citation

Other reports: ▸Search Summary [Taxonomy reports] [Multiple alignment]

Graphic Summary

Distribution of 1 Blast Hits on the Query Sequence

EHK47354 hypothetical protein TRIATDRAFT_129734 [Trichoderma atr.. S=13 E=4.4

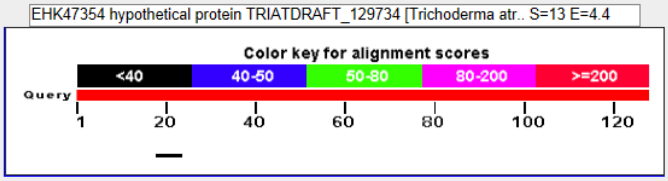


Figure 3.24BLAST result for the alignment of the two proteins containing a WD 40 domain.

Amino acid sequence of the WD 40 domain containing proteingi|358392256detected in gel piece number 9(UniProtKB Entryname: G9NP82_HYPAI):

```
  1 MATKQPLKTT FDVERVIRPI YTGGSVAVDN KAQILATTLG EDAILTNPSN
 51 GKHLAQIEGD GEAISTLTLT PSGSHLIICS RSLSMRIFTL KWSSEGDSIE
101 ASLVRTLKPH TTPVIVIAVD RTGTLLATGG TDGAIKVWDI SGGYVTHTFR
151 GPSVLVSALR FFEVAARSAS SRNSKGVKNQ SKAADEEDEE ETDNATTTNF
201 RLASGSQDGK VRIWDLNKRS CIANLDSHVS DVQAIDYSPT QHAIVTASRD
251 KTLIWWDAKS WKIRKVVPCL ELVEAAGFLD DGNLTYSAGA NGCLRIWDTD
301 KGAELTPKQS SKSEEEGIFA GIYRPELPFI LLVQVDHTLA LYELASKAST
351 ATFATPEPFR RISGTHDEII DMAYLLPDHS ILALATNSED VRLVSVADTK
401 QDASEMTWTK SETPYFGQDV ALLRGHDDIV IALDVDWSGH WVATGAKDNT
451 AKLWRIDPAN GSHICWATFS GHAESLGAVA LPRTLPAEGS AARTDPLNHP
501 PPFLITGSQD QTIKKWEIPR TPQQRDQKTN ARSAFTRKAH DKDINAITVH
551 HAGQLFASAS QDKTVKVWSV EEGEVQGILR GHKRGVWTVQ FSPAQMPALQ
601 GEDGPITGKG VVLTGSGDKS IKLWNLADYT CIRTFEGHSN SVLKVAWLNM
651 TSRPEQSRGL VQFASAGGDG LVKIWNANSG EAECTLDNHE DRVWALAVHP
701 DTNAVVSGSG DSTVTFWKDT TSQTQAAASQ AALKLIEQEQ ELENHMHAGS
```

```
751  YREAITLALQ  LNHPGRLLSL  FTSVVTTSKP  EQGSLCGIKA  VDQVLATLSD
801  DQIYLLLLRL  RDWNTNARSA  PVAQRILRTL  IKSYPASKFS  NLQVKGSRGE
851  KSLKDVLHGL  RVYTERHYKR  MEELVDESYL  VEYTLQEMDS  LAPTLQGDVS
901  LNADTIMIS
```

Amino acid sequence of the WD 40 domain containing proteingi|358397996detected in gel piece number 11(UniProtKB Entryname: G9P803_HYPAI):

```
  1  MATPTLNFIT  FNQDHSCLAV  GTSKGFGIYH  TDPFSRIFSS  DDGNIAIIEM
 51  LFSTSLVALI  LSPRHLIIQN  TKRASVICEL  TFPSAVLAVR  LNRKRLAVVL
101  EEEIYLYDIS  NMSLLYTIPT  SPNPSAICAL  SASSENCYIA  YPLPKPREES
151  DNRRPSHAPP  QSAYVAPTSG  EVLMFDTLTL  KAVNVVEAHR  SPLSCISLNS
201  EGTMLATASE  TGTIIRIFSV  PRGQKLYQFR  RGTYPSTIYS  MSFNLSSTLL
251  CVSSASDTVH  IFRLSAPPGH  TTPAGAPIES  LGSPRQDRWS  RGRSHDGADS
301  PSNNSATESP  KSETAELAGN  GTAPDSSSQP  VNRKQSGSFS  SMLRRSSQIM
351  GRGVAGVVGS  YLPQSVTEMW  EPLRDFAYIK  IPKSTGLGAG  ARPPGQGSNP
401  LRSVVAMSSS  SPQVMVVTSD  GGFYVYNIDM  EHGGEGYLVK  QFSVLEGDSK
451  SDPSAYTG
```

The identified peptide sequences are shown in bold red. The only similarity between these proteins is the existence of a WD 40 domain which could be determined by comparison of these protein sequences. The conserved domains of the sequences are shown in Figure 3.26. These annotations were accomplished by NCBI´s Conserved Domain Database (CDD) [Marchler-Bauer et al., 2011]. The presence of the same sequence pattern in two proteins normally indicates that they share a conserved biochemical function and/or substrate. The WD repeat is a conserved motif that is found in a variety of a large family of proteins [Smith et al., 1999]. Generally, the WD motif (also called Trp-Asp motif) is an approximately 40 amino acids stretch typically ending with a Trp - Asp dipeptide and is found in over 100 proteins with diverse cellular functions [Di Benedetto et al., 2001]. Almost all structurally characterized WD-repeat proteins are composed of seven such repeats and fold into seven-bladed propellers, which you can see in Figure 3.25.

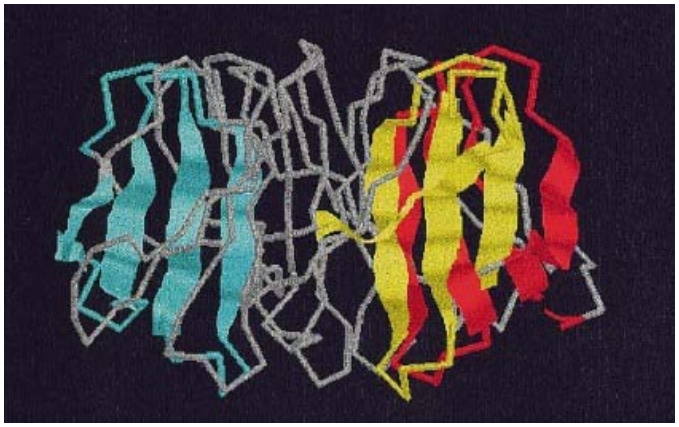


Figure 3.25 Structure of a WD - repeat protein
Side view of a structure of a WD – repeat protein. Each blade (one is colored in blue) of the typical propeller of the WD 40 domain consists of a single four stranded antiparallel β-sheet. The N – terminus is colored in red and the C – terminus in yellow.
Modified by [Smith et al., 1999]

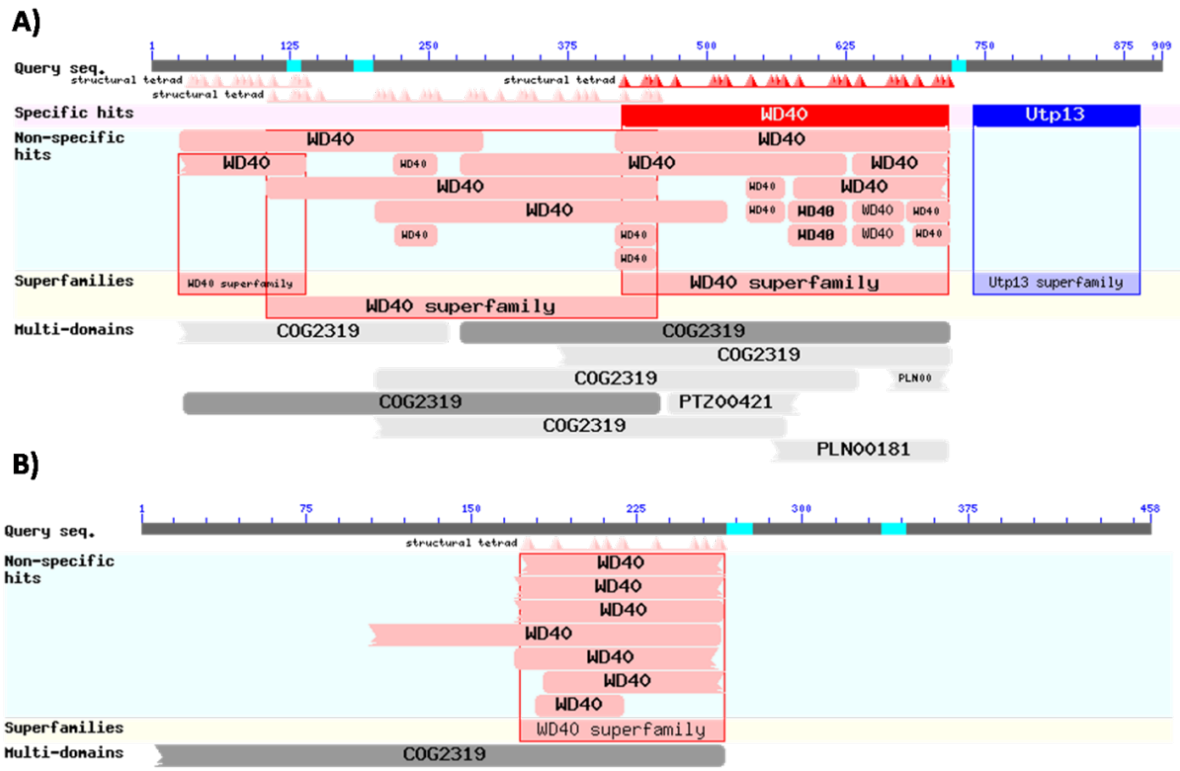


Figure 3.26 Conserved domain annotation of the WD 40 domain containing proteinby NCBI´s CDD
A) Conserved domains of the detected WD 40 domain containing protein in the gel part number 9 and B) Conserved domains of the detected WD 40 domain containing protein in the gel part number 11. The WD 40 domain exists in both proteins but the proteins themselves are not the same.

The same was found out aligning the different peptide sequences, **TLSLSSDQITVYSLAKTSNR** and **YGKTPVSKAVENSR** (see Figure 3.27) and protein sequences (see Figure 3.28). No significant similarities were found aligning the peptide sequences. However, aligning the protein sequences, coverage of 12 % was determined.

Figure 3.27 BLAST result for the alignment of the two sequences for Ankyrin repeat containing protein

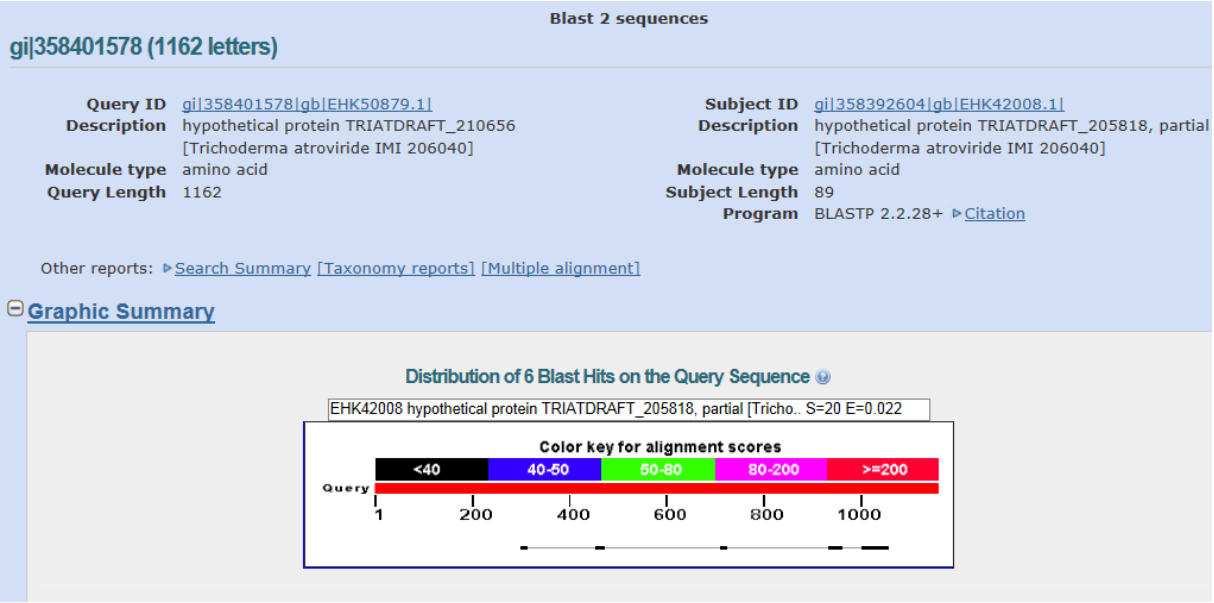


Figure 3.28 BLAST result for the alignment of the two proteins containing an Ankyrin repeat

Amino acid sequence of the Ankyrin repeat containing proteingi|358401578detected in gel piece number 5(UniProtKB Entryname:G9NEI1_HYPAI):

```
   1 MSASSGTQKV  FRLRRLPESI  SSRKDVAKLL  GKTLSLSSDQ  ITVYSLAKTS
  51 NRWGSMSKVA  TVQFKSIPPI  LDPEPPGAQW  KFPIPESQHN  DVLILDTHFR
 101 GMTVLNDVEK  ENHRTDCIAI  SGLASHPFGS  WQPHGPDKSF  MWIRDELPTS
 151 VPGVRAILYG  YDSRLKDSKS  FQSIEDIAGC  LILNLKSGGW  NLPKSRPIIF
 201 LAHSLGGIVL  KEAIKQMAGN  SDRREADILN  NLLGAIMFGV  PNLGMEQSHL
 251 MAMVEGQDNE  TLVQDLSRNN  GRNYVRQLDE  KFNGLSTVHT  LKILWAYETE
 301 SLTIPINKNH  SDMVKFSQGD  EDLETIIFSL  NDILKERLGQ  PLLAPNDASQ
 351 SQQTLLGANL  DYQSTDEGVL  TEDEKVLKDL  GSFLLSIQGI  HDELYSPELD
 401 SRINQIEDPS  QNTFNWIFSL  PLFSQWLRKK  SGLFWISGKP  GSGKSTLMKH
 451 VFQSQSTKDL  SHKWETSSID  IKAGFFFHYR  GTAIQKSLEG  VLRSLIIHIL
 501 KPHRIAFQKK  YQGTWEIFQS  FIQRYRTLEG  QRASFEYELD  AIVEEKMVGD
 551 IKQQLSLLHR  RMEEVSKRSL  DFREREPELQ  QKLKQVRADI  AAVSRSISSL
 601 AEKARPYQTQ  PETRFLRSLV  NELQNDSNSQ  VDKLEQILRL  LLDQDIMNIN
 651 LVLFFDALDE  FDGHIENISD  FLTNLLERST  TSKTQIKVCF  SSRPQESLND
 701 HFTKYPGFRL  QDYTTEDIEQ  YAKISLARSE  IMNFSQREEF  MKIIPSIIAR
 751 ANGVFLWVRL  AMKELFDTAG  GSPEAELFGR  LKKKLQELPD  DLLKFYKHII
 801 ERISGANRRY  TFALLELLAR  HAGLSVSVTD  IWGAVLTSGC  TTFEESLEVL
 851 QKISGNTGQK  IATDSDRDQR  AISDISAWAG  GLVEIKAQNN  LQLMHQTVLE
 901 FTRDQTFKNW  IDESPDQLRR  IFRQGAQPPL  LTYLAFEPAS  GVLLKGHVTT
 951 ARLLLEKGYN  IAKDTRFFPS  LLEKIWKAEA  MAAVQGGFSE  SHAQTAIARI
1001 LQELATVVLD  NGQNPNISCS  IFSRDNLQRC  TPLHIAPPGL  AAKLIRCDAD
1051 VNMPDSWGKK  PLDWVLNPPR  WSPRWSCARR  YEMCRLLVKA  GALMSESTPD
1101 EDWIGALAEF  DLAGHDVEVL  QRNEPRPLAA  AAPSSGDPNA  QNSKERHRRR
1151 ALSFLVGLFR  KK
```

Amino acid sequence of the WD 40 domain containing proteingi|358392604detected in gel piece number 12(UniProtKB Entryname:G9P4M2_HYPAI):

```
  1 KTPLSLAAEY GHLAVVIFLA GKGANFERPD ISHKTPLSLA VEKGHFEVVK
 51 FLAGKGANTE SKDRYGKTPV SKAVENSRLD IVKFLVEMC
```

The identified peptide sequences are shown in bold red. As well as the WD 40 domain containing protein the conserved domain annotation shows only the appearance of Ankyrin repeats but no other similarities. The CDD results are shown in Figure 3.29

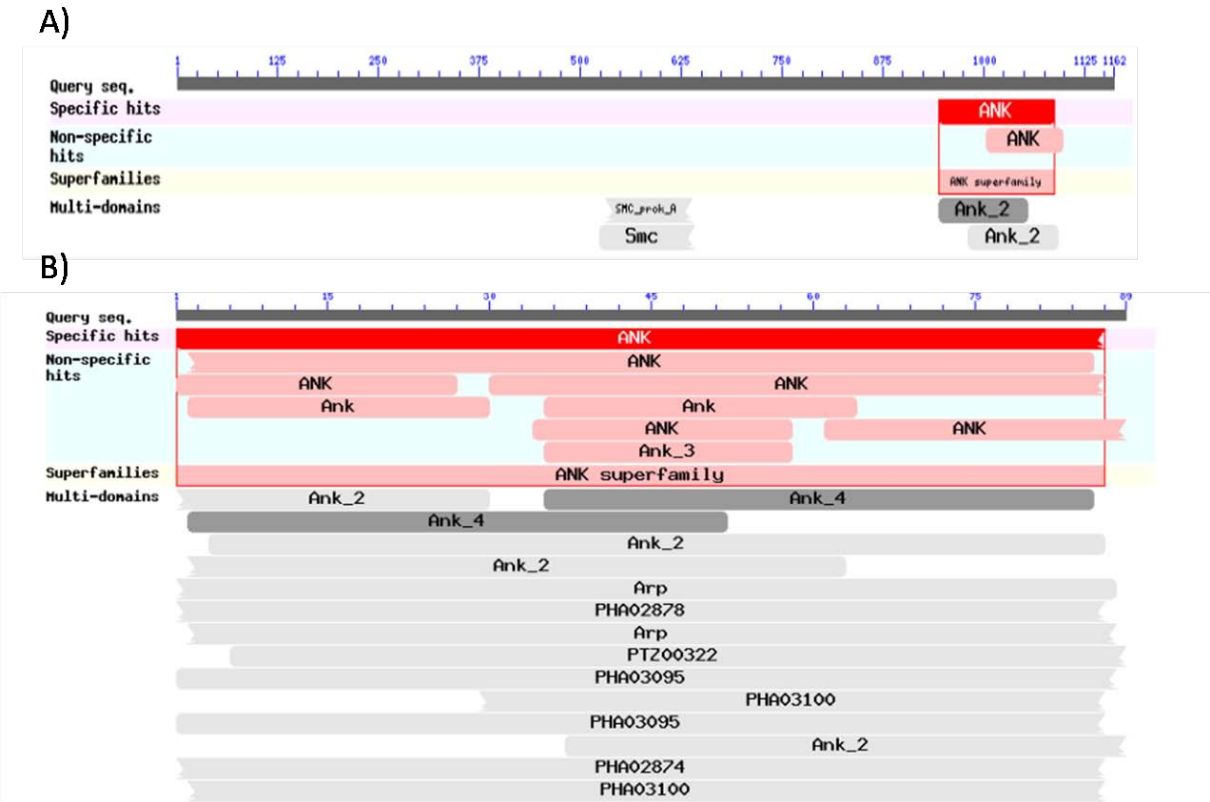


Figure 3.29 Conserved domain annotation of the Ankyrin repeat containing protein by NCBI´s CDD
A) Conserved domains of the detected Ankyrin repeat containing protein in the gel part number 5 and B) Conserved domains of the detected Ankyrin repeat containing protein in the gel part number 12. The Ankyrin repeat domain exists in both but there are non others similarity.

Ankyrin repeats mediate protein-protein interactions in very diverse families of proteins and the number can range from 2 to over 20. They may occur in combinations with other types of domains. The structural repeat unit contains two anti-parallel helices and a beta-hairpin, repeats are stacked in a super-helical arrangement; this alignment contains 4 consecutive repeats (Figure 3.30) [Sedgwick and Smerdon, 1999].

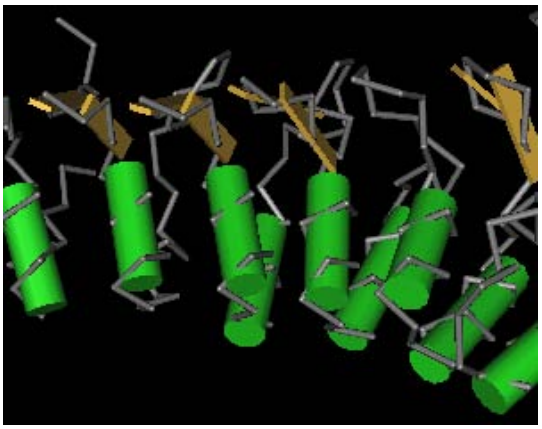


Figure 3.30 Structure of an Ankyrin repeat containing protein
The typical Ankyrin repeat consist of two antiparallel helices (colored in green) and a beta-hairpin (colored in yellow).

Nevertheless, no significant identification of a phosphorylated protein was possible.

Therefore, proteins without a detected phosphogroup were under investigation. 8 proteins in *T. atroviride* wild type and 12 proteins in the *T. atroviride* mutant were detected. In Table 3.13 the proteins without a phosphogroup are summarized. Again, this does not exclude the possibility that those proteins can carry a phosphogroup but in lower concentration, so the identification of them is hindered.

Table 3.13 Detected proteins without phospho-residues either in the *Trichoderma atroviride* wild type or in the mutant

T. atroviride$_{wt}$ vs. R. solani (induced Mycoparasitism)					
(Score/TH)*	NCBI DB**	Protein	Gel piece	theoretical MW [kDa]	MW area on the gel [kDa]
30/56	gi|358391622	Carboxypeptidase A	7	47.505	30-40
21/56	gi|358396599	DEAD – like helicases containing protein	2	104.578	110-160
64/55	gi|358395844	F – actin capping protein (!)	8	31.312	30-40
65/55	gi|358395844		8	31.312	30-40
88/56	gi|358395844		8	31.312	30-40
13/53	gi|358395489	MedA like protein	10	77.943	20-30
53/58	gi|358393615	NAC domain containing protein	12	16.614	16-18
58/58	gi|358396009	p23 hB – ind1 like protein (!)	10	23.459	20-30
32/58	gi|358396009		10	23.459	20-30
20/56	gi|358400387	Pentatricopeptide repeat – containing protein	8	93.271	30-40
22/56	gi|35839368	Rossmann – fold NAD(P)$^+$ - binding protein (GDP dissociation inhibitor)	6	51.177	40-50
T. atroviride $_{tmk1}$ vs. R. solani (reduced Mycoparasitism)					
(Score/TH)	NCBI DB	Protein	Gel piece	theoretical MW [kDa]	MW area on the gel [kDa]
26/57	gi|358395995	60S ribosomal protein L5	8	33.971	30-40
23/54	gi|358399725	60S ribosomal protein L16	4	27.731	60-75-
26/57	gi|358399676	Dihydrolipoamide succinyltransferase	6	46.786	40-50
48/55	gi|358400765	Enolase	6	47.443	40-50
24/55	gi|358395434	Fructose bisphosphate aldolase, class II	8	39.446	30-40
26/55	gi|358389969	Geranylgeranyl reductase family protein	6	45.538	40-50
87/57	gi|358397635	Glutamate ammonia ligase (!)	7	40.508	30-40

82/56	gi|358398848	Molecular chaperon bip 1 (!)	4	72.450	60-75
26/56	gi|358390537	Necrosis inducing protein	10	31.144	20-30
16/55	gi|358393449	Phosphatidylinositol transfer protein	9	33.161	30-40
29/57	gi|358390255	Protein phosphatase PTC2	7	47.539	30-40
13/54	gi|358391305	Ribosomal RNA – processing protein 7	5	35.575	50-60

*TH…Threshold <0.05 **NCBI DB…NCBI Database Name

(!) Significant identified proteins

As you can see in both samples, in the *Trichoderma* samples with induced as well as with reduced mycoparasitism, two proteins were identified significantly. In *Trichoderma atroviride* $_{wt}$ F – actin capping protein and p23 hB – ind1 like protein and in *Trichoderma atroviride* $_{tmk1}$ glutamate ammonia ligase and molecular chaperon bip1 were identified. In Figure 3.31 to Figure 3.34 the annotated PSD spectra are listed. Detailed information about the Mascot Results are given in chapter6, appendix.

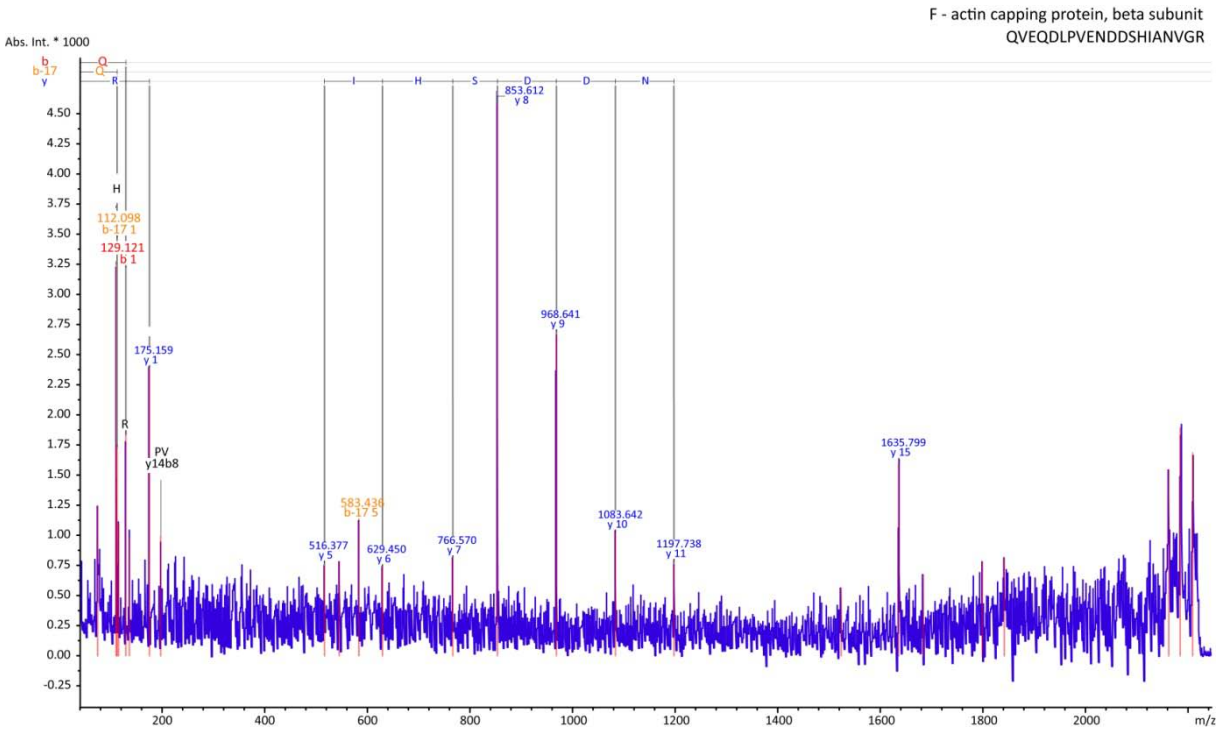


Figure 3.31 PSD spectrum of m/z 2235.011 Da identified as F - actin capping protein, beta subunit

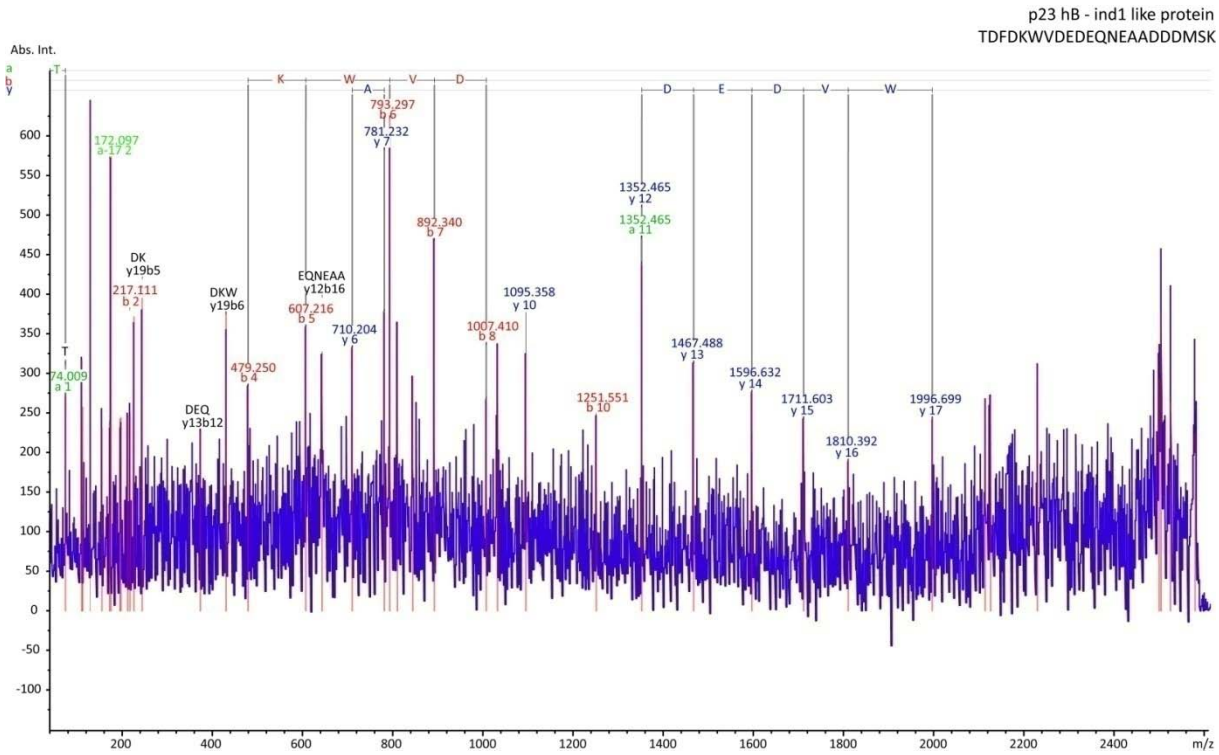


Figure 3.32 PSD spectrum of m/z 2602.647 Da identified as p23 hB-ind1 like protein

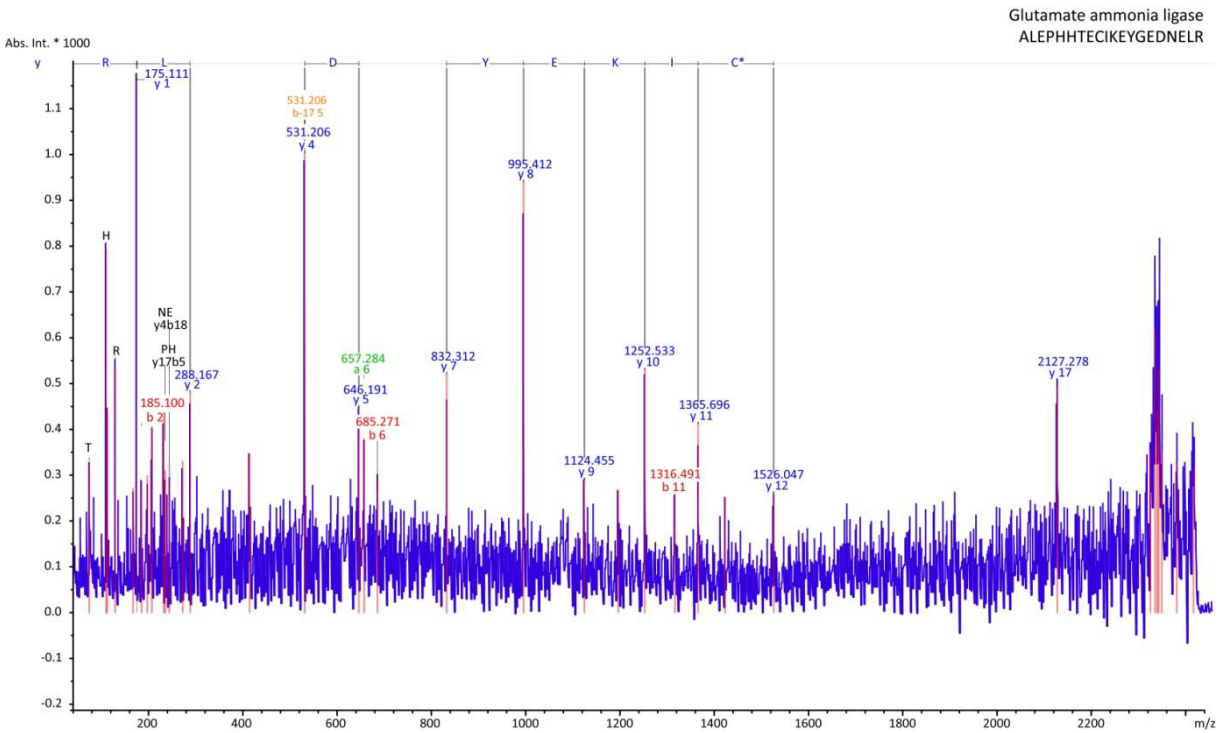


Figure 3.33 PSD spectrum of m/z 2439.821 Da identified as glutamte ammonia ligase

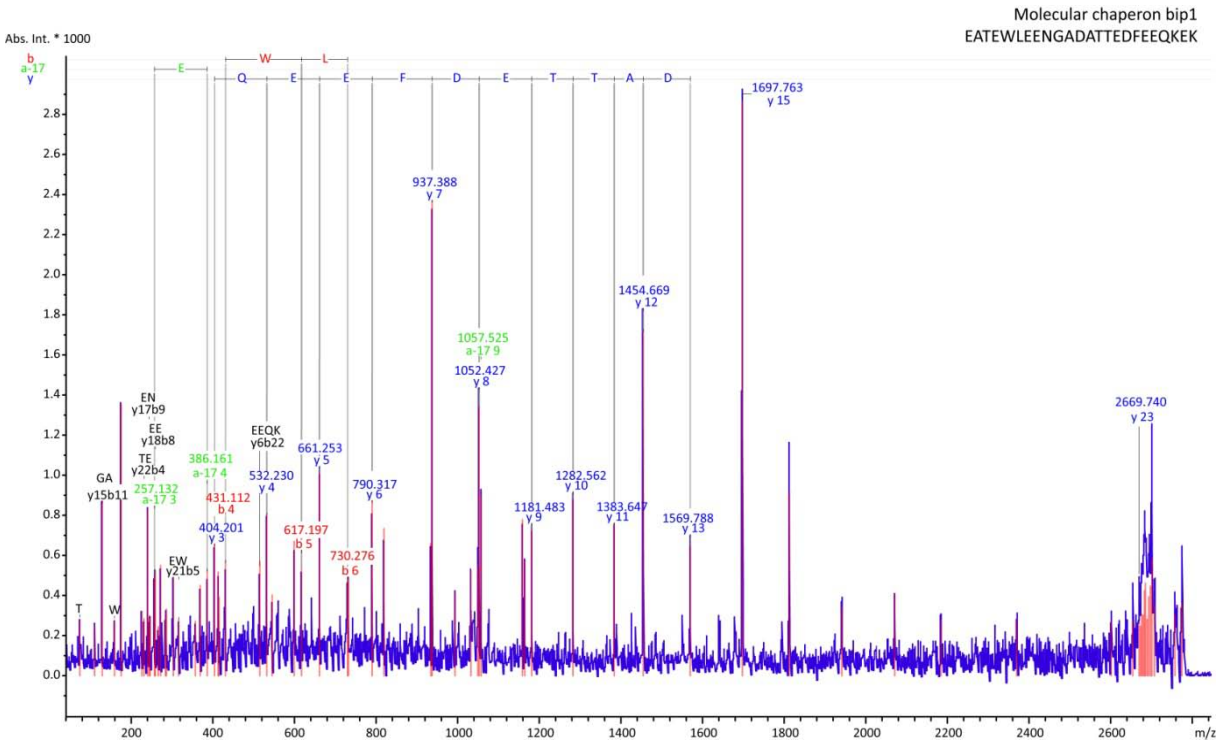


Figure 3.34 PSD spectrum of m/z 2799.119 Da identified as molecular chaperon bip1

3.3.3.1 Biological Function of the significant identified Proteins

F-actin capping protein, beta subunit

(UniProtKB Entryname: G9NW69_HYPAI)

F-actin capping protein blocks the ends of actin filaments by binding in a calcium independent manner [Maruyama, 1990]. The protein itself consists of a heterodimer (alpha subunit 268-286 amino acid residues and beta unit 280 amino acid residues).

p23 hB-ind1 like protein

(UniProtKB Entryname:G9NWP5_HYPAI)

p23 like domain found in human (h) butyrate-induced transcript 1 (B—ind1). hB-ind1 participates in signaling by the GTPase Rac1 by means of activation of nuclear factor κB and c-Jun N-terminal kinase [Felts and Toft, 2003]. It interacts with heat shock protein Hsp90 and therefore playing a role in the RNA replication and particle production of Hepatitis C virus. p23 hB-ind1 like proteins includes a co-chaperon of the Hsp90, namely the *Saccharomyces cerevisia* Sba1. This co-chaperon shows to be required for telomere length maintenance and may modulate telomerase DNA binding activity.

Glutamate ammonia ligase

(UniProtKB Entryname:G9NNY9_HYPAI)

Glutamate - ammonia ligase is an enzyme involved in the ATP-consumptive transfer of an ammonium to glutamate to produce glutamine [Liaw et al., 1995]. It plays an important role in the metabolism of

nitrogen by the catalyzing the glutamine production, the detoxification of ammonia and the assimilation of ammonia. The glutamate - ammonia ligase consists of 477 amino acid residues.

Molecular chaperon bip1

(UniProtKB Entryname:G9NMR9_HYPAI)

The molecular chaperon bip1 belongs to the heat shock protein hsp70 family. This protein family assists in protein folding and assembly and also directs miss folded proteins towards degradation [Daugaard, 2007]. The hsp70 proteins consist of a nucleotide-binding domain (NBD) and a substrate-binding domain (SBD). The two subdomains of the NBD change their conformation between ATP-bound, ADP-bound and nucleotide-free states. If ATP binds, the SBD opens the binding site; substrate binds and increases the rate of ATP hydrolysis. The molecular-chaperon bip1 consists of 622 amino acid residues.

3.3.4 Summary of the Phosphoprotein Identification

Analyzing the whole lysate of the different Trichoderma atroviride samples (un-induced, induced and reduced mycoparasitism) turned out to be not the best way to identify those proteins playing a key role in the activation of mycoparasitic response. High abundance proteins (e.g. housekeeping proteins) suppress the MS-signal in the spectra. Therefore, a 1D – SDS –PAGE step was included to increase protein identification rate and phosphoprotein recovery. Using this workflow, it was possible to detect 69 proteins. The results are no strict statements; it concerns only general tendencies, because of biological and methodical issues, which are discussed in detail on page 76. Proteins detected in the self confrontation sample (*Trichoderma atroviride*$_{wt}$ v. *Trichoderma atroviride*$_{wt}$) with un-induced mycoparasitism are assumed to have no relevance in the activation of the mycoparasitic cascade and were excluded from further discussion. Therefore, 21 proteins were determined only in the sample with induced mycoparasitism (*Trichoderma atroviride* $_{wt}$ vs. *Rhizoctonia solani*) and 13 only at reduced mycoparasitism (*Trichoderma atroviride* $_{tmk1}$ vs. *Rhizoctonia solani*). Unfortunately, no phosphorylated protein was identified significantly neither with induced nor with reduced mycoparasitism. Investigations on the proteins detected without phosphogroups revealed that in both samples, in the *Trichoderma* samples with induced as well as with reduced mycoparasitism, two proteins were identified significantly; namely, F – actin capping protein and p23 hB – ind1 like protein in the wild type and glutamate ammonia ammonia ligase and molecular chaperon bip1 in the mutant.

4 CONCLUSION

Mycoparasitic species, like *Trichoderma atroviride*, are used as biocontrol agents in agriculture to antagonize phytopathogenic fungi. This antifungal activity is in today´s focus to increase sustainable agriculture and biological control as a good alternative to chemical pesticides. The mechanism of *Trichoderma atroviride* is based on the one hand on the stimulation of the plant´s own defense mechanism and on the other hand on the mycoparasitism. The mycoparasitic activity includes the host recognition, the attachment to the host hyphae and the secretion of antibiotics and cell-wall degrading enzymes to kill the parasite. In recent years, investigations on the underlying signal transduction pathways revealed that G-protein signalling and pathways including mitogen-activated protein kinases (MAPKs) play important roles in the mycoparasitic response. Analyzing the *Trichoderma atroviride* wild type and a mutant missing the MAPK-encoding *tmk1* gene (*Trichoderma atroviride* $_{tmk1}$) should offer the identification of proteins which are regulated by the MAPK and therefore contributing to mycoparasitism.

First of all, an evaluation of sample preparation techniques was carried out to gain a method which enables the detection of phosphorylated peptides by MALDI - MS. The best MALDI – matrix, a proper desalting method and the best performing enrichment strategy were evaluated.An optimized sample preparation method was developed including desalting with HyperSep 96 C_{18} well plate, enrichment using a Magnetic Titatnium Dioxide Phosphopeptide Enrichment Kit. The MALID - MS analyses were carried out using 3 mg/ml CHCA.

After the establishment of a proper sample preparation technique, the *Trichoderma atroviride*s amples were analyzed. Since, the analyses of the whole lysate failed, due to high abundance proteins, which assumed to have no regulatory implications, a 1D – SDS – PAGE step was included into the workflow. Based on this workflow, 69 proteins could be detected (31proteins in the sample with un-induced mycoparasitism, 45 in the sample with induced and 39 in the sample with reduced mycoparasitism). However, methodical and biological issues of this approach make conclusions complex. The results are rather tendencies than strict statements and in this context possible correlations can only be assumed.

The *Trichoderma atroviride*$_{wt}$ vs. *Trichoderma atroviride*$_{wt}$ sample was under investigation to estimate the proteins expressed during growth in the presence of another fungus. However, up and down regulations cannot be determined with this approach and therefore, the proteins occurring in the self confrontation sample are assumed to have no relevance in mycoparasitism. Thus, 25 proteins were

determined in the wild type grown against *R. solani* and 17 in the mutant. Unfortunately no phosphorylated protein could be identified significantly, with a threshold < 0.05. Due to the difficulties implicated by analyzing phosphorylated proteins, proteins without phosphorylations were investigated. In both, the wild type and the mutant missing the *tmk1* MAPK, two proteins were identified (TH<0.05), namely, F – actin capping protein and p23 hB – ind1 like protein in the sample with induced mycoparasitism (wild type) and glutamate-ammonia ammonia ligase and molecular chaperon bip1 in the sample with reduced mycoparasitism (mutant).

With this approach, first insights into the proteome of *Trichoderma atroviride* with different states of mycoparasitic activities can be assumed. Although no phosphorylated protein was detected significantly, tendencies of proteins occurring at induced mycoparasitism can be considered. Further investigations can be directed on the same approach. Also a workflow including another enrichment step is a possibility. The main disadvantage of the used enrichment strategy *Pierce® Magnetic Titanium Dioxide Phosphopeptide Enrichment Kit* is the preferred enrichment of mono phosphorylated peptides. Information about a protein with multiply phosphorylated residues disappears and the coverage of the phosphoproteom of the *Trichoderma atroviride* sample is limited. One alternative to MOAC is the use of an IMAC based enrichment step or the combination of both, exploited by Thingholm et al. in 200, called SIMAC (sequential elution from IMAC) [Thingholm et al., 2008]. The complementary distribution with acidic or basic elution prior MS analyses, obtained from separate affinity media enables the sequentially separation of mono-phosphorylated and multiple phosphorylated peptides from highly complex biological samples.

By understanding the mycoparasitic process and the influence of MAPK, a suitable application of biological fungicides in agriculture is revealed. Therefore the identification of proteins, playing a key role during the activation of the mycoparasitic cascade is of utmost importance.

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6 APPENDIX

6.1 Analyzing the Cell Lysate without prior Separation

6.1.1 PSD Spectra of *T. atroviride* related PMF peaks without Enrichment

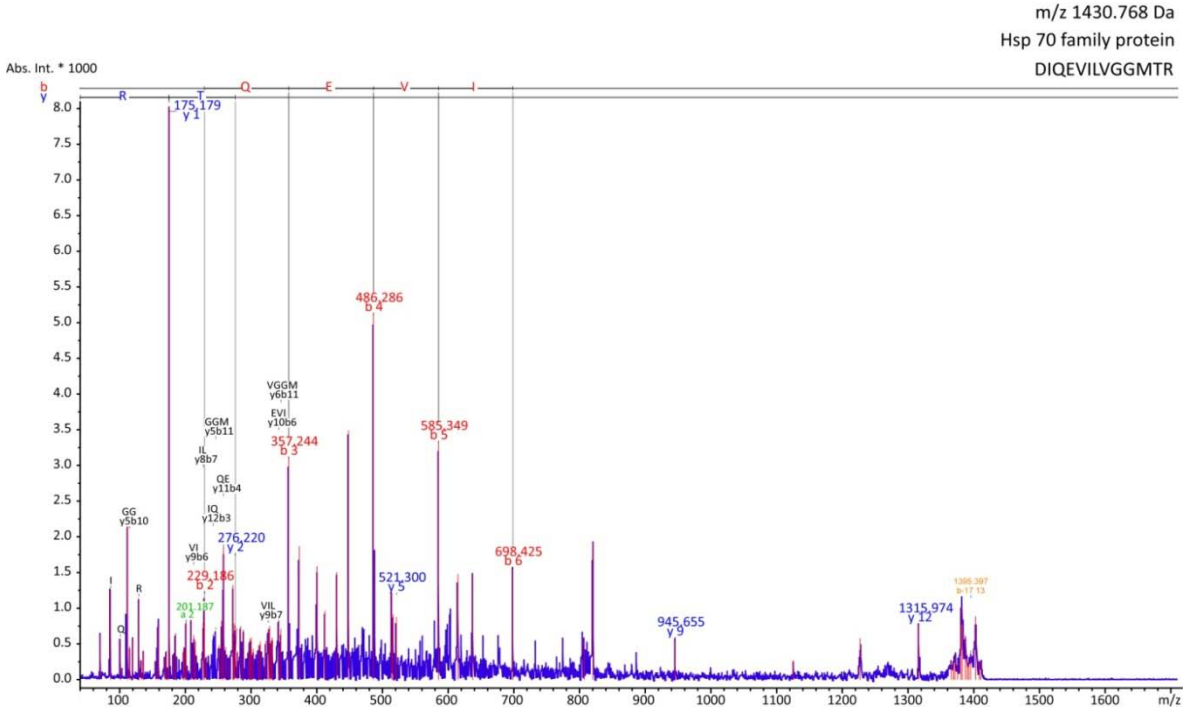


Figure 6.1 PSD spectrum of m/z 1430.768 Da at un-induced mycoparasitism

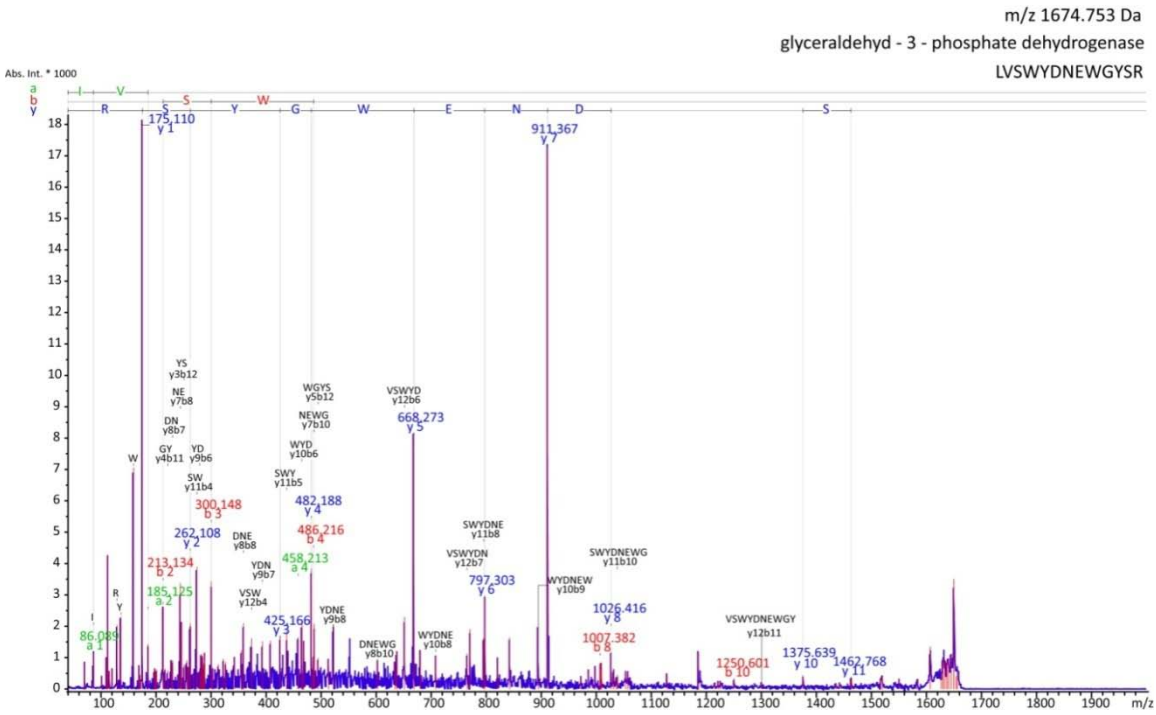


Figure 6.2 PSD spectrum of m/z 1674.753 Da at un-induced mycoparasitism

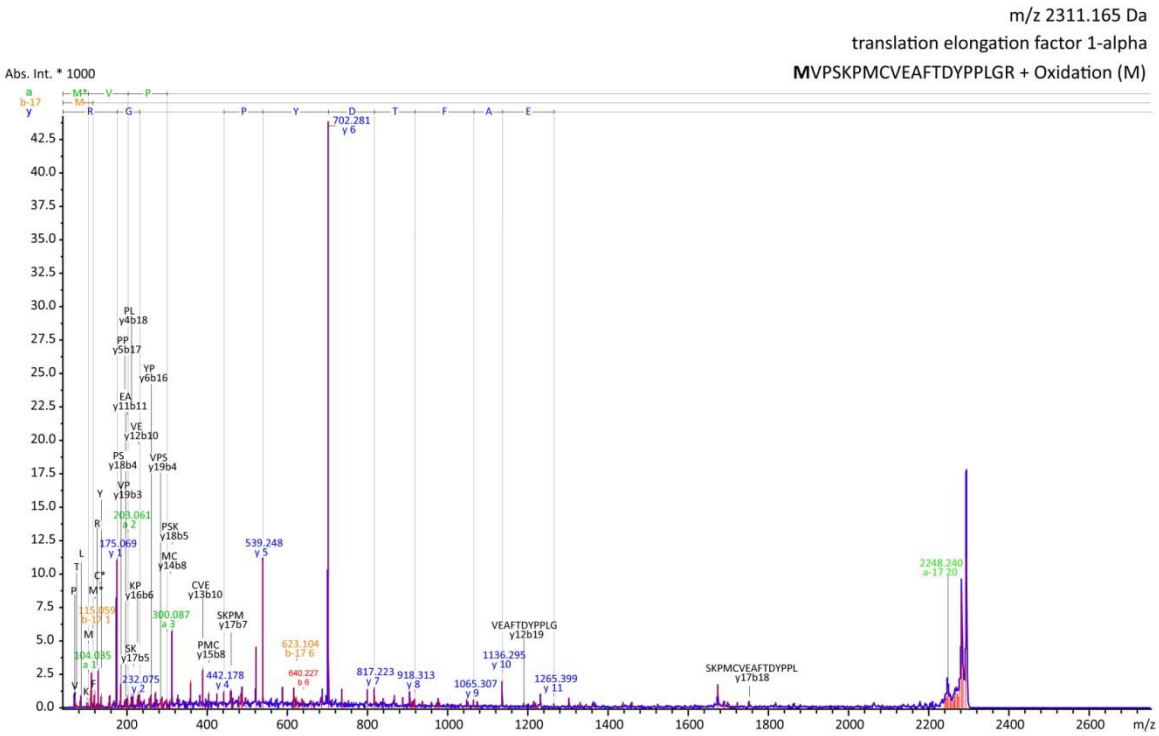


Figure 6.3 PSD spectrum of m/z 2311.165 Da at un-induced mycoparasitism

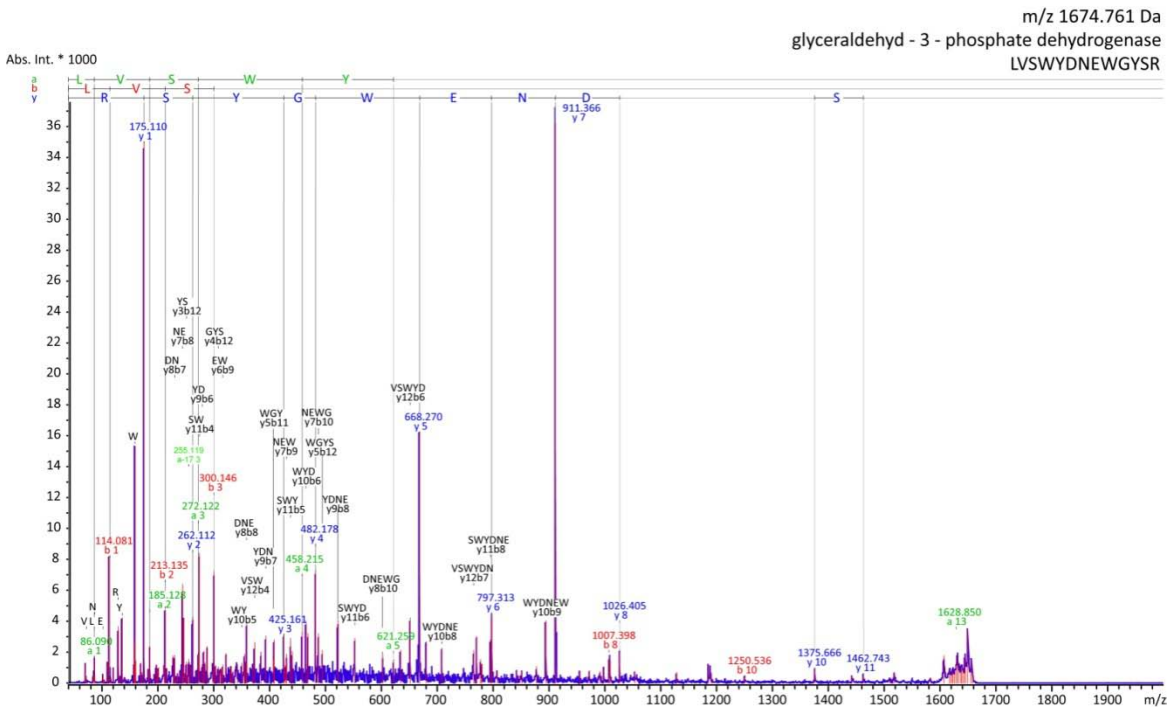


Figure 6.4 PSD spectrum of m/z 1674.761 Da at induced mycoparasitism

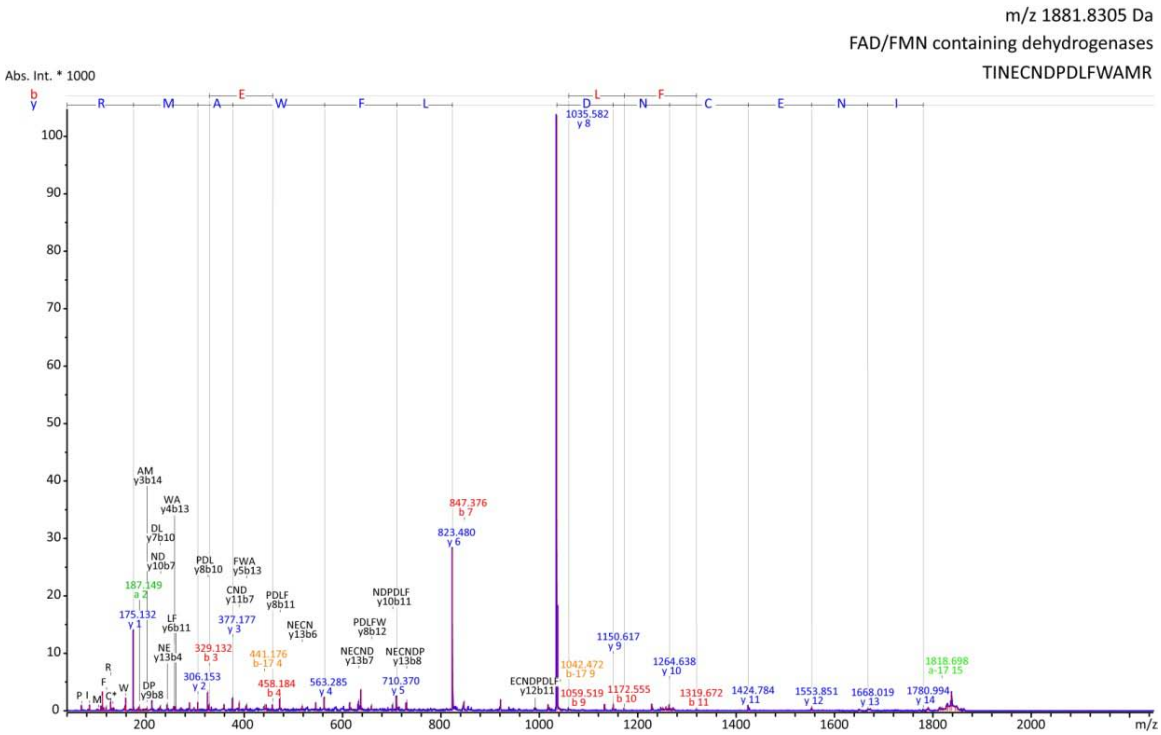


Figure 6.5 PSD spectrum of m/z 1881.830 Da at induced mycoparasitism

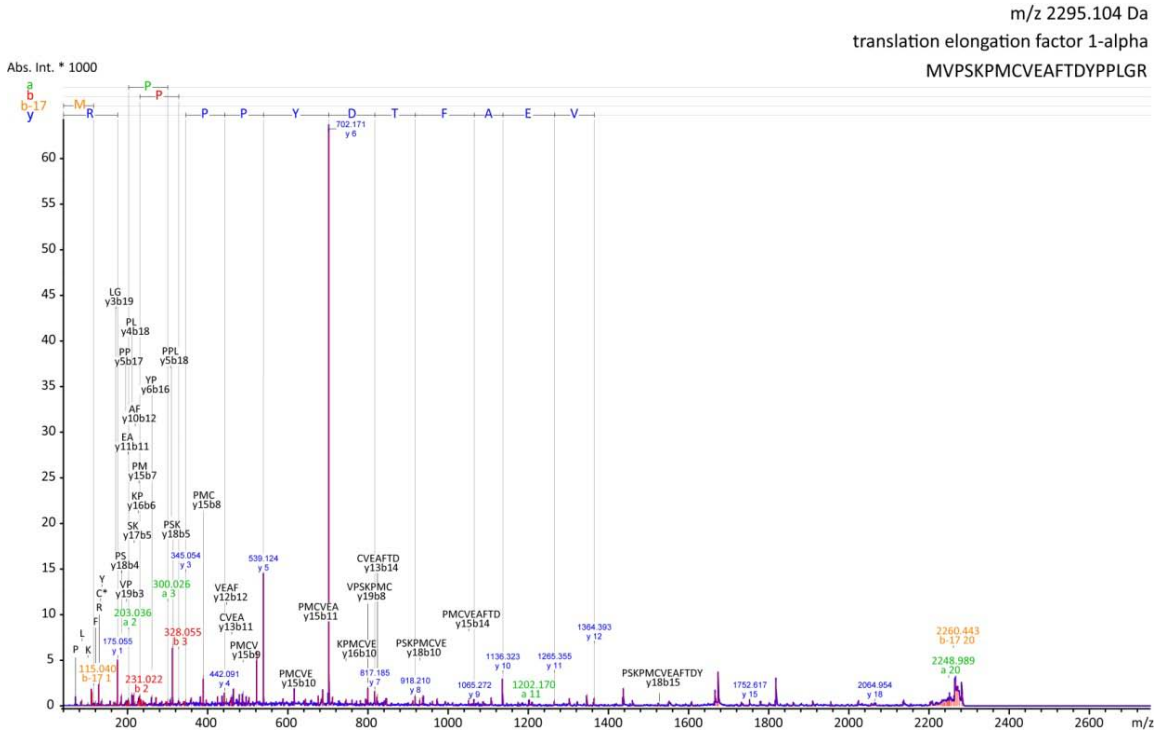


Figure 6.6 PSD spectrum of m/z 2295.104 Da at induced mycoparasitism

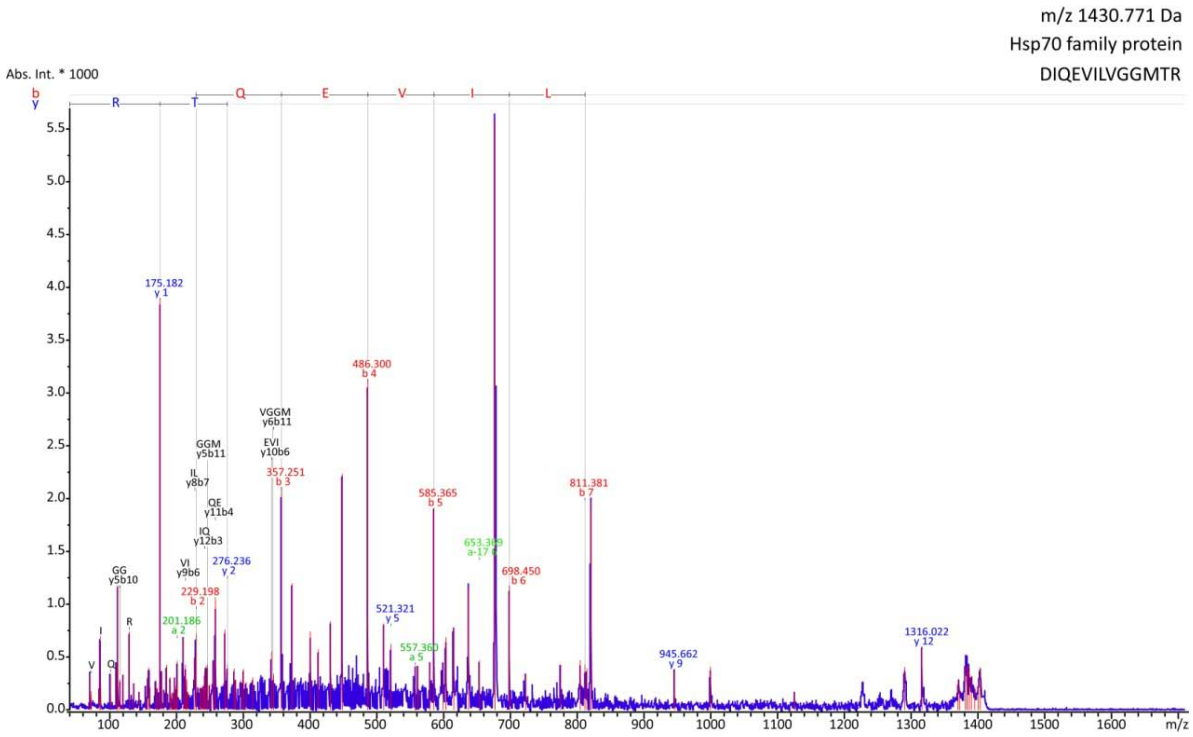


Figure 6.7 PSD spectrum of m/z 1430.771 Da at reduced mycoparasitism

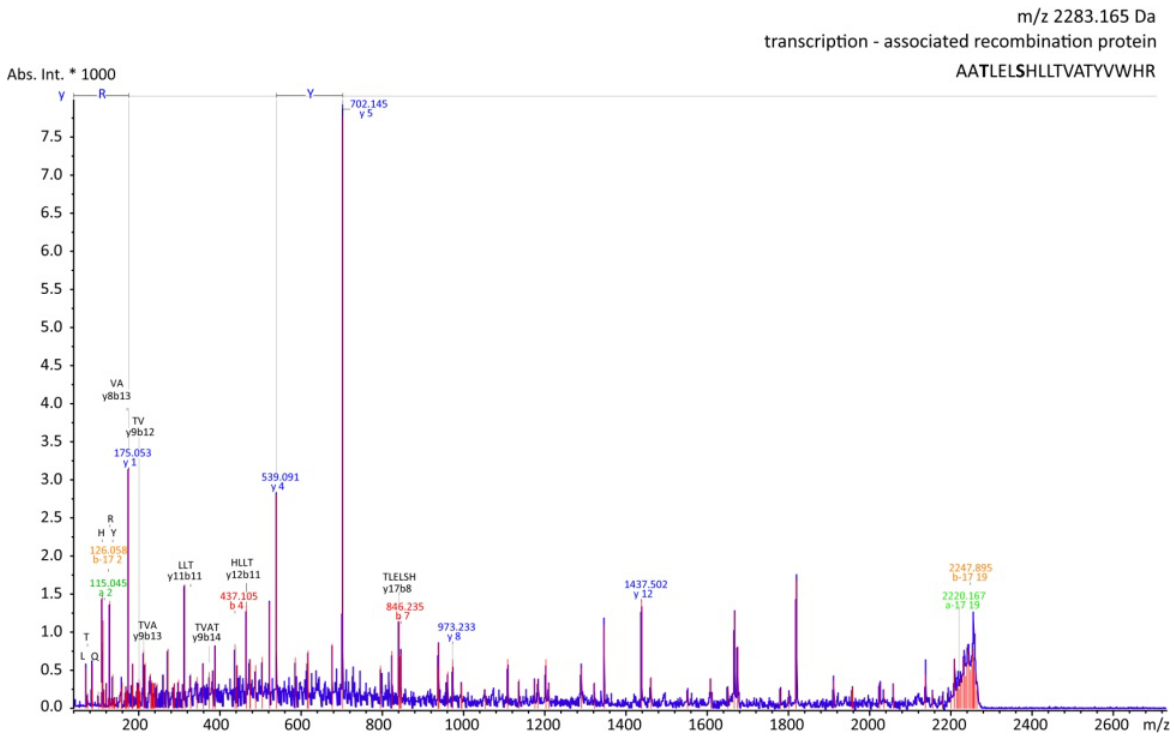


Figure 6.8PSD spectrum of m/z 2283.165 Da at reduced mycoparasitism

6.1.2 PSD Spectrum of *T. atroviride* related PMF peaks with prior Enrichment

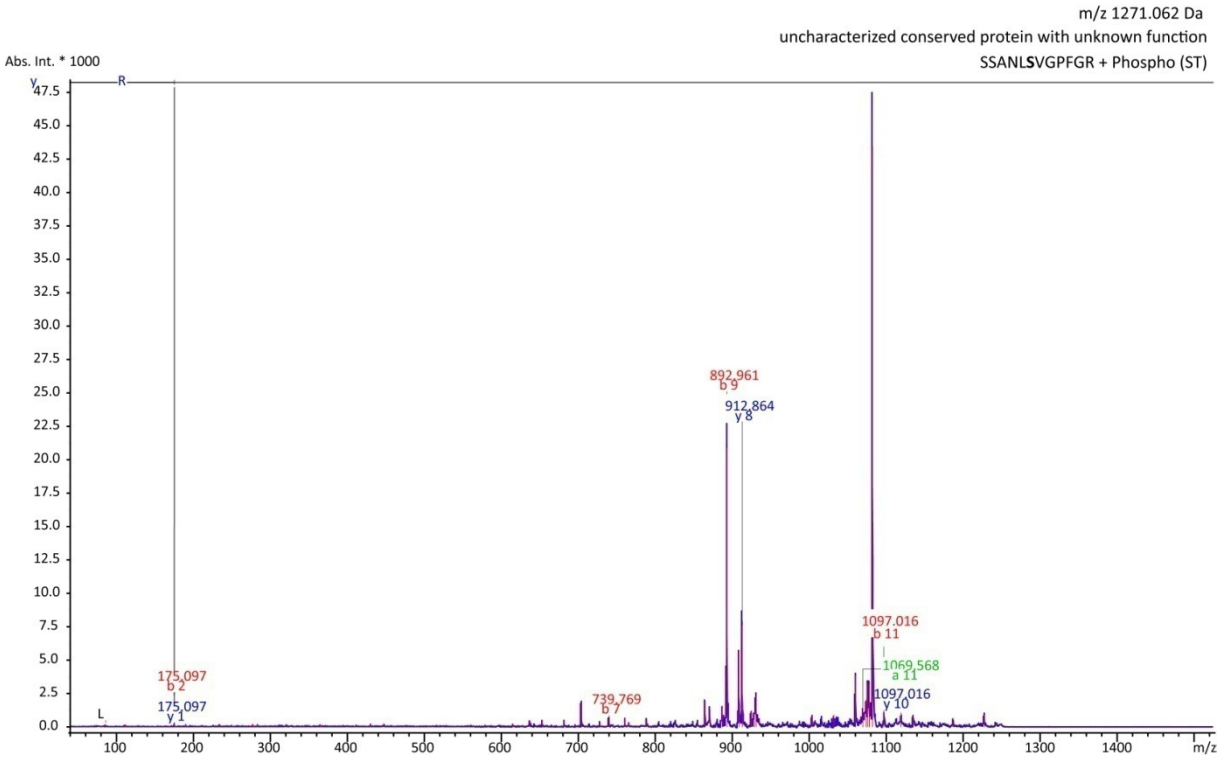


Figure 6.9 PSD spectrum of m/z 1271.062 Da

6.2 Analyzing the Phosphoproteins of *Trichoderma atroviride* including a separation via 1D – SDS – PAGE

In the following pages the PMF spectra of every gel piece are shown. Annotated are only those peaks which used for PSD analyses. Below every spectrum, the m/z values are listed and their measured mass lists as well as the relationship to *Trichoderma atroviride*. The pictures are named due to a number code. The first number describes the *Trichoderma* sample (1 = *Trichoderma atroviride* $_{wt}$ vs. *Trichoderma atroviride* $_{wt}$; 2 = *Trichoderma atroviride* $_{wt}$ vs. *Rhizoctonia solani*; 3 = *Trichoderma atroviride* $_{tmk1}$ vs. *Rhizoctonia solani*), the second number is for the replication (1 or 2) and the last number stands for the gel piece which was digested, desalted, enriched and measured by MALDI – MS (1-14). For example 1_2_12 is the second replicate of the sample with inactive mycoparasitism *Trichoderma atroviride* $_{wt}$vs. *Trichoderma atroviride* $_{wt}$ and the PMF was carried out with the gel piece 14.

6.2.1 Summarized Mass List of the Gel Blank and the Trypsin Blank

Table 119.1 Summary of the peaks, occurred in the gel blank or in the trypsin blank

	Mass list
Gel Blank	1013,237; 1022,170; 1033,191; 1035,204; 1041,197; 1044,253; 1047,483; 1047,579; 1059,204; 1060,114; 1062,259; 1066,127; 1067,269; 1077,174; 1077,215; 1079,170; 1079,226; 1082,097; 1089,128; 1091,138; 1093,202; 1095,222; 1098,062; 1099,199; 1103,535; 1105,223; 1107,217; 1115,172; 1118,311; 1121,183; 1131,134; 1133,271; 1161,284; 1173,151; 1201,117; 1203,076; 1309,142; 1610,951; 1612,957; 1615,947; 1689,928; 1691,920; 1694,911; 1812,946
Trypsin Blank	1009,276; 1013,231; 1033,186; 1035,181; 1047,597; 1059,200; 1061,187; 1062,261; 1067,273; 1075,165; 1077,205; 1079,223; 1089,121; 1093,206; 1095,219; 1099,182; 1105,211; 1107,203; 1115,160; 1119,203; 1121,190; 1129,127; 1131,126; 1133,259; 1139,125; 1145,139; 1159,104; 1161,247; 1211,817; 1264,215; 1266,246; 1309,122; 1362,722; 1430,786; 1610,933; 1612,935; 1614,917; 1691,898; 1694,884; 1851,084; 2048,133; 2081,168; 2148,244; 2161,802; 2930,422; 3012,430

Masses, which occurred either in the gel blank or in the trypsin blank, were excluded for further PSD analysis. The most frequent contaminations are matrix clusters, keratin and tryptic autolysis peaks.

6.2.2 *Trichoderma atroviride* $_{wt}$ vs. *Trichoderma atroviride* $_{wt}$ (un-incuded mycoparasitism)

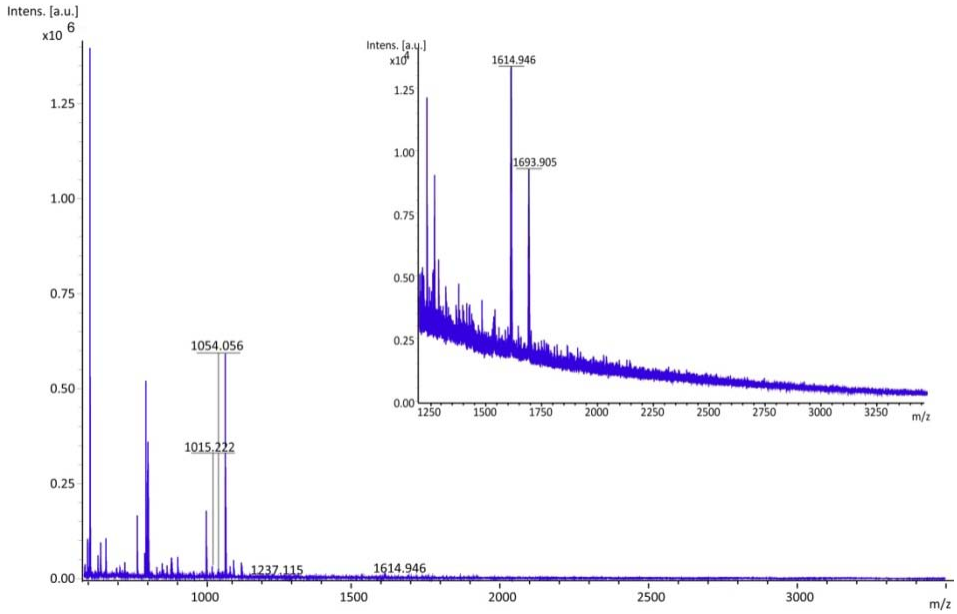


Figure 6.10 Positive ion reflector TOF - MALDI mass spectrum of 1_1_1

$[MH]^+$ 1015.222 Da	
Fragement masses	86.107; 107.085; 110.107; 112.119; 115.116; 123.126; 129.130; 136.111; 141.127; 154.114; 158.125; 172.107; 175.141; 187.128; 189.150; 195.146; 197.152; 200.160; 208.131; 210.135; 212.124; 214.130; 216.137; 227.120; 231.154; 235.136; 246.149; 248.121; 250.124; 257.177; 268.141; 288.172; 294.115; 311.137; 782.117; 821.953; 825.110; 827.253; 867.363; 933.391; 947.350; 960.569; 970.175; 972.453; 977.351; 984.782; 988.770; 991.004; 994.491
T. atroviride	**Not related**
[MH]+ 1054.056 Da	
Fragment masses	107.065; 110.077; 112.093; 129.099; 147.070; 154.099; 166.129; 172.067; 175.123; 184.147; 190.068; 195.128; 197.119; 212.110; 228.116; 231.110; 234.076; 240.131; 250.094; 252.125; 270.141; 294.102; 311.094; 585.179; 676.017; 697.919; 713.821; 731.161; 821.140; 857.808; 859.903; 864.076; 866.226; 869.436; 940.171; 995.690; 999.383; 1.008.596; 1.023.172; 1.031.916
T. atroviride	**Not related**
$[MH]^+$ 1237.115 Da	
Fragment masses	84.068; 107.060; 110.076; 112.089; 129.104; 147.065; 154.090; 172.083; 175.117; 181.095; 195.102; 197.122; 212.114; 214.105; 227.103; 229.119; 240.119; 243.133; 246.117; 253.128; 257.148; 264.126; 268.111; 271.143; 276.110; 288.162; 294.086; 297.103; 314.130; 435.178; 563.198; 692.261; 787.190; 810.985; 857.036; 940.363; 1.000.856; 1.040.809; 1.043.830; 1.046.005; 1.074.067; 1.129.100; 1.188.272; 1.200.664; 1.213.239; 1.216.833
T. atroviride	**Not related**
$[MH]^+$ 1614.115 Da	
Fragment masses	110.069; 112.081; 129.112; 154.104; 172.098; 175.123; 197.128; 445.194; 734.026; 736.025; 815.009; 905.469; 1.410.365; 1.414.514; 1.425.929; 1.467.018; 1.519.031; 1.530.968; 1.534.182; 1.536.988; 1.561.045; 1.584.514
T. atroviride	Not related
$[MH]^+$ 1693.905 Da	
Fragment masses	110.080; 112.087; 154.096; 175.130; 197.144; 288.187; 734.988; 814.008; 1.483.338; 1.496.568; 1.545.905; 1.611.067; 1.632.630; 1.657.127; 1.667.088
T. atroviride	Not related

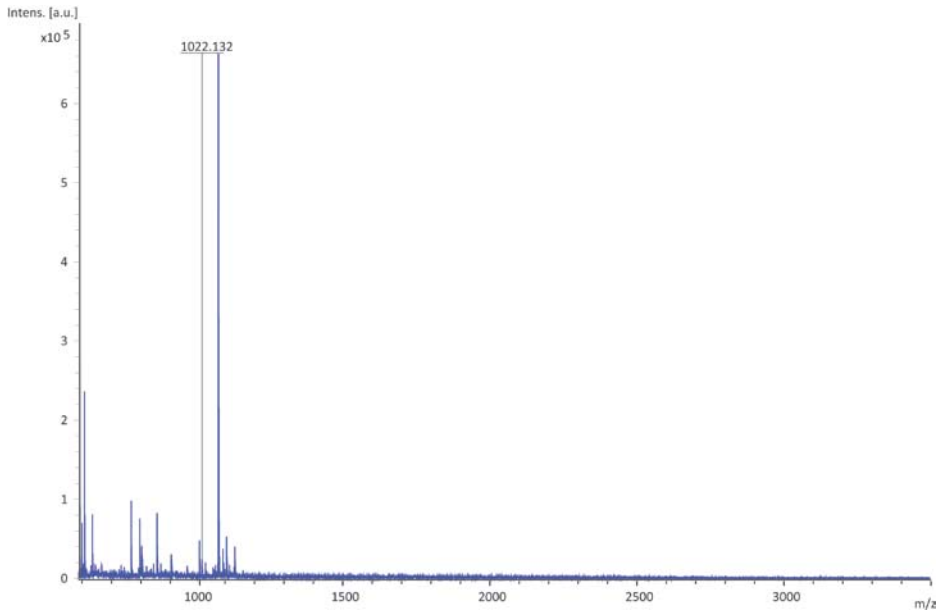


Figure 6.11 Positive ion reflector TOF - MALDI mass spectrum of 1_1_2

$[MH]^+$ 1022.132 Da	
Fragment masses	70.059; 86.092; 98.084; 100.098; 110.089; 112.105; 115.110; 125.113; 127.113; 129.116; 143.111; 146.107; 154.116; 157.125; 167.118; 169.123; 172.103; 175.142; 184.131; 186.134; 190.119; 195.134; 197.144; 200.136; 202.130; 209.139; 212.138; 214.151; 218.158; 223.143; 226.131; 229.149; 231.145; 240.149; 242.153; 244.156; 246.164; 248.156; 250.126; 252.140; 254.159; 257.166; 260.150; 268.156; 271.173; 285.164; 288.188; 294.119; 311.138; 313.190; 577.858; 593.927; 599.128; 637.906; 644.073; 666.368; 681.890; 697.909; 766.870; 782.951; 820.393; 826.938; 833.260; 864.278; 870.884; 908.241; 933.049; 959.533; 972.170; 975.454; 996.178
T. atroviride	**Not related**

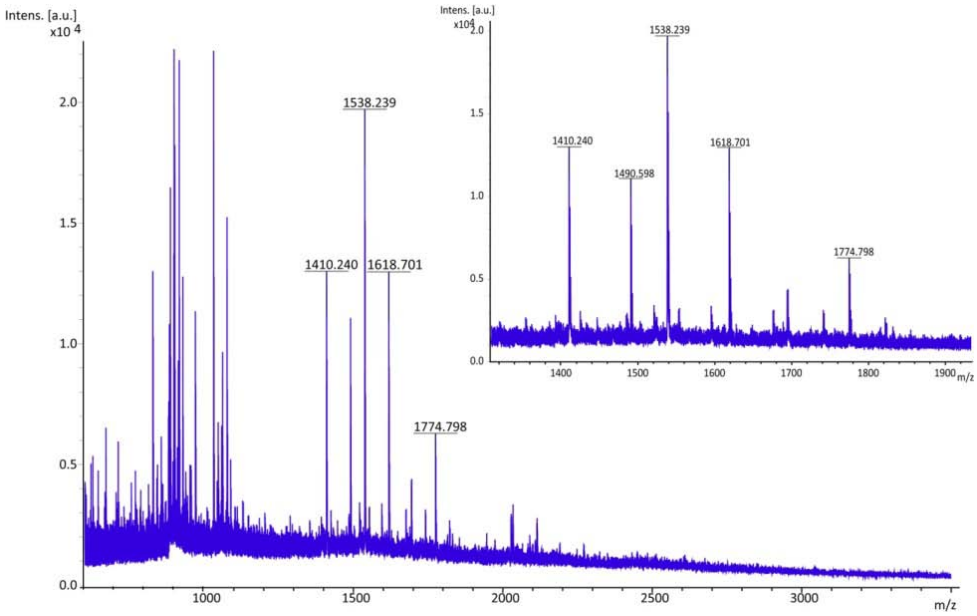


Figure 6.12 Positive ion reflector TOF - MALDI mass spectrum of1_1_3

$[MH]^+$ 1410.240 Da

Fragment masses	70.069; 84.099; 102.092; 110.117; 112.137; 115.139; 120.139; 129.164; 154.169; 157.186; 167.180; 169.199; 172.185; 175.208; 185.198; 187.182; 197.222; 201.211; 213.206; 215.223; 226.231; 229.239; 232.236; 240.240; 244.237; 247.240; 251.238; 255.247; 257.263; 259.233; 268.272; 270.277; 272.280; 284.254; 288.291; 298.267; 314.276; 316.255; 326.273; 332.259; 343.309; 385.339; 413.293; 427.308; 444.336; 455.303; 472.325; 902.342; 1.279.208; 1.300.454; 1.306.699; 1.318.451
T. atroviride	**Not related**
$[MH]^+$ 1490.598 Da	
Fragment masses	70.037; 84.065; 110.072; 112.090; 115.093; 120.088; 129.114; 141.119; 154.109; 157.125; 167.115; 169.135; 172.121; 175.143; 185.124; 187.112; 192.135; 197.151; 209.122; 214.155; 217.135; 226.159; 230.133; 232.164; 240.159; 242.167; 244.143; 255.148; 257.171; 259.150; 268.168; 270.185; 272.177; 282.154; 284.155; 288.197; 298.157; 314.190; 316.163; 326.167; 343.168; 444.201; 455.172; 472.201; 508.270; 543.237; 571.247; 718.313; 787.338; 902.378; 1.032.403; 1.146.572; 1.261.677; 1.273.278; 1.279.714; 1.289.564; 1.375.925; 1.384.409; 1.392.901; 1.410.918; 1.441.393; 1.466.409
T. atroviride	**Elongation Factor 3 (EF-3) K.RGEEVFSDEDDL.- + Phospho (significant)**
$[MH]^+$ 1583.239 Da	
Fragment masses	69.840; 83.836; 100.841; 109.804; 111.812; 114.814; 119.808; 128.815; 140.802; 153.785; 156.800; 166.776; 168.788; 170.790; 174.792; 184.771; 196.780; 200.773; 210.765; 212.745; 225.770; 228.752; 230.719; 239.758; 242.769; 244.715; 246.744; 250.743; 258.699; 267.764; 271.744; 284.769; 287.747; 297.706; 315.680; 325.701; 331.672; 341.682; 425.677; 442.699; 454.641; 470.677; 554.631; 571.653; 582.614; 599.628; 653.630; 670.640; 1.029.400; 1.031.472; 1.406.026; 1.430.266; 1.433.504; 1.450.355; 1.488.366; 1.510.959; 1.518.911
T. atroviride	**Not related**
$[MH]^+$ 1618.701 Da	
Fragment masses	84.079; 110.081; 112.100; 120.095; 129.119; 141.124; 154.114; 172.120; 175.149; 185.116; 197.148; 226.164; 243.157; 268.171; 285.192; 316.156; 342.196; 443.251; 471.264; 572.316; 583.300; 600.317; 671.395; 682.363; 699.397; 818.480; 846.474; 915.516; 933.500; 1.030.572; 1.048.585; 1.091.567; 1.274.758; 1.298.245; 1.389.826; 1.401.330; 1.407.879; 1.417.593; 1.420.809; 1.487.887; 1.493.122; 1.503.038; 1.505.333; 1.512.514; 1.521.037; 1.530.617; 1.539.074
T. atroviride	**Elongation Factor 3 (EF-3) R.KRGEEVFSDEDDL.- + Phospho (significant)**
$[MH]^+$ 1774.798 Da	
Fragment masses	70.065; 84.085; 110.092; 112.109; 115.108; 129.128; 141.129; 154.121; 157.134; 172.131; 175.153; 197.168; 399.227; 441.280; 528.261; 627.362; 756.420; 854.500; 1.071.570; 1.106.695; 1.169.637; 1.186.667; 1.204.764; 1.284.783; 1.414.957; 1.430.901; 1.448.916; 1.503.746; 1.529.972; 1.546.145; 1.557.423; 1.564.099; 1.635.325; 1.643.875; 1.660.336; 1.672.960; 1.677.278; 1.695.317
T. atroviride	Not related

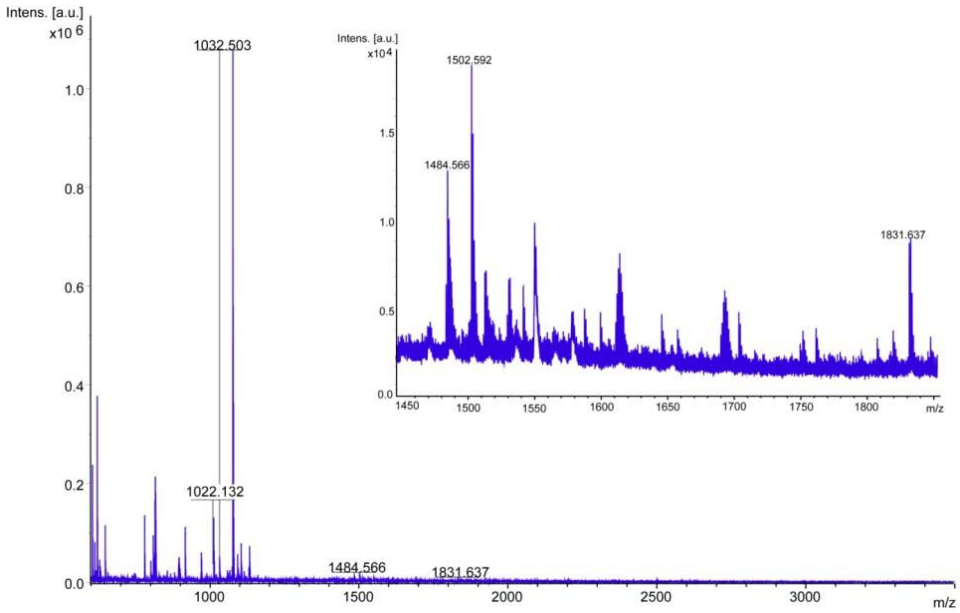


Figure 6.13 Positive ion reflector TOF - MALDI mass spectrum of 1_1_4

$[MH]^+$ 1022.132 Da	
Fragment masses	70.057; 84.075; 86.099; 107.059; 110.082; 113.091; 115.094; 129.115; 136.089; 154.096; 158.101; 167.100; 171.110; 172.106; 175.125; 181.104; 184.104; 188.113; 190.110; 195.096; 197.126; 209.111; 212.114; 216.105; 227.113; 229.117; 232.139; 238.123; 240.131; 249.145; 253.100; 268.137; 270.141; 278.134; 279.104; 286.146; 288.167; 296.133; 306.138; 310.115; 328.185; 345.216; 355.196; 365.152; 377.122; 382.170; 392.148; 393.137; 410.159; 416.150; 421.131; 473.157; 491.129; 508.211; 525.186; 593.905; 599.091; 600.041; 637.872; 644.021; 660.258; 681.845; 688.169; 697.900; 782.860; 826.859; 830.021; 833.150; 870.876; 908.209; 932.943; 959.434; 971.991 976.434
T. atroviride	**Not related**
$[MH]^+$ 1032.503 Da	
Fragment masses	70.065; 86.100; 100.076; 110.078; 113.086; 115.087; 129.119; 133.094; 136.082; 143.098; 154.087; 158.096; 167.096; 172.103; 175.121; 178.070; 181.102; 188.111; 190.116; 195.088; 198.093; 201.105; 207.089; 212.105; 215.111; 225.101; 229.109; 232.137; 238.110; 242.119; 249.154; 253.090; 262.094; 268.132; 270.122; 273.112; 279.095; 286.141; 288.148; 292.102; 296.128; 303.156; 306.113; 310.110; 324.126; 328.187; 338.138; 345.218; 355.188; 365.143; 377.111; 382.176; 386.394; 393.144; 398.134; 410.176; 416.154; 421.135; 445.167; 449.143; 453.208; 473.184; 481.170; 491.196; 508.296; 518.260; 525.220; 529.239; 574.236; 586.274; 606.317; 623.357; 643.297; 660.322; 663.429; 671.293; 681.682; 688.342; 700.664; 743.442; 760.483; 773.468; 801.500; 817.549; 858.555; 876.605; 918.727; 953.727; 971.808; 982.058; 986.551; 997.747
T. atroviride	**FAD/FMN-containing dehydrogenases K.NTGHDYLGR.S (significant)**
$[MH]^+$ 1484.566 Da	
Fragment masses	84.086; 86.099; 110.087; 112.099; 115.090; 129.121; 131.111; 136.095; 154.112; 157.113; 158.112; 167.118; 172.128; 175.143; 185.187; 190.138; 195.111; 197.153; 212.123; 213.179; 216.136; 225.140; 226.155; 227.145; 232.158; 242.201; 249.173; 253.117; 268.175; 271.162; 277.162; 279.123; 286.169; 288.192; 296.149; 310.137; 326.212; 328.201; 339.188; 345.229; 355.204; 382.195; 393.153; 401.197; 411.170; 416.159; 421.139; 473.183; 491.196; 508.276; 518.255; 525.198; 538.244; 568.344; 574.215; 586.245; 588.247; 606.273; 623.303; 653.275; 660.280; 688.263; 743.325; 760.366; 766.336; 817.387; 835.506; 863.453; 908.793; 918.449; 978.529; 1.015.488; 1.032.503;

	1.097.735; 1.116.739; 1.286.653; 1.290.831; 1.302.758; 1.404.889; 1.440.877; 1.449.819; 1.456.829
T. atroviride	**P-type ATPase-like protein R.TKRDSGYGDLGR.N + 2x Phospho (NOT significant)**
$[MH]^+$ 1502.589 Da	
Fragment masses	69.974; 83.981; 86.006; 109.983; 111.999; 114.995; 129.015; 135.993; 153.990; 158.002; 166.997; 172.008; 175.023; 181.007; 185.063; 190.014; 194.987; 197.022; 213.056; 216.003; 226.012; 232.022; 242.068; 249.030; 252.982; 268.010; 270.024; 272.019; 277.023; 278.981; 285.997; 288.023; 296.008; 309.982; 326.049; 328.031; 339.021; 345.061; 355.023; 382.003; 392.986; 410.993; 415.977; 472.986; 508.061; 518.028; 524.980; 588.004; 606.009; 623.026; 816.968; 1.015.035; 1.032.179; 1.119.512; 1.285.299; 1.288.350; 1.302.363; 1.308.525; 1.387.518; 1.404.510; 1.422.552; 1.467.351; 1.484.431
T. atroviride	**Not related**
$[MH]^+$ 1831.637 Da	
Fragment masses	84.084; 110.079; 112.094; 115.101; 129.115; 154.111; 175.136; 197.148; 232.143; 250.082; 345.138; 508.280; 623.310; 1.015.525; 1.032.521; 1.288.673; 1.302.699; 1.405.802; 1.467.809; 1.481.672; 1.484.820; 1.493.851; 1.502.838; 1.582.841; 1.723.596; 1.733.243; 1.751.349; 1.778.212; 1.800.785
T. atroviride	**Not related**

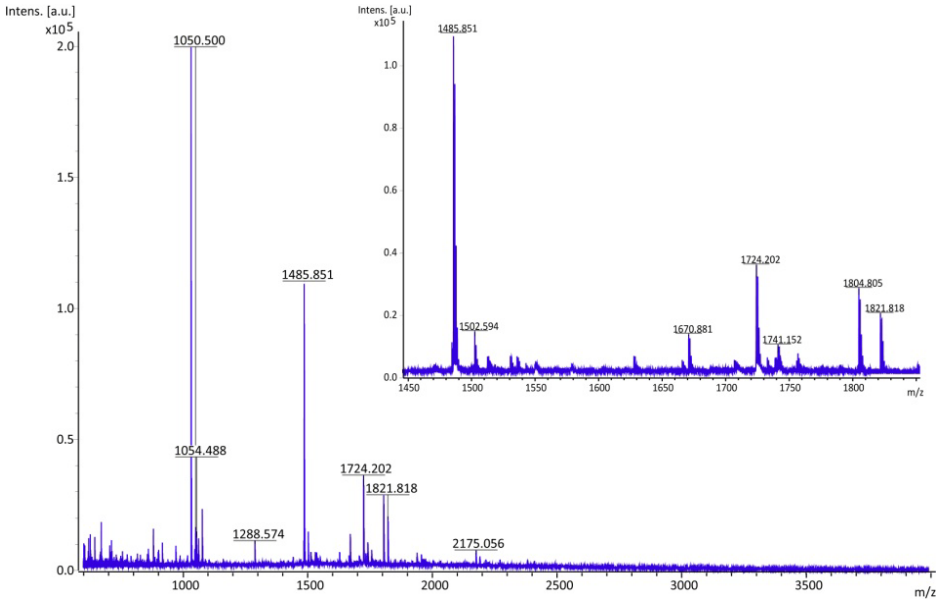


Figure 6.14 Positive ion reflector TOF - MALDI mass spectrum of1_1_5

$[MH]^+$ 1050.500 Da	
Fragment masses	70.079; 86.112; 110.107; 112.121; 115.118; 120.119; 129.146; 136.117; 154.135; 157.151; 167.143; 172.130; 175.170; 181.153; 184.176; 195.148; 197.171; 204.166; 212.171; 216.156; 225.163; 227.169; 232.199; 242.180; 253.157; 268.191; 279.174; 288.230; 294.167; 296.198; 311.160; 345.267; 382.230; 410.235; 508.249; 525.271; 731.123; 1.031.447
T. atroviride	**FAD/FMN-containing dehydrogenases R.NTGHDYMGR.S (NOT significant)**
$[MH]^+$ 1054.488 Da	
Fragment masses	70.068; 86.111; 107.090; 110.108; 112.126; 115.126; 129.143; 136.124; 146.111; 154.135; 158.144; 167.148; 172.123; 175.173; 181.149; 185.154; 190.133; 195.152; 197.170; 204.183; 209.160; 212.155; 216.160; 231.181; 237.184; 253.158; 279.181; 288.225; 294.177; 311.164; 382.242; 410.247; 508.247; 525.285; 585.249; 645.443; 651.193; 660.435; 676.105; 688.436; 731.208; 782.541; 851.582; 898.624; 940.801; 1.005.418; 1.031.709

T. atroviride	**FAD/FMN-containing dehydrogenases R.NTGHDYYGK.S (NOT significant)**
$[MH]^+$ 1288.574 Da	
Fragment masses	110.072; 112.088; 129.106; 154.101; 175.128; 197.132; 226.124; 232.144; 243.130; 249.143; 253.117; 255.107; 258.136; 268.149; 288.169; 345.199; 508.293; 666.256; 709.299; 781.339; 916.555; 944.570; 1.032.631; 1.187.711; 1.264.607
T. atroviride	**Not related**
$[MH]^+$ 1485.851 Da	
Fragment masses	70,056; 84,096; 86,115; 110,096; 112,113; 129,136; 154,127; 158,131; 167,139; 172,145; 175,164; 185,197; 195,144; 197,178; 213,201; 216,154; 232,184; 242,225; 249,199; 253,147; 271,186; 277,203; 279,154; 286,2; 296,18; 310,161; 326,245; 328,218; 345,257; 355,229; 382,212; 393,198; 401,242; 411,201; 416,202; 473,217; 508,31; 525,218; 606,31; 623,325; 653,305; 688,317; 743,319; 760,408; 817,431; 835,49; 918,516; 978,516; 1015,442; 1032,543; 1302,789; 1440,869; 1442,567
T. atroviride	**FAD/FMN-containing dehydrogenases R.IVLKNTGHDYLGR.S (significant)**
$[MH]^+$ 1502.594 Da	
Fragment masses	110.086; 112.114; 129.132; 154.112; 158.131; 167.135; 172.138; 175.161; 185.180; 195.134; 197.164; 213.204; 216.145; 232.180; 242.228; 253.146; 272.204; 279.160; 286.185; 310.164; 345.252; 411.217; 508.304; 525.230; 588.274; 606.262; 623.301; 817.231; 1.015.465; 1.032.530; 1.288.801; 1.302.738; 1.399.558; 1.404.960; 1.423.023; 1.467.810; 1.484.711
T. atroviride	**Not related**
$[MH]^+$ 1670.881 Da	
Fragment masses	110.074; 112.089; 115.089; 129.112; 154.105; 175.136; 197.133; 267.118; 508.210; 514.247; 542.244; 759.298; 983.540; 1.032.454; 1.084.589; 1.112.673; 1.266.545; 1.324.813; 1.483.993; 1.552.168
T. atroviride	**Not related**
$[MH]^+$ 1724.202 Da	
Fragment masses	70.058; 86.081; 101.076; 112.090; 115.096; 120.092; 129.111; 147.117; 154.098; 157.122; 172.109; 175.135; 185.114; 197.129; 200.117; 213.112; 217.102; 221.140; 230.123; 244.134; 249.127; 255.118; 259.130; 305.178; 311.163; 328.171; 370.145; 568.234; 633.362; 761.354; 816.307; 902.368; 1.030.478; 1.130.394; 1.145.473; 1.260.607; 1.485.298; 1.578.266; 1.616.575; 1.627.253; 1.706.039
T. atroviride	**Ribosome-associated chaperone zuotin R.TFSEDDRIQAQESAK.K (NOT significant)**
$[MH]^+$ 1741.152 Da	
Fragment masses	70.044; 84.076; 86.089; 101.077; 110.073; 112.090; 115.091; 120.085; 129.111; 147.114; 154.100; 157.115; 167.103; 172.115; 175.127; 185.128; 195.100; 197.142; 200.131; 217.113; 221.153; 231.101; 242.166; 244.129; 249.146; 255.141; 259.157; 345.180; 370.190; 508.237; 1.030.472; 1.145.451; 1.187.458; 1.596.296; 1.641.059; 1.706.395; 1.723.773
T. atroviride	**Not related**
$[MH]^+$ 1804.805 Da	
Fragment masses	101,104; 110,105; 112,119; 115,114; 120,115; 129,142; 154,132; 157,157; 175,171; 197,18; 562,337; 761,455; 833,43; 1030,689; 1110,672; 1145,751; 1216,58; 1260,838; 1389,978; 1579,153; 1590,211; 1663,345; 1666,841; 1676,04; 1689,412; 1692,432; 1697,689; 1701,02; 1707,381; 1725,416
T. atroviride	**Ribosome-associated chaperone zuotin R.TFSEDDRIQAQESAK.N + Phospho (significant)**
$[MH]^+$ 1821.818 Da	
Fragment masses	112,118; 129,139; 175,161; 250,141; 304,141; 345,18; 373,202; 487,212; 656,36; 687,393; 705,398; 785,367; 1030,653; 1037,596; 1145,623; 1260,657; 1351,811; 1389,66; 1469,64; 1485,375; 1578,493; 1596,248; 1689,465; 1706,431; 1714,76; 1721,283; 1724,413; 1742,453
T. atroviride	**Putative aminotransferase R.RFSNAEPSTNEFQSK.V + Phospho (NOT significant)**
$[MH]^+$ 2175.056 Da	

Fragment masses	70,062; 110,092; 112,108; 115,108; 129,129; 136,102; 175,15; 197,164; 226,184; 255,163; 272,189; 472,186; 542,26; 878,423; 892,444; 1118,593; 1199,689; 1486,823; 1604,026; 2034,735; 2042,307; 2048,279; 2059,139; 2060,787; 2065,66; 2077,725
T. atroviride	**Not related**

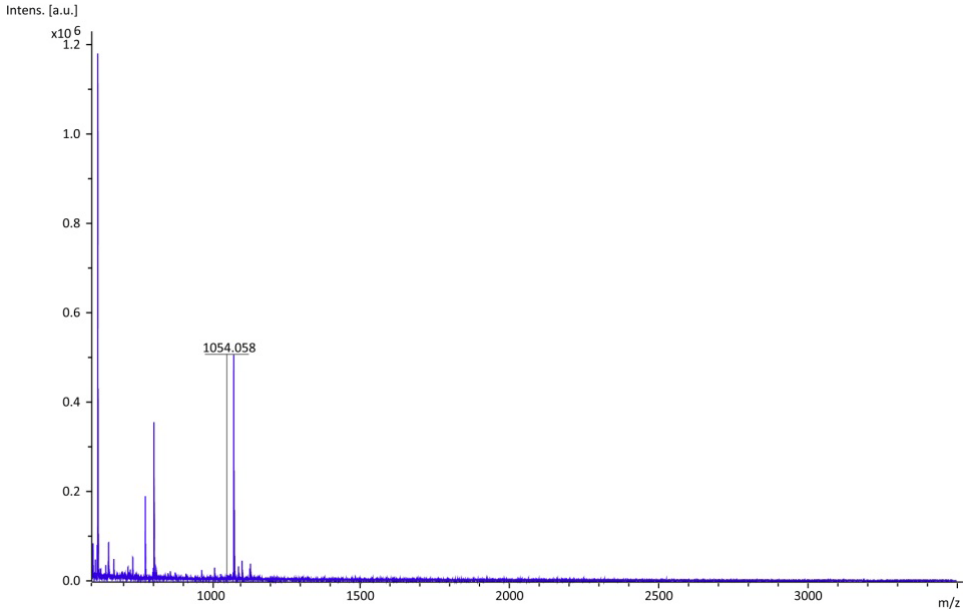


Figure 6.15 Positive ion reflector TOF - MALDI mass spectrum of 1_1_6

$[MH]^+$ 1054.058 Da	
Fragment masses	70,06; 84,077; 86,088; 107,052; 110,075; 112,088; 115,087; 129,106; 136,085; 147,082; 154,091; 158,102; 167,095; 172,076; 175,12; 181,098; 184,132; 186,109; 195,107; 197,121; 211,119; 214,123; 216,116; 226,122; 228,126; 231,116; 240,123; 250,104; 253,108; 257,13; 268,131; 288,161; 294,105; 311,09; 410,175; 508,112; 525,162; 585,116; 651,095; 676,002; 713,799; 731,1; 856,854; 858,888; 861,032; 863,109; 865,194; 961,313; 1008,571; 1026,819; 1031,611
T. atroviride	**Not related**

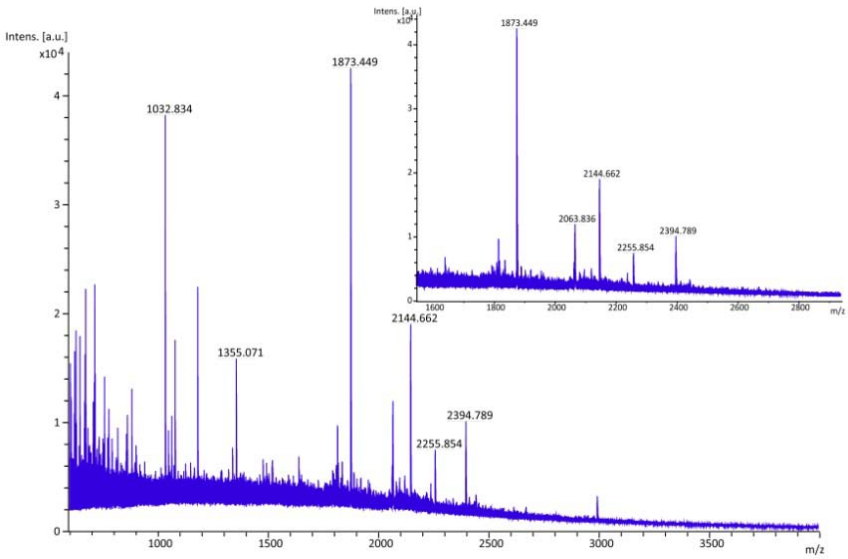


Figure 6.16 Positive ion reflector TOF - MALDI mass spectrum of 1_1_7

$[MH]^+$ 1032.546 Da	
Fragment masses	58,011; 70,065; 72,064; 84,076; 86,091; 95,07; 100,089; 102,073; 107,071; 110,086; 112,096; 115,096; 121,091; 123,101; 125,094; 129,111; 132,105; 136,087; 139,099; 141,102; 143,124; 149,099; 151,077; 154,095; 158,1; 161,096; 167,099; 169,105; 172,086; 175,123; 179,091; 181,099; 185,101; 187,097; 190,091; 192,098; 197,119; 202,107; 207,096; 209,107; 212,108; 215,118; 218,118; 223,094; 225,103; 227,105; 232,125; 235,098; 240,116; 242,12; 245,104; 253,099; 260,113; 268,113; 270,139; 288,147; 294,085; 310,11; 345,175; 382,144; 410,143; 473,136; 508,253; 525,174; 660,240; 688,267; 837,840; 840,973; 845,258; 917,889; 924,189; 966,141; 971,647; 981,983; 984,056; 986,371; 988,682; 991,896; 997,483; 1005,951; 1008,029
T. atroviride	**FAD/FMN-containing dehydrogenases K.NTGHDYLGR.S (significant)**
$[MH]^+$ 1355.071 Da	
Fragment masses	70,029; 84,063; 86,08; 101,075; 110,083; 112,101; 115,102; 129,131; 136,111; 154,133; 157,144; 167,143; 172,146; 175,169; 185,164; 197,182; 200,17; 202,158; 209,172; 212,181; 216,182; 223,19; 226,185; 229,173; 235,183; 237,185; 240,198; 243,196; 245,168; 249,187; 251,192; 254,204; 257,191; 259,184; 263,201; 266,194; 268,204; 271,197; 275,197; 277,201; 283,263; 286,211; 288,237; 296,207; 303,244; 310,211; 314,221; 348,194; 355,217; 366,197; 373,232; 718,426; 1240,005; 1304,412; 1308,786; 1320,754; 1332,57; 1335,422
T. atroviride	**Not related**
$[MH]^+$ 1873.449 Da	
Fragment masses	70,063; 86,108; 112,118; 115,118; 129,143; 175,16; 199,21; 212,152; 227,211; 244,161; 262,184; 311,209; 405,21; 422,212; 535,225; 623,261; 641,316; 698,437; 754,424; 778,395; 865,434; 964,522; 1061,537; 1095,678; 1158,698; 1175,664; 1304,757; 1418,879; 1690,299; 1775,518; 1793,54; 1825,003
T. atroviride	**Glycogen synthetase kinase 3 K.ILVENEPNVSYICSR.Y + Phospho (significant)**
$[MH]^+$ 2063.781 Da	
Fragment masses	110,085; 112,094; 129,116; 136,088; 175,132; 197,148; 343,256; 382,19; 486,284; 614,404; 628,275; 638,45; 729,476; 901,494; 1113,58; 1284,666; 1604,542; 1956,737; 2017,877
T. atroviride	**Not related**
$[MH]^+$ 2144.662 Da	
Fragment masses	112,092; 129,116; 136,089; 175,13; 197,139; 296,186; 343,225; 382,199; 424,283; 442,209; 528,28; 638,438; 739,448; 766,566; 895,615; 914,43;

	1081,703; 1196,766; 1265,758; 1363,741; 1704,035; 2028,521; 2046,519; 2064,543; 2089,879; 2112,925
T. atroviride	**Elicitor protein R.FAYLGNDSDGEEKPVVPVK.T + Phospho (significant)**
$[MH]^+$ 2255.857 Da	
Fragment masses	110,086; 112,102; 129,124; 311,141; 853,656; 999,66; 1096,631; 1211,741; 1430,951; 2127,884; 2209,987
T. atroviride	**Not related**
$[MH]^+$ 2394.778 Da	
Fragment masses	110,086; 129,12; 175,132; 381,147; 452,257; 480,218; 595,215; 724,219; 966,434; 1037,455; 1066,354; 1194,625; 1200,535; 1328,639; 1357,609; 1428,757; 1514,884; 1556,876; 1629,007; 1672,078; 1800,081; 1905,196; 2151,824; 2298,786
T. atroviride	**Cinnamyl-alcohol dehydrogenase family protein K.GGEHVDENKAYKWNCDETNK.L (significant)**

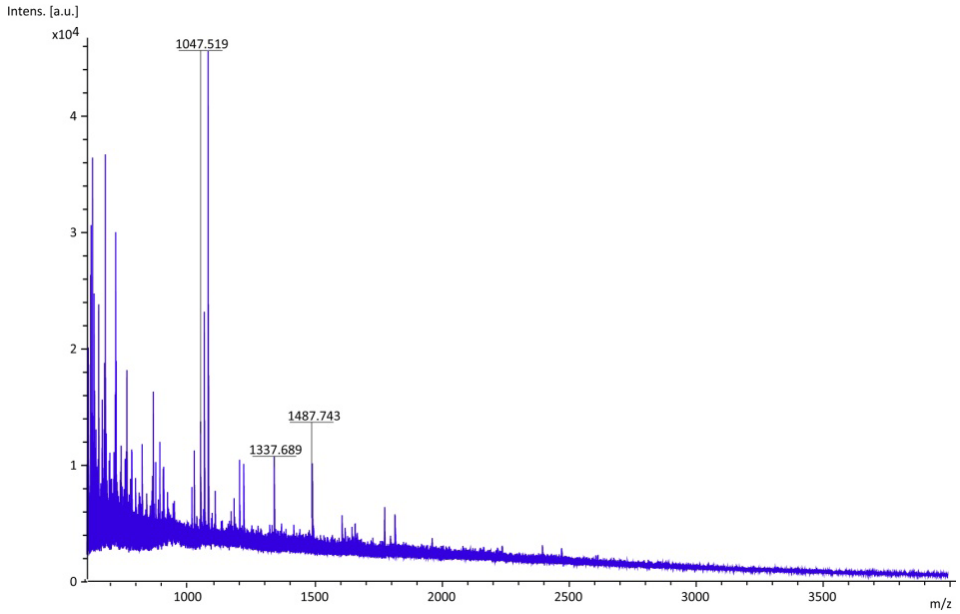


Figure 6.17 Positive ion reflector TOF - MALDI mass spectrum of 1_1_8

$[MH]^+$ 1047.519 Da	
Fragment masses	107,107; 110,123; 112,142; 115,132; 129,155; 154,156; 172,145; 175,189; 181,173; 185,183; 197,196; 211,202; 213,194; 223,193; 226,199; 231,195; 239,222; 257,228; 288,265; 294,207; 311,189; 585,274; 651,241; 666,126; 731,207; 849,901; 857,275; 961,267; 997,326; 999,424; 1014,514
T. atroviride	**Not related**
$[MH]^+$ 1337.689 Da	
Fragment masses	70,042; 84,077; 110,094; 112,114; 115,118; 129,146; 136,133; 154,145; 171,165; 175,179; 185,169; 197,19; 212,194; 223,209; 226,204; 240,201; 251,209; 254,209; 257,223; 268,221; 272,236; 286,205; 288,24; 361,255; 488,267; 587,376; 751,483; 954,835; 1095,828; 1135,659; 1146,108
T. atroviride	**Proteinkinase C-related kinase homology K.IATTHEVMSLR.G + Phospho (NOT significant)**
$[MH]^+$ 1487.743 Da	
Fragment masses	110,069; 112,09; 129,113; 154,103; 171,132; 175,142; 197,146; 211,155; 227,151; 288,184; 631,3; 1016,675; 1172,738; 1292,904; 1331,952; 1440,627; 1464,195; 1470,173
T. atroviride	**Not related**

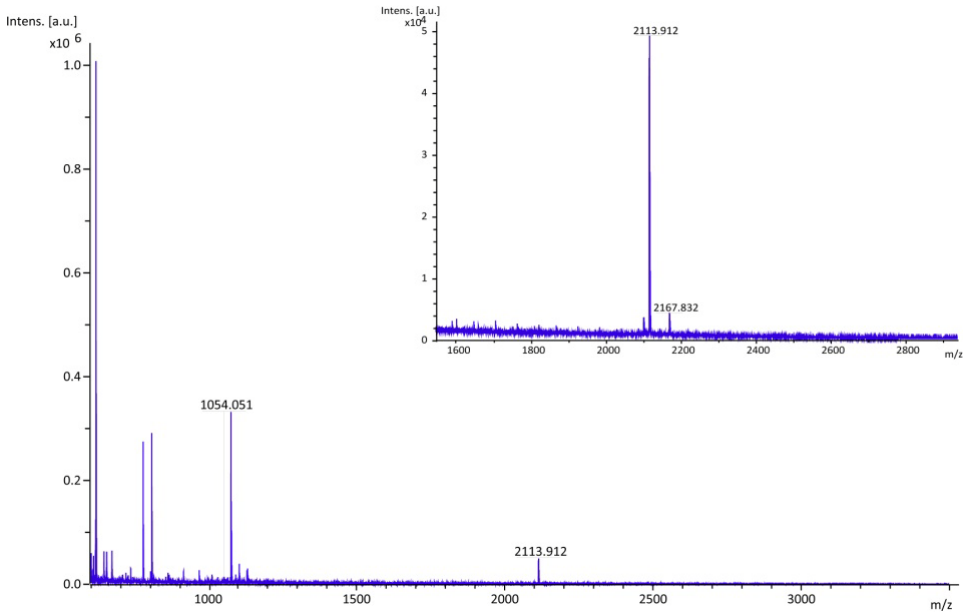


Figure 6.18 Positive ion reflector TOF - MALDI mass spectrum of 1_1_9

$[MH]^+$ 1054.051 Da	
Fragment masses	154,1; 172,08; 175,128; 184,154; 195,115; 197,125; 294,111; 311,103; 385,271; 585,209; 674,044; 676,049; 697,958; 712,883; 731,203; 820,268; 857,862; 859,947; 862,066; 864,135; 961,362; 1008,621; 1031,776
T. atroviride	**Not related**
$[MH]^+$ 2113.912 Da	
Fragment masses	110,059; 112,066; 129,085; 175,096; 498,155; 587,131; 626,238; 658,219; 685,26; 697,223; 754,314; 756,305; 772,303; 786,283; 826,31; 882,372; 885,352; 900,359; 915,31; 954,383; 971,386; 996,358; 1014,395; 1026,421; 1044,389; 1083,442; 1100,445; 1125,51; 1143,457; 1196,42; 1214,502; 1229,514; 1231,518; 1324,559; 1342,568; 1358,567; 1429,618; 1510,733; 1557,731; 1581,798; 1686,891; 1710,859; 1841,013; 1968,242; 1999,252; 2016,407; 2042,244; 2064,794; 2088,336
T. atroviride	**40S ribosomal protein S3 R.VAEQEGAAEEEAQPAAEEQQ.- (significant)**
$[MH]^+$ 2167.832 Da	
Fragment masses	70,053; 112,102; 129,115; 175,142; 213,122; 244,203; 301,228; 345,18; 384,292; 409,276; 416,236; 487,272; 516,406; 539,401; 587,426; 799,54; 997,624; 1125,718; 1337,746; 1396,686; 1569,666; 1811,756; 2027,648; 2040,618; 2042,828; 2061,802; 2065,657; 2113,33; 2136,561; 2138,379
T. atroviride	**Not related**

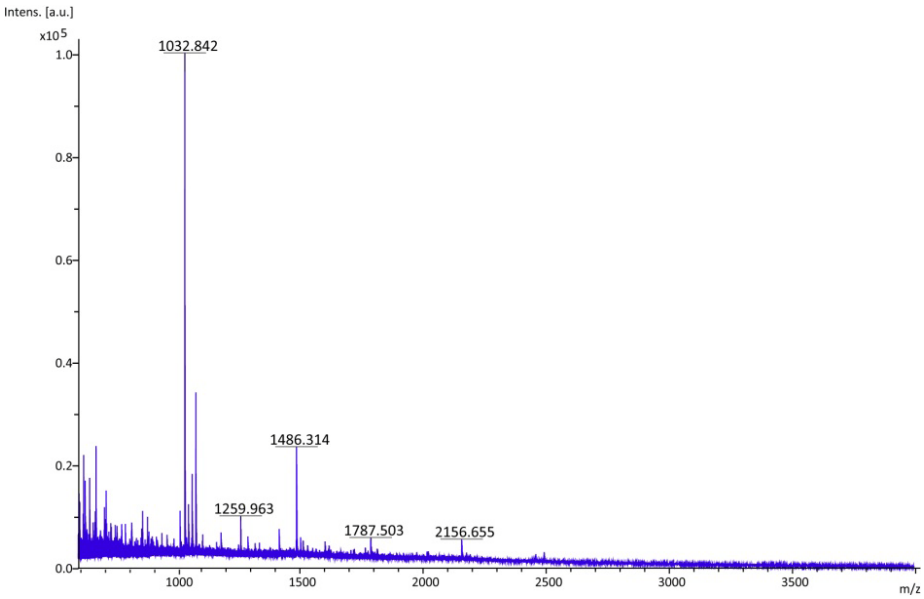


Figure 6.19 Positive ion reflector TOF - MALDI mass spectrum of 1_1_10

$[MH]^+$ 1032.842 Da	
Fragment masses	70,081; 84,096; 86,115; 110,105; 113,117; 115,117; 129,138; 136,118; 154,124; 158,134; 167,129; 172,128; 175,157; 181,125; 185,135; 188,152; 190,137; 195,141; 197,16; 209,145; 211,153; 215,151; 225,141; 227,153; 232,178; 249,181; 253,141; 257,185; 266,186; 268,181; 279,147; 284,153; 288,201; 294,144; 296,178; 310,164; 328,217; 345,263; 365,193; 382,23; 410,231; 473,241; 508,358; 525,283; 623,444; 660,376; 688,424; 801,574; 817,694; 924,215; 964,522; 988,853
T. atroviride	**FAD/FMN containing dehydrogenases R.NTGHDYLGR.S (NOT significant)**
$[MH]^+$ 1259.963 Da	
Fragment masses	70,04; 84,068; 110,078; 112,097; 115,1; 129,119; 147,093; 154,111; 175,138; 197,145; 211,165; 221,13; 226,142; 237,134; 240,143; 250,124; 256,145; 284,151; 288,179; 294,14; 397,208; 494,243; 814,541; 942,23; 951,982; 963,399; 1040,169; 1119,892; 1123,438; 1144,909; 1152,239; 1161,945
T. atroviride	**Not related**
$[MH]^+$ 1486.314 Da	
Fragment masses	110,109; 112,127; 129,153; 154,154; 158,152; 175,182; 195,159; 197,19; 213,218; 226,177; 232,206; 242,234; 253,174; 288,235; 310,183; 345,274; 411,229; 508,338; 525,235; 606,352; 623,345; 688,342; 817,468; 918,52; 942,413; 1015,585; 1032,551; 1097,944; 1286,808; 1440,933
T. atroviride	**FAD/FMN containing dehydrogenases R.IVLKNTGHDYLGR.S (significant)**
$[MH]^+$ 1787.503 Da	
Fragment masses	110,081; 112,093; 129,115; 608,323; 649,292; 706,302; 764,343; 776,414; 863,398; 874,452; 913,462; 1011,438; 1028,593; 1081,541; 1126,528; 1144,56; 1241,607; 1291,751; 1371,887; 1470,948; 1671,176; 1689,195; 1708,27; 1752,732
T. atroviride	**Not related**
$[MH]^+$ 2156.655 Da	
Fragment masses	70,055; 110,089; 112,098; 115,106; 129,127; 175,163; 197,16; 397,252; 763,385; 794,399; 799,468; 811,436; 876,456; 892,353; 894,447; 910,39; 924,528; 942,534; 956,31; 1022,523; 1040,514; 1056,556; 1104,568; 1120,527; 1125,732; 1134,652; 1152,668; 1164,759; 1232,62; 1250,654; 1283,661; 1299,706; 1337,743; 1381,644; 1397,712; 1403,757; 1413,708; 1511,781; 1569,927; 1812,341; 1988,145; 1997,833; 2028,22; 2044,438; 2047,779; 2051,849; 2061,415; 2063,382; 2079,763; 2112,538; 2114,443; 2135,115
T. atroviride	**Not related**

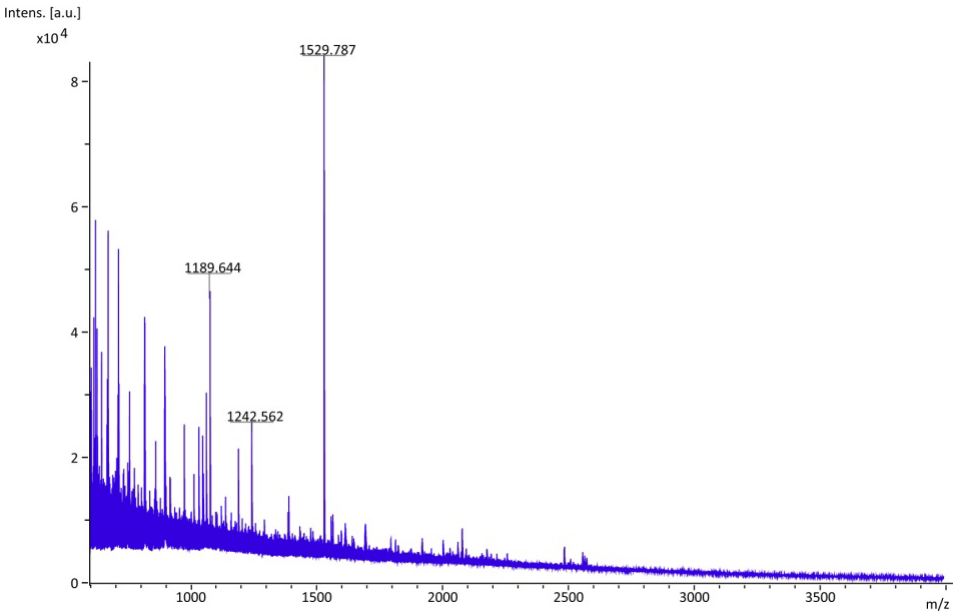


Figure 6.20 Positive ion reflector TOF - MALDI mass spectrum of 1_1_11

$[MH]^+$ 1189.644 Da	
Fragment masses	110,09; 112,11; 115,109; 129,127; 136,108; 141,126; 143,116; 154,116; 157,134; 172,113; 175,152; 197,14; 209,142; 211,134; 225,15; 227,147; 237,152; 239,148; 286,163; 288,176; 1169,193
T. atroviride	**Not related**
$[MH]^+$ 1242.562 Da	
Fragment masses	110,089; 112,106; 115,105; 129,128; 136,102; 154,116; 172,123; 175,149; 197,149; 254,151; 257,167; 288,189; 295,171; 312,188
T. atroviride	**Not related**
$[MH]^+$ 1529.787 Da	
Fragment masses	84,115; 110,123; 112,135; 129,166; 154,168; 172,177; 175,197; 186,199; 195,192; 197,214; 199,194; 212,221; 226,224; 232,226; 240,223; 242,254; 252,228; 258,222; 270,239; 283,238; 302,228; 333,278; 371,291; 399,289; 461,339; 512,376; 590,399; 699,447; 718,462; 769,498; 831,594; 1031,706; 1229,863; 1415,251; 1486,214
T. atroviride	**Cyclophilin K.DGKPTAEIKEQTGR.I (significant)**

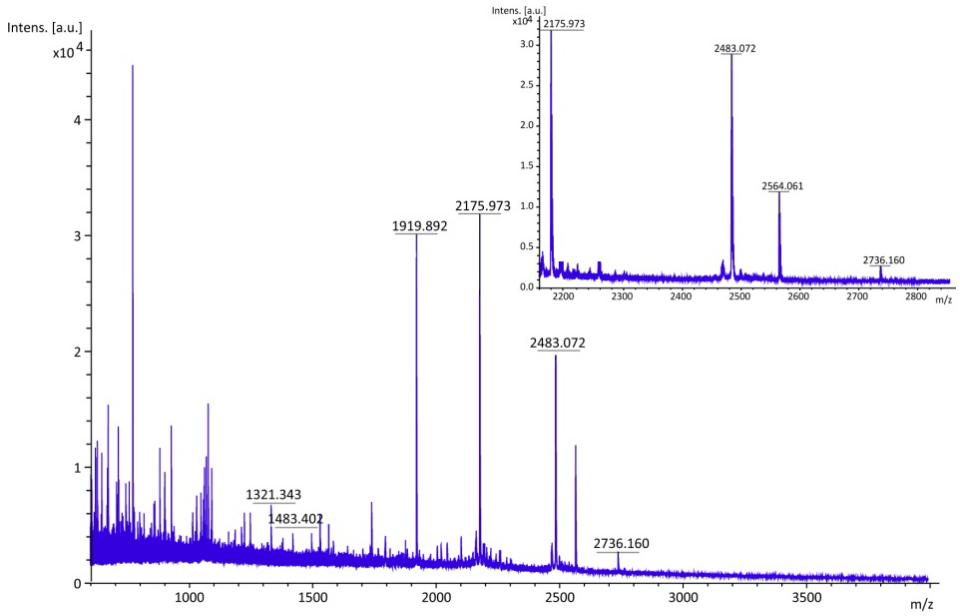


Figure 6.21 Positive ion reflector TOF - MALDI mass spectrum of 1_1_12

$[MH]^+$ 1321.343 Da	
Fragment masses	112,107; 115,11; 129,132; 154,128; 157,15; 172,137; 175,165; 195,158; 197,17; 240,182; 244,182; 254,204; 271,231; 279,199; 286,203; 288,221; 296,211; 313,244; 442,325; 597,359; 1130,024; 1272,458; 1296,933
T. atroviride	**Not related**
$[MH]^+$ 1483.402 Da	
Fragment masses	110,101; 112,116; 115,116; 129,144; 175,193; 197,195; 313,285; 1030,729; 1418,55; 1441,078
T. atroviride	**Not related**
$[MH]^+$ 1919.892 Da	
Fragment masses	84,096; 112,12; 129,141; 175,155; 226,132; 431,205; 530,306; 547,371; 618,41; 687,315; 765,56; 1031,657; 1048,748; 1119,762; 1176,826; 1233,854; 1548,277; 1805,462; 1849,793; 1872,907
T. atroviride	**Plectin/S10 domain containing protein R.DAGEGKEGGAPGEFAPQFR.G (significant)**
$[MH]^+$ 2175.973 Da	
Fragment masses	112,091; 129,115; 136,08; 275,18; 449,194; 466,325; 547,264; 564,236; 693,368; 804,404; 821,466; 1084,652; 1483,764; 1856,078; 2072,026; 2113,577; 2137,092
T. atroviride	**Not related**
$[MH]^+$ 2483.072 Da	
Fragment masses	244,185; 315,282; 326,198; 425,285; 455,192; 487,277; 554,314; 574,337; 584,251; 673,402; 683,369; 782,422; 802,445; 812,355; 866,372; 883,397; 901,412; 911,462; 1030,557; 1159,554; 1258,592; 1357,564; 1565,617; 1583,73; 1654,684; 2029,318; 2449,19
T. atroviride	**Not related**
$[MH]^+$ 2564.061 Da	
Fragment masses	112,099; 129,11; 227,11; 229,127; 244,178; 259,121; 298,159; 300,14; 315,2; 326,167; 331,162; 358,152; 397,22; 407,219; 412,178; 425,225; 430,198; 455,18; 457,222; 469,206; 487,224; 496,234; 526,246; 554,269; 558,223; 574,264; 584,217; 586,258; 610,28; 625,283; 655,306; 665,314; 673,335; 683,313; 698,255; 754,353; 764,354; 767,32; 782,38; 784,37; 795,285; 802,39; 812,309; 848,334; 853,411; 866,335; 883,356; 893,432; 901,456; 911,43; 964,393; 982,412; 1010,518; 1030,522; 1081,529; 1092,451; 1097,553; 1109,486; 1141,575; 1159,589; 1191,502; 1208,549; 1240,653; 1251,616; 1258,669; 1269,641; 1322,682; 1340,681; 1357,759; 1486,825; 1547,815; 1565,871; 1583,922; 1655,81; 1704,560; 1751,986; 1769,071; 1847,862; 1883,196;

	2012,305; 2141,444; 2240,548; 2260,170; 2355,701; 2432,730; 2439,011; 2444,903; 2449,845; 2455,259; 2463,727; 2467,542; 2484,858
T. atroviride	**Not related**
$[MH]^+$ 2736.160 Da	
Fragment masses	425,262; 1032,285; 1145,4; 1357,463; 1591,82; 1706,128; 1821,399; 2167,429; 2256,141; 2467,312; 2513,774; 2525,079; 2562,904; 2626,6; 2668,792; 2691
T. atroviride	**Not related**

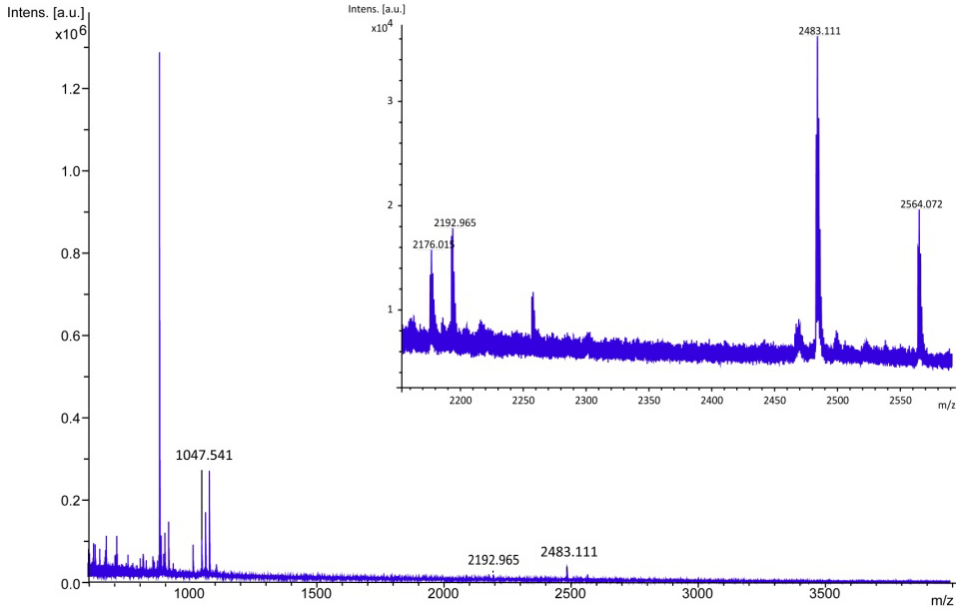


Figure 6.22 Positive ion reflector TOF - MALDI mass spectrum of 1_1_13

$[MH]^+$ 1047.541 Da	
Fragment masses	70,051; 84,075; 86,082; 98,081; 100,088; 107,062; 110,077; 112,094; 115,093; 123,112; 129,109; 136,092; 143,103; 147,082; 151,09; 154,103; 167,118; 172,086; 175,13; 181,113; 184,116; 186,132; 197,133; 202,121; 211,134; 215,127; 227,133; 229,137; 231,133; 244,137; 246,138; 250,113; 252,151; 271,174; 288,176; 294,104; 311,102; 487,083; 585,122; 651,122; 665,982; 712,977; 731,098; 855,087; 857,154; 924,224; 961,188; 997,314; 999,376; 1014,519; 1023,031; 1025,861
T. atroviride	**Not related**
$[MH]^+$ 2176.015 Da	
Fragment masses	112,092
T. atroviride	**Not related**
$[MH]^+$ 2192.965 Da	
Fragment masses	Fragmentation was not possible
T. atroviride	**-**
$[MH]^+$ 2483.111 Da	
Fragment masses	244,163; 326,182; 487,243; 574,292; 673,36; 683,323; 802,391; 812,299; 866,303; 883,343; 901,401; 911,424; 1030,467; 1159,527; 1258,562; 1357,676; 1583,597; 1654,64; 2464,856
T. atroviride	**Not related**

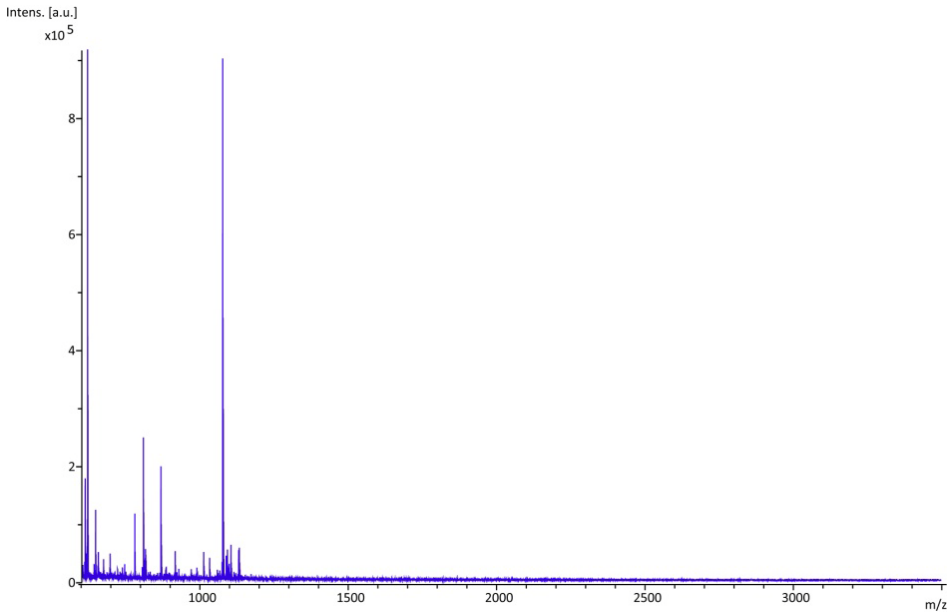


Figure 6.23 Positive ion reflector TOF - MALDI mass spectrum of 1_1_14

No relevant Peaks for PSD analysis

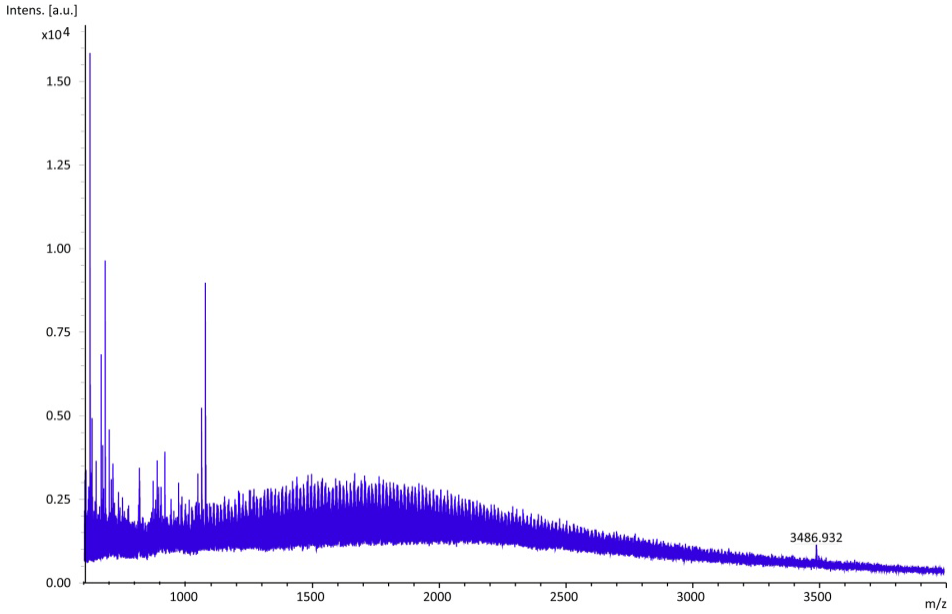


Figure 6.24 Positive ion reflector TOF - MALDI mass spectrum of 1_2_1

$[MH]^+$ 3486.932 Da	
Fragment masses	74,083; 130,118; 154,103; 156,163; 168,087; 173,198; 197,151; 211,164; 228,186; 242,173; 254,179; 266,136; 268,164; 285,205; 297,181; 338,178; 381,188; 398,188; 424,174; 438,191; 513,208; 626,184; 1726,567; 1783,685; 1880,658; 2009,613; 2760,605; 2925,122; 3207,435; 3286,955; 3378,966; 3424,507; 3431,662; 3436,482; 3440,195; 3443,414; 3446,689; 3451,413; 3455,399; 3459,692; 3463,59
T. atroviride	**Not related**

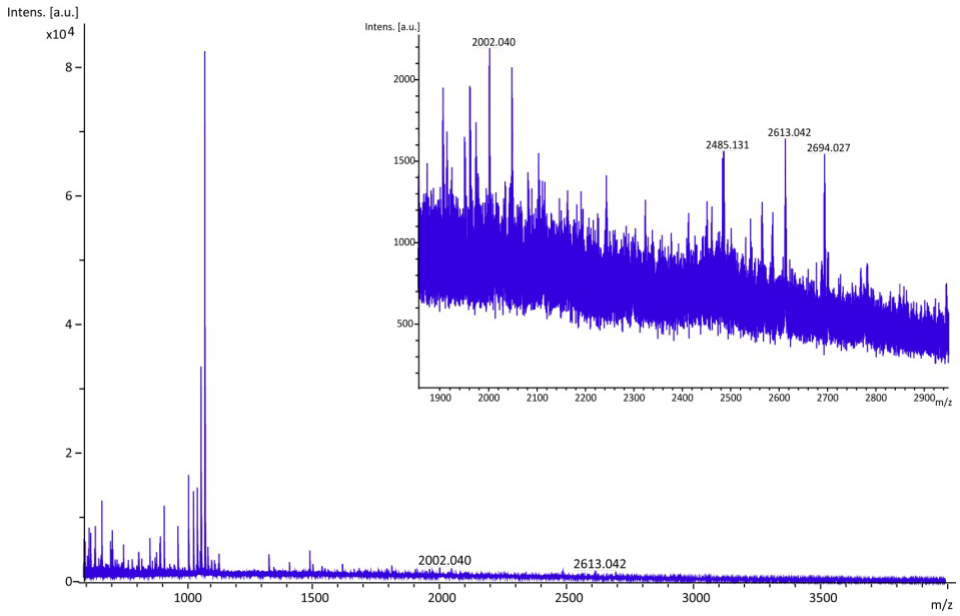


Figure 6.25 Positive ion reflector TOF - MALDI mass spectrum of 1_2_2

$[MH]^+$ 2002.04 Da	
Fragment masses	70,036; 74,189; 84,05; 86,073; 102,04; 110,055; 112,069; 115,068; 120,072; 129,087; 136,066; 141,078; 158,085; 167,081; 169,086; 172,081; 175,103; 181,084; 183,1; 185,091; 187,075; 195,079; 197,104; 202,084; 209,085; 212,105; 217,081; 226,109; 228,104; 232,117; 272,129; 701,187; 898,326; 1013,271; 1089,229; 1881,05; 1887,152; 1890,307; 1896,459; 1899,71; 1911,604; 1970,317; 1976,098; 1978,869; 1983,504; 1986,713
T. atroviride	**Not related**
$[MH]^+$ 2485.131 Da	
Fragment masses	110,045; 112,064; 129,087; 158,071; 169,071; 175,091; 197,088; 227,078; 232,112; 244,104; 270,096; 272,15; 298,111; 301,117; 347,125; 386,141; 715,239; 816,27; 858,289; 935,276; 963,306; 1050,295; 1064,334; 1069,368; 1087,373; 1151,376; 1250,426; 1363,465; 1589,672; 1660,639; 1761,626; 1832,779; 1904,449; 2102,071; 2370,627; 2376,718; 2381,535; 2384,532; 2388,567; 2395,105; 2412,598; 2465,48
T. atroviride	**Translation initiations factor 3 R.ESSPTAATAPEIVSTFTPDDIQK.V + Phospho (significant)**
$[MH]^+$ 2613.042 Da	
Fragment masses	70,007; 74,068; 112,074; 115,072; 129,095; 136,062; 158,084; 169,101; 175,109; 185,084; 195,095; 197,104; 215,103; 226,112; 232,133; 244,108; 273,107; 288,11; 301,121; 386,171; 401,161; 403,184; 502,248; 780,318; 895,336; 1010,343; 1087,424; 1125,311; 1310,405; 1882,608; 2314,363; 2475,161; 2482,122; 2489,542; 2492,339; 2499,371; 2502,333; 2505,168; 2510,097; 2517,639; 2583,973; 2588,8; 2594,332
T. atroviride	**TRP-repeat protein K.SAEIVVDSDEEEANDDDYDVLDR.A (NOT significant)**
$[MH]^+$ 2694.027 Da	
Fragment masses	74,083; 112,096; 129,13; 158,118; 175,146; 195,127; 201,136; 213,152; 229,171; 232,17; 273,152; 288,166; 290,177; 312,201; 333,217; 401,237; 403,248; 502,304; 591,31; 600,321; 617,33; 780,391; 878,43; 895,43; 975,441; 1010,463; 1051,452; 1125,498; 1166,54; 1222,574; 1240,493; 1310,577; 1439,594; 1568,657; 1680,712; 1697,784; 1812,778; 1881,757; 1979,882; 2257,481; 2548,33; 2568,693; 2572,532; 2578,158; 2596,757; 2612,975; 2615,875
T. atroviride	**Not related**

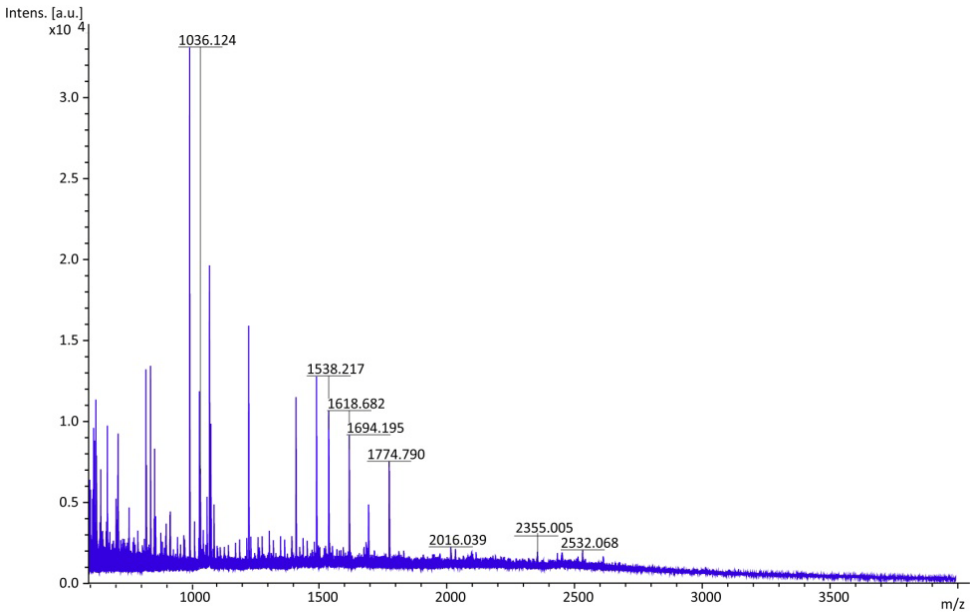


Figure 6.26 Positive ion reflector TOF - MALDI mass spectrum of 1_2_3

$[MH]^+$ 1036.124Da	
Fragment masses	58,005; 70,04; 72,043; 81,037; 86,073; 95,055; 97,059; 100,062; 104,088; 107,04; 110,059; 112,074; 115,067; 120,065; 123,078; 125,072; 129,084; 135,082; 139,076; 141,076; 144,076; 147,049; 149,083; 154,065; 158,077; 162,076; 167,073; 172,036; 175,1; 181,075; 184,057; 190,061; 195,075; 197,095; 207,067; 209,078; 211,082; 213,073; 215,083; 217,081; 223,08; 227,086; 232,101; 245,072; 253,07; 257,134; 266,063; 268,085; 270,098; 294,053; 310,068; 345,142; 382,102; 505,004; 508,173; 525,101; 614,007; 632,063; 651,872; 658,091; 661,128; 669,873; 676,127; 688,134; 695,581; 697,792; 780,309; 785,233; 796,883; 803,266; 820,094; 821,956; 829,292; 831,007; 834,614; 836,694; 840,864; 847,291; 865,328; 930,435; 957,686; 970,900; 974,441; 988,299; 992,511; 1008,919; 1010,927; 1013,729; 1016,580
T. atroviride	**Not related**
$[MH]^+$ 1538.217 Da	
Fragment masses	70,052; 72,067; 84,081; 86,084; 101,096; 104,105; 110,074; 112,092; 115,096; 120,096; 129,115; 136,095; 141,119; 144,116; 147,11; 154,107; 157,125; 159,112; 167,113; 169,132; 172,109; 175,14; 185,128; 187,111; 197,144; 201,137; 203,122; 205,113; 207,127; 209,148; 211,131; 213,133; 215,149; 217,14; 221,124; 223,149; 225,144; 227,136; 229,148; 232,151; 235,133; 237,153; 240,163; 243,172; 245,136; 247,159; 251,159; 254,151; 256,145; 258,144; 260,151; 262,156; 268,186; 272,156; 275,151; 277,138; 279,142; 285,199; 288,183; 292,145; 294,151; 296,148; 298,153; 300,161; 303,174; 312,150; 314,190; 316,141; 326,166; 328,164; 332,150; 335,159; 342,164; 345,186; 400,190; 443,228; 455,192; 471,229; 508,239; 555,230; 572,240; 583,225; 600,238; 654,250; 671,242; 818,273; 1030,172; 1032,241; 1139,491; 1161,758; 1180,411; 1273,835; 1328,411; 1330,433; 1333,499; 1337,747; 1340,694; 1346,121; 1351,465; 1406,899; 1432,265; 1434,451; 1450,191; 1490,677; 1493,933; 1509,230; 1512,240; 1519,478
T. atroviride	**Not related**
$[MH]^+$ 1618.682 Da	
Fragment masses	70,057; 72,069; 84,065; 86,068; 100,074; 104,095; 110,06; 112,08; 115,074; 120,075; 129,097; 136,081; 141,094; 144,092; 154,089; 157,103; 167,094; 169,108; 172,083; 175,114; 181,105; 183,106; 185,093; 187,085; 197,116; 200,117; 202,095; 212,124; 214,134; 217,107; 227,104; 242,11; 244,112; 268,158; 272,116; 288,137; 316,116; 399,204; 431,209; 1136,28; 1308,576; 1479,309; 1491,475; 1493,667; 1497,816; 1500,961; 1510,576; 1548,485;

	1576,817; 1590,521; 1633,993; 1642,336; 1657,755; 1671,678; 1674,534
T. atroviride	**Elongation factor 3 (EF-3) R.KRGEEVFSDEDDL.- (NOT significant)**
$[MH]^+$ 1694.195 Da	
Fragment masses	70,057; 72,069; 84,065; 86,068; 100,074; 104,095; 110,06; 112,08; 115,074; 120,075; 129,097; 136,081; 141,094; 144,092; 154,089; 157,103; 167,094; 169,108; 172,083; 175,114; 181,105; 183,106; 185,093; 187,085; 197,116; 200,117; 202,095; 212,124; 214,134; 217,107; 227,104; 242,11; 244,112; 268,158; 272,116; 288,137; 316,116; 399,204; 431,209; 1136,28; 1308,576; 1479,309; 1491,475; 1493,667; 1497,816; 1500,961; 1510,576; 1548,485; 1576,817; 1590,521; 1633,993; 1642,336; 1657,755; 1671,678; 1674,534
T. atroviride	**Not related**
$[MH]^+$ 1774.790 Da	
Fragment masses	70,051; 72,061; 84,079; 86,088; 104,1; 110,074; 112,095; 115,094; 120,096; 129,11; 136,099; 141,098; 144,113; 154,106; 157,117; 159,094; 167,107; 172,096; 175,13; 181,135; 185,114; 197,142; 212,131; 227,149; 268,176; 288,196; 399,236; 441,254; 627,31; 756,314; 1071,444; 1186,547; 1204,549; 1392,987; 1407,996; 1411,115; 1539,22; 1546,916; 1563,874; 1582,213; 1635,086; 1638,497; 1643,076; 1649,148; 1660,154; 1677,076; 1695,126; 1744,896; 1752,367
T. atroviride	**Not related**
$[MH]^+$ 2016.039 Da	
Fragment masses	70,026; 72,05; 84,044; 86,074; 104,098; 110,062; 112,08; 115,081; 129,097; 136,075; 141,099; 144,09; 154,084; 157,098; 167,081; 169,103; 172,075; 175,116; 181,105; 185,084; 197,117; 212,113; 214,119; 227,115; 244,12; 246,13; 768,265; 1066,285; 1467,631; 1623,633; 1638,766; 1808,254; 1810,084; 1812,517; 1815,462; 1908,372; 1912,694; 1968,796; 1992,842
T. atroviride	**Not related**
$[MH]^+$ 2355.005 Da	
Fragment masses	70,05; 74,035; 84,065; 86,075; 110,055; 112,074; 115,077; 129,09; 141,079; 157,083; 167,081; 169,097; 172,068; 175,098; 181,081; 195,072; 197,09; 212,096; 226,094; 232,1; 272,116; 288,129; 589,186; 783,268; 853,181; 946,309; 1024,264; 1581,319; 1767,389; 1870,16; 1956,182; 2140,772; 2146,678; 2245,217; 2248,589; 2331,128; 2334,873
T. atroviride	**Not related**
$[MH]^+$ 2532.068 Da	
Fragment masses	70,026; 74,048; 86,045; 110,071; 112,084; 115,081; 129,098; 154,075; 167,092; 175,115; 181,112; 186,118; 195,097; 197,115; 201,104; 212,122; 226,124; 232,14; 244,13; 246,151; 272,167; 288,174; 386,186; 873,415; 988,425; 1058,414; 1076,43; 1227,442; 1340,503; 1358,513; 1451,482; 1543,416; 2041,445; 2142,963; 2317,166; 2332,007; 2335,241; 2374,515; 2381,988; 2399,387; 2405,913; 2415,26; 2420,306; 2423,532; 2430,216; 2433,107; 2439,168; 2450,347
T. atroviride	**Not related**

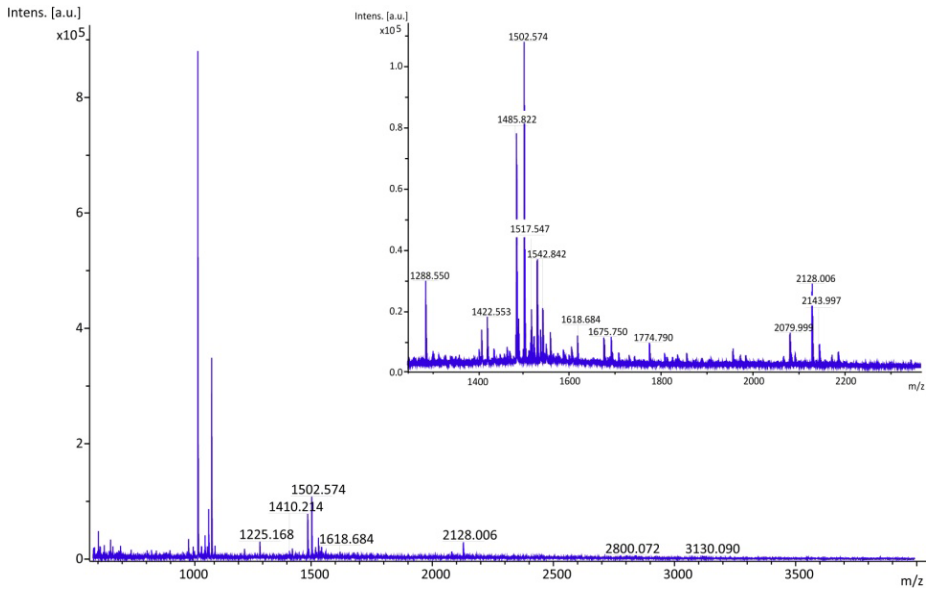


Figure 6.27 Positive ion reflector TOF - MALDI mass spectrum of 1_2_4

$[MH]^+$ 1225.168 Da	
Fragment masses	70,022; 84,051; 86,074; 100,06; 110,066; 112,079; 115,076; 123,099; 129,091; 136,069; 141,095; 143,115; 154,08; 158,091; 167,082; 172,086; 175,117; 177,048; 181,076; 184,095; 191,06; 197,112; 201,087; 203,112; 212,1; 215,097; 217,097; 226,1; 228,091; 232,095; 240,1; 249,987; 253,071; 265,951; 286,087; 288,128; 310,065; 508,098; 1028,912; 1031,211; 1087,351; 1162,598; 1175,236; 1177,452; 1179,611; 1195,902; 1198,105; 1202,555; 1204,662
T. atroviride	**Not related**
$[MH]^+$ 1288.550 Da	
Fragment masses	69,999; 86,058; 100,048; 110,04; 112,063; 115,053; 129,083; 136,05; 141,073; 143,092; 154,061; 159,06; 167,063; 172,061; 175,096; 181,065; 188,083; 190,051; 197,089; 215,071; 217,069; 226,082; 232,095; 240,082; 249,06; 253,047; 257,054; 265,97; 288,092; 310,052; 345,137; 366,056; 508,213; 524,977; 709,19; 781,218; 899,641; 916,335; 946,643; 1030,9; 1089,553; 1093,845; 1228,834; 1233,02; 1241,458; 1244,788; 1262,214; 1264,264; 1266,375; 1269,748
T. atroviride	**Not related**
$[MH]^+$ 1410.214 Da	
Fragment masses	70,04; 84,066; 86,094; 101,087; 110,093; 112,111; 115,111; 120,103; 129,141; 136,122; 141,14; 143,16; 147,135; 154,141; 159,155; 167,152; 172,162; 175,182; 181,15; 197,195; 201,157; 203,163; 215,188; 219,155; 226,195; 232,203; 240,21; 242,201; 249,207; 253,177; 257,197; 264,195; 270,22; 275,184; 288,236; 311,177; 345,257; 373,136; 508,294; 525,205; 1015,448; 1032,464; 1208,529; 1250,627; 1289,67; 1306,628; 1315,62; 1324,661; 1342,543; 1360,639; 1383,594; 1386,932; 1389,676
T. atroviride	**Type a willebrand factor domain containing proteinR.HSGPACGSRRIGR.V (NOT significant)**
$[MH]^+$ 1422.553 Da	
Fragment masses	70,061; 84,075; 86,094; 110,09; 112,113; 115,116; 129,136; 136,124; 154,126; 167,143; 172,14; 175,172; 197,178; 215,16; 217,158; 232,193; 240,175; 253,156; 257,172; 275,158; 277,179; 288,202; 293,159; 311,169; 345,26; 373,125; 387,15; 393,176; 508,32; 525,216; 588,265; 606,273; 623,316; 688,248; 1015,434; 1032,607; 1302,854; 1305,902; 1307,992; 1324,954; 1343,007; 1378,871
T. atroviride	**Not related**
$[MH]^+$ 1485.822 Da	
Fragment masses	70,04; 86,071; 110,066; 112,086; 115,088; 129,107; 136,077; 141,092; 143,128; 154,091; 158,104; 167,102; 172,108; 175,132; 181,097; 185,151; 188,134; 190,109;

	195,103; 197,134; 203,12; 213,164; 216,118; 219,104; 226,134; 232,149; 242,189; 249,15; 253,105; 268,115; 273,125; 279,113; 288,147; 296,12; 310,118; 345,202; 393,107; 411,134; 416,09; 473,13; 508,234; 525,123; 588,142; 606,195; 623,235; 688,114; 817,308; 918,419; 1015,261; 1032,265; 1089,285; 1284,877; 1302,705; 1366,594; 1370,788; 1375,021; 1381,431; 1384,622; 1387,825; 1399,508; 1404,85; 1421,769; 1432,771; 1441,940; 1448,984; 1460,285; 1462,654; 1466,774
T. atroviride	**FAD/FMN containing dehydrogenases R.MIIKNTGHDYLGR.S (significant)**
$[MH]^+$ 1502.574 Da	
Fragment masses	70,031; 84,064; 86,077; 110,063; 112,082; 115,073; 129,102; 136,071; 139,075; 141,098; 154,092; 158,095; 167,097; 172,096; 175,124; 185,15; 190,109; 195,102; 197,118; 213,158; 216,105; 227,109; 232,14; 242,171;326,146; 328,16; 345,195; 355,142; 382,125; 393,104; 411,113; 416,097; 473,113; 508,21; 518,17; 525,105; 588,166; 606,152; 623,172; 660,088; 688,078; 760,119; 817,087; 918,068; 1015,052; 1032,408; 1088,864; 1284,867; 1288,702; 1302,72; 1361,909; 1387,872; 1392,07; 1404,859; 1422,903; 1440,938; 1443,967; 1450,206; 1467,799; 1484,803
T. atroviride	**Not related**
$[MH]^+$ 1517.547 Da	
Fragment masses	70,035; 86,074; 110,066; 112,085; 115,083; 129,109; 136,087; 141,106; 143,146; 154,096; 158,108; 167,107; 172,116; 175,141; 181,122; 185,16; 188,135; 190,122; 195,113; 197,142; 213,175; 215,13; 226,148; 232,164; 242,188; 249,163; 253,121; 257,127; 259,133; 275,13; 277,148; 279,113; 286,154; 288,169; 296,132; 310,131; 328,184; 345,224; 355,193; 382,16; 411,134; 416,116; 473,132; 508,232; 518,194; 525,127; 588,179; 606,165; 623,191; 688,091; 1015,139; 1032,208; 1284,993; 1287,92; 1302,018; 1317,918; 1360,977; 1378,09; 1387,071; 1403,938; 1411,318; 1414,556; 1421,966; 1432,592; 1438,947; 1450,296; 1458,851; 1466,997; 1484,438; 1492,673; 1495,702
T. atroviride	**FAD/FMN containing dehydrogenases R.MIIKNTGHDYLGR.S (NOT significant)**
$[MH]^+$ 1542.842 Da	
Fragment masses	154,095; 158,11; 167,114; 175,141; 197,145; 213,171; 232,168; 242,176; 253,115; 310,126; 345,223; 355,177; 402,108; 410,156; 473,158; 482,068; 508,245; 518,178; 525,137; 588,191; 606,199; 623,214; 688,121; 817,18; 918,222; 988,304; 1015,083; 1032,211; 1060,246; 1070,374; 1089,46; 1092,015; 1276,088; 1301,583; 1316,165; 1383,797; 1390,166; 1402,985; 1415,248; 1417,465; 1420,996; 1425,746; 1432,127; 1435,25; 1438,523; 1442,723; 1450,157; 1462,891; 1466,029; 1483,834; 1488,085; 1494,808; 1498,207; 1500,888; 1505,7; 1512,098; 1515,209; 1517,343; 1519,854; 1522,932
T. atroviride	**FAD/FMN containing dehydrogenases R.LRIKNTGHDYLGR.S (significant)**
$[MH]^+$ 1618.864 Da	
Fragment masses	70,039; 84,061; 86,071; 110,058; 112,076; 115,077; 129,09; 136,07; 141,092; 143,11; 154,082; 158,092; 167,091; 172,094; 175,118; 181,095; 187,102; 197,119; 201,11; 205,082; 209,105; 211,117; 213,128; 215,112; 217,107; 226,119; 232,132; 235,116; 240,12; 244,113; 253,099; 270,143; 272,13; 286,123; 288,157; 310,112; 312,104; 314,139; 345,19; 508,226; 525,138; 546,102; 582,1; 588,181; 606,161; 623,169; 688,129; 801,104; 817,151; 1015,123; 1032,193; 1089,268; 1483,885; 1506,065; 1508,123; 1511,327; 1514,499; 1520,923; 1525,088; 1540,013; 1569,425; 1584,796; 1586,871; 1591,437; 1594,735; 1598,838
T. atroviride	**Not related**
$[MH]^+$ 1675.750 Da	
Fragment masses	70,03; 84,053; 86,07; 101,057; 110,053; 112,072; 115,071; 120,067; 129,088; 136,062; 141,088; 143,122; 147,086; 154,078; 158,087; 167,088; 172,087; 175,115; 181,101; 183,122; 185,106; 197,127; 213,12; 217,098; 229,113; 232,128; 240,138; 244,117; 250,115; 270,146; 272,129; 474,175; 508,206; 589,188; 659,143; 1000,493; 1015,029; 1032,148; 1089,241; 1202,53; 1483,589; 1519,905; 1577,986; 1615,953; 1634,037; 1640,875; 1647,433; 1650,594; 1653,749
T. atroviride	**Not related**
$[MH]^+$ 1774.790 Da	

Fragment masses	70,045; 84,07; 86,083; 110,073; 112,089; 115,093; 129,111; 136,096; 139,11; 141,111; 143,147; 147,094; 154,102; 158,106; 167,117; 169,125; 172,12; 175,138; 183,142; 185,141; 187,118; 197,149; 201,122; 213,166; 226,156; 232,161; 240,154; 242,181; 250,136; 255,156; 288,183; 508,288; 1015,331; 1017,283; 1032,269; 1089,16; 1133,261; 1306,096; 1315,846; 1324,108; 1386,924; 1403,957; 1418,344; 1484,256; 1660,351; 1665,546; 1669,812; 1677,273; 1739,673; 1742,431; 1746,488; 1749,148; 1752,059; 1756,571
T. atroviride	**Not related**
$[MH]^+$ 2079.999 Da	
Fragment masses	70,03; 84,064; 101,073; 110,064; 112,075; 115,071; 129,096; 136,069; 141,092; 154,079; 158,084; 167,085; 169,106; 172,085; 175,109; 181,092; 186,115; 195,091; 197,113; 201,093; 212,119; 226,121; 228,119; 232,12; 240,116; 244,117; 250,098; 258,113; 270,144; 272,148; 274,112; 284,122; 286,145; 288,139; 292,127; 303,156; 316,113; 360,18; 508,238; 560,222; 689,269; 804,295; 933,278; 1032,287; 1089,257; 1485,376; 1681,986; 1959,892; 1964,279; 1968,519; 1981,346; 1995,605; 2008,603; 2034,456; 2042,391; 2046,074; 2049,843; 2052,841; 2055,982; 2059,557
T. atroviride	**Not related**
$[MH]^+$ 2128.006 Da	
Fragment masses	70,018; 84,058; 102,037; 110,057; 112,069; 115,066; 129,089; 136,053; 141,085; 154,063; 158,078; 167,078; 169,093; 175,098; 181,08; 186,102; 197,114; 201,079; 217,1; 226,102; 240,12; 250,106; 258,123; 272,135; 274,102; 286,142; 292,135; 303,154; 316,126; 343,146; 360,175; 560,218; 689,264; 804,249; 933,275; 1032,32; 1481,608; 1682,03; 2008,201; 2015,49; 2061,223; 2063,922; 2078,926; 2092,139; 2094,459; 2097,383; 2100,714; 2107,493
T. atroviride	**Poly(ADP-ribose) polymerase K.HTHASLEQLVRSLGGSVTR.S + Phospho (NOT significant)**
$[MH]^+$ 2143.997 Da	
Fragment masses	70,04; 84,065; 110,064; 112,084; 115,079; 129,101; 136,069; 141,101; 154,086; 159,097; 167,102; 169,1; 175,123; 186,125; 197,125; 201,101; 203,095; 217,127; 226,143; 240,134; 245,114; 258,145; 272,171; 274,116; 292,155; 303,194; 316,142; 343,195; 360,239; 403,191; 489,246; 560,306; 689,337; 787,285; 804,331; 933,353; 1032,386; 1190,409; 1481,493; 1681,474; 2051,648; 2062,258; 2065,05; 2076,778; 2080,448; 2108,064; 2111,075; 2115,878; 2119,195; 2127,502
T. atroviride	**Not related**
$[MH]^+$ 2800.072 Da	
Fragment masses	74,01; 110,032; 112,042; 129,064; 175,086; 185,079; 195,057; 197,087; 213,082; 215,081; 226,081; 230,086; 240,094; 244,094; 246,114; 254,092; 257,115; 259,059; 272,118; 284,087; 300,089; 314,1; 369,114; 379,121; 386,114; 404,145; 413,113; 415,107; 429,131; 431,088; 515,151; 532,185; 599,14; 661,209; 937,344; 1052,366; 1180,273; 1282,518; 1390,373; 1454,572; 1697,746; 1812,862; 2425,568; 2566,719; 2664,376; 2668,553; 2677,871; 2685,498; 2759,203; 2763,572; 2767,55; 2774,37; 2779,861; 2784,822
T. atroviride	**Not related**
$[MH]^+$ 3130.090 Da	
Fragment masses	129,108; 175,15; 226,169; 240,17; 244,177; 258,177; 272,186; 342,165; 358,194; 457,192; 528,205; 560,299; 599,274; 617,284; 716,37; 728,317; 827,401; 947,505; 1032,402; 1076,514; 1191,668; 1459,641; 1589,876; 1684,699; 1959,172; 2081,346; 2203,386; 2415,751; 3010,702; 3074,44; 3104,971; 3113,294
T. atroviride	**Not related**

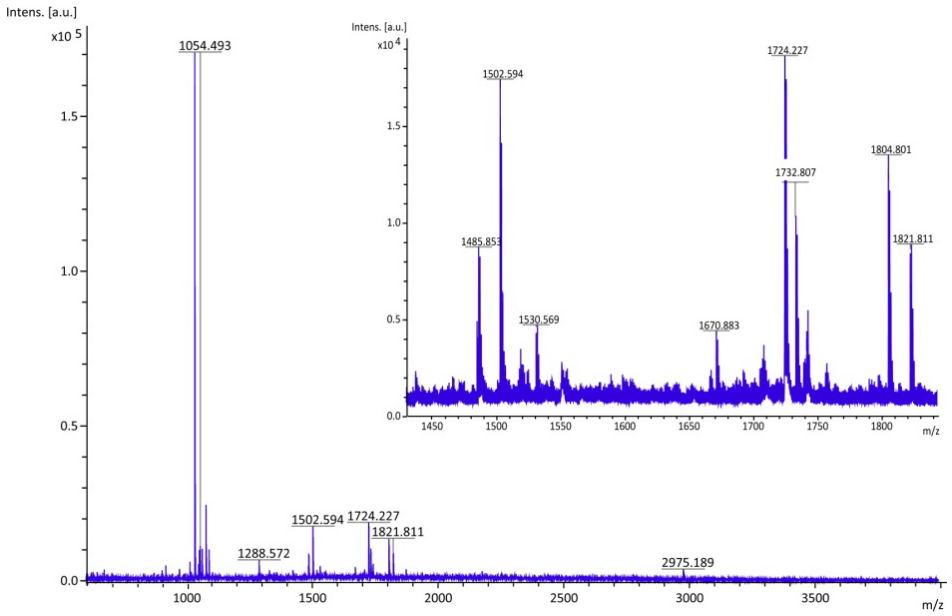


Figure 6.28 Positive ion reflector TOF - MALDI mass spectrum of 1_2_5

$[MH]^+$ 1054.493 Da	
Fragment masses	70,047; 84,073; 86,097; 110,086; 113,097; 120,098; 129,121; 136,093; 139,099; 143,127; 147,108; 154,107; 158,111; 167,107; 172,109; 175,14; 181,117; 184,151; 186,113; 188,123; 190,108; 195,105; 197,13; 204,146; 207,116; 212,125; 216,121; 225,121; 227,127; 232,153; 235,108; 238,128; 240,156; 242,133; 245,127; 253,109; 279,116; 286,163; 296,139; 311,113; 345,191; 362,182; 365,15; 367,187; 379,198; 382,179; 386,414; 393,143; 410,180; 416,145; 421,126; 473,141; 508,14; 525,204; 530,269; 585,183; 645,307; 651,193; 660,288; 672,229; 681,893; 688,321; 731,209; 782,462; 823,450; 839,500; 851,490; 856,737; 858,798; 860,959; 863,099; 865,172; 898,555; 908,580; 940,645; 961,329; 1006,293; 1010,665; 1014,567; 1026,601; 1031,52
T. atroviride	**FAD/FMN dontaining dehydrogenases R.NTGHDYYGK.S (NOT significant)**
$[MH]^+$ 1288.572 Da	
Fragment masses	70,014; 84,039; 86,066; 101,048; 110,047; 112,069; 115,068; 120,065; 129,084; 133,054; 136,06; 139,081; 141,069; 147,066; 154,068; 158,075; 167,073; 172,077; 175,102; 181,078; 183,091; 185,087; 187,071; 195,067; 197,097; 201,074; 203,072; 205,065; 207,070; 209,075; 212,098; 215,090; 219,069; 221,070; 226,09; 229,079; 232,104; 235,079; 237,084; 240,089; 242,093; 244,088; 246,076; 249,091; 253,07; 255,084; 257,069; 259,083; 262,085; 264,076; 266,087; 268,103; 270,099; 272,099; 276,108; 279,072; 284,08; 286,085; 288,108; 290,101; 296,088; 310,077; 312,098; 314,084; 329,098; 345,149; 349,086; 366,085; 508,228; 525,099; 606,172; 623,216; 666,172; 709,215; 763,185; 781,231; 899,347; 908,881; 916,353; 944,332; 1031,719; 1081,270; 1086,463; 1091,639; 1097,999; 1183,200; 1187,506; 1190,797; 1220,215; 1238,196; 1241,442; 1244,774; 1263,012; 1266,237; 1269,295
T. atroviride	**Not related**
$[MH]^+$ 1485.853 Da	
Fragment masses	70,061; 84,079; 86,086; 101,068; 110,077; 112,097; 115,081; 120,084; 129,115; 136,086; 147,102; 154,102; 158,115; 167,111; 172,117; 175,142; 181,119; 183,128; 185,14; 187,114; 195,118; 197,151; 201,131; 213,164; 215,142; 217,119; 226,141; 232,162; 240,148; 242,174; 244,134; 253,124; 256,138; 258,133; 262,148; 264,155; 268,163; 270,148; 272,173; 277,156; 279,12; 286,147; 288,163; 290,151; 301,145; 303,166; 310,136; 314,158; 328,184; 330,165; 332,145; 334,158; 339,166; 345,214; 355,179; 359,171; 385,179; 393,153; 398,157; 411,161; 508,257; 518,214; 525,180; 588,226; 606,230; 623,255; 688,196; 817,283; 918,362; 1015,373; 1032,401; 1097,628; 1112,350; 1116,568; 1286,544; 1290,738; 1292,949; 1302,668; 1376,975;

	1380,211; 1383,469; 1386,716; 1389,949; 1393,164; 1404,747; 1422,473; 1425,402; 1440,742; 1457,789; 1465,767
T. atroviride	**FAD/FMN dontaining dehydrogenases R.IVLKNTGHDYLGR.S (significant)**
$[MH]^+$ 1502.594 Da	
Fragment masses	70,052; 84,073; 86,089; 101,075; 110,074; 112,092; 115,088; 120,09; 129,114; 136,087; 154,106; 158,104; 167,103; 172,118; 175,137; 181,116; 185,131; 195,109; 197,131; 215,128; 227,127; 229,128; 232,149; 242,152; 244,129; 249,147; 253,11; 255,131; 257,122; 259,118; 270,142; 272,152; 279,102; 286,146; 288,146; 290,141; 304,158; 310,125; 316,145; 328,160; 330,14; 332,133; 334,136; 345,205; 355,185; 358,145; 365,142; 367,152; 369,153; 371,146; 373,139; 375,144; 385,141; 387,131; 389,151; 398,154; 400,181; 410,156; 427,162; 453,121; 508,240; 518,200; 525,167; 588,206; 606,209; 623,229; 633,190; 688,162; 1015,308; 1032,418; 1285,591; 1288,608; 1302,645; 1308,784; 1318,530; 1361,807; 1387,826; 1391,872; 1399,442; 1404,816; 1422,851; 1443,043; 1450,060; 1459,813; 1467,715; 1484,344
T. atroviride	**Not related**
$[MH]^+$ 1530.569Da	
Fragment masses	57,815; 59,286; 64,802; 67,512; 71,23; 74,175; 77,981; 85,048; 89,074; 92,28; 95,399; 97,761; 100,574; 102,607; 104,153; 110,107; 112,118; 114,53; 116,803; 120,077; 121,508; 124,338; 127,109; 129,165; 143,09; 149,775; 153,157; 157,141; 160,768; 163,47; 165,218; 167,113; 169,728; 172,455; 175,175; 179,104; 185,666; 187,13; 190,782; 192,196; 197,157; 204,587; 208,153; 211,172; 216,161; 219,509; 221,169; 224,532; 227,162; 232,181; 238,832; 241,170; 244,17; 247,213; 249,098; 253,144; 264,184; 266,198; 269,245; 273,210; 276,15; 279,957; 281,213; 284,132; 289,507; 292,167; 294,521; 298,236; 303,253; 312,191; 315,218; 329,214; 331,210; 333,150; 345,258; 349,175; 354,149; 358,230; 374,264; 380,200; 385,192; 389,685; 394,136; 402,155; 411,195; 413,083; 425,132; 429,258; 437,177; 441,156; 446,209; 464,091; 466,098; 473,239; 477,192; 508,322; 515,287; 518,339; 532,849; 538,145; 542,219; 561,237; 597,3; 623,372; 754,489; 1032,573; 1050,455; 1091,498; 1415,983; 1432,846; 1436,345; 1440,646; 1450,894; 1484,784; 1487,743; 1492,461; 1503,372; 1506,124; 1511,777; 1514,032; 1521,145; 1524,253; 1527,802; 1530,899; 1533,392
T. atroviride	**Not related**
$[MH]^+$ 1670.883 Da	
Fragment masses	70,045; 84,063; 86,077; 101,06; 110,061; 112,077; 115,077; 120,076; 129,099; 133,07; 136,076; 139,084; 141,089; 143,104; 147,092; 155,09; 157,098; 159,093; 167,096; 169,103; 172,097; 175,12; 181,102; 183,115; 185,105; 187,088; 195,097; 197,12; 200,115; 209,105; 212,113; 214,11; 217,084; 221,095; 226,117; 229,11; 232,133; 240,131; 242,133; 244,12; 249,107; 251,104; 255,11; 258,118; 262,143; 267,104; 272,142; 276,126; 329,139; 508,22; 759,285; 983,43; 1032,28; 1050,331; 1089,399; 1266,674; 1324,69; 1466,433; 1483,739; 1537,55; 1551,978; 1555,093; 1559,104; 1563,368; 1567,545; 1569,794; 1573,000; 1591,026; 1603,662; 1609,093; 1626,947; 1646,125
T. atroviride	**Not related**
$[MH]^+$ 1724.227 Da	
Fragment masses	70,058; 84,061; 86,08; 101,066; 110,063; 112,079; 115,079; 120,074; 129,098; 136,067; 140,079; 147,103; 154,081; 157,094; 159,085; 167,081; 169,096; 171,083; 175,113; 183,102; 185,093; 187,084; 195,092; 197,116; 200,103; 203,086; 209,092; 213,106; 217,091; 221,117; 225,13; 227,100; 230,112; 232,113; 234,121; 242,134; 244,103; 249,108; 255,108; 259,118; 267,097; 270,122; 272,147; 276,133; 287,126; 305,164; 314,123; 318,137; 330,176; 345,144; 370,138; 416,198; 429,146; 434,192; 447,147; 562,222; 568,195; 611,190; 633,272; 659,244; 761,280; 797,223; 816,245; 833,252; 925,302; 1017,329; 1030,409; 1032,318; 1145,366; 1479,564; 1484,172; 1504,560; 1513,111; 1521,568; 1529,920; 1539,539; 1578,131; 1596,089; 1602,572; 1610,034; 1616,365; 1619,475; 1622,702; 1627,014; 1637,497; 1647,183; 1651,423; 1660,020; 1662,153; 1681,067; 1688,390; 1699,330; 1706,056
T. atroviride	**Not related**
$[MH]^+$ 1732.807 Da	

Fragment masses	70,047; 84,062; 86,078; 101,072; 110,064; 112,082; 115,085; 120,084; 129,098; 136,078; 139,077; 141,096; 143,095; 147,106; 155,084; 157,098; 159,089; 167,091; 169,098; 172,097; 175,119; 181,103; 183,116; 185,099; 189,082; 195,087; 197,118; 200,116; 203,096; 207,103; 209,097; 212,114; 217,095; 221,118; 226,125; 228,127; 230,111; 232,125; 234,138; 240,121; 242,144; 244,114; 249,12; 255,114; 259,133; 267,094; 270,126; 272,141; 276,138; 287,144; 305,177; 311,149; 318,150; 345,159; 370,152; 434,21; 482,150; 488,199; 546,221; 562,222; 568,198; 611,174; 633,279; 645,259; 668,196; 687,253; 797,233; 808,325; 816,254; 925,288; 936,362; 1014,338; 1030,411; 1032,322; 1060,358; 1088,355; 1099,347; 1122,472; 1145,399; 1187,437; 1244,499; 1251,580; 1358,611; 1388,716; 1457,770; 1483,738; 1521,243; 1529,537; 1539,039; 1577,982; 1586,849; 1595,65; 1603,928; 1615,985; 1619,074; 1622,197; 1625,381; 1628,536; 1631,833; 1635,017; 1659,396; 1662,498; 1665,717; 1680,373; 1688,977; 1705,938
T. atroviride	**Rossmann-fold NAD(P)$^+$ - binding proteins (FAD-binding domain containing protein, FAD-Monooxygenase) R.DTQHEGEQYVGNVEK.H (significant)**
$[MH]^+$ 1804.801 Da	
Fragment masses	70,07; 84,083; 86,107; 101,092; 110,093; 112,111; 115,114; 120,111; 129,133; 136,107; 147,137; 155,126; 157,14; 167,145; 171,147; 175,163; 181,145; 185,15; 187,124; 195,145; 197,168; 200,15; 209,142; 212,166; 232,182; 242,186; 244,177; 255,166; 259,188; 272,195; 305,21; 329,288; 345,244; 562,283; 633,342; 751,522; 761,388; 773,427; 816,345; 833,367; 887,465; 902,448; 1013,527; 1030,601; 1033,443; 1110,571; 1127,599; 1145,66; 1216,734; 1225,678; 1243,636; 1260,725; 1389,828; 1447,443; 1458,825; 1579,07; 1590,055; 1596,084; 1606,879; 1634,133; 1663,225; 1666,724; 1671,010; 1672,920; 1677,146; 1680,953; 1689,274; 1691,822; 1694,487; 1697,997; 1700,830; 1707,246; 1725,285; 1741,547
T. atroviride	**Ribosome assoziated chaperone zuotin R.TFSEDDRIQAQESAK.N + Phospho (NOT significant)**
$[MH]^+$ 1821.811 Da	
Fragment masses	70,063; 84,077; 86,098; 101,087; 110,091; 112,109; 115,109; 120,106; 129,128; 136,103; 141,127; 147,137; 157,134; 167,125; 172,138; 175,157; 181,149; 185,150; 195,139; 197,16; 250,128; 259,179; 272,205; 276,181; 304,181; 329,241; 373,208; 391,217; 488,234; 586,238; 656,282; 659,348; 677,366; 687,339; 705,364; 757,371; 785,315; 833,416; 1014,478; 1030,549; 1032,477; 1037,522; 1087,547; 1128,507; 1145,505; 1219,507; 1260,503; 1351,753; 1389,474; 1467,598; 1484,926; 1578,313; 1589,503; 1596,135; 1607,009; 1613,113; 1662,274; 1665,823; 1676,161; 1680,144; 1689,324; 1693,251; 1696,913; 1706,269; 1709,321; 1713,538; 1717,760; 1724,246; 1742,279; 1770,629; 1804,034;
T. atroviride	**Not related**
$[MH]^+$ 2975.189 Da	
Fragment masses	69,992; 73,926; 110,024; 112,053; 129,082; 169,078; 175,112; 198,102; 212,1; 216,091; 226,106; 232,123; 240,092; 244,1; 247,109; 256,108; 258,09; 267,088; 269,12; 272,132; 275,094; 285,138; 295,108; 297,115; 299,123; 301,063; 313,118; 327,113; 330,128; 339,131; 341,132; 343,127; 355,119; 360,134; 375,151; 382,126; 384,131; 386,15; 394,138; 396,127; 400,155; 412,139; 414,172; 430,149; 447,151; 456,193; 471,171; 518,131; 534,173; 582,211; 628,212; 640,166; 697,275; 825,325; 908,41; 1034,411; 1041,484; 1051,444; 1122,499; 1139,5; 1209,554; 1296,594; 1383,643; 1454,697; 1608,738; 1679,761; 1935,053; 2516,542; 2732,877; 2776,961; 2794,166; 2811,993; 2831,338; 2855,708; 2859,878; 2865,126; 2868,973; 2873,219; 2875,717; 2892,377; 2930,437; 2945,84
T. atroviride	**Dihydrolipoamide acetyltransferase component K.KDSEPAPQSTPASAPQSSSAPEQYSSQGR.I (significant)**

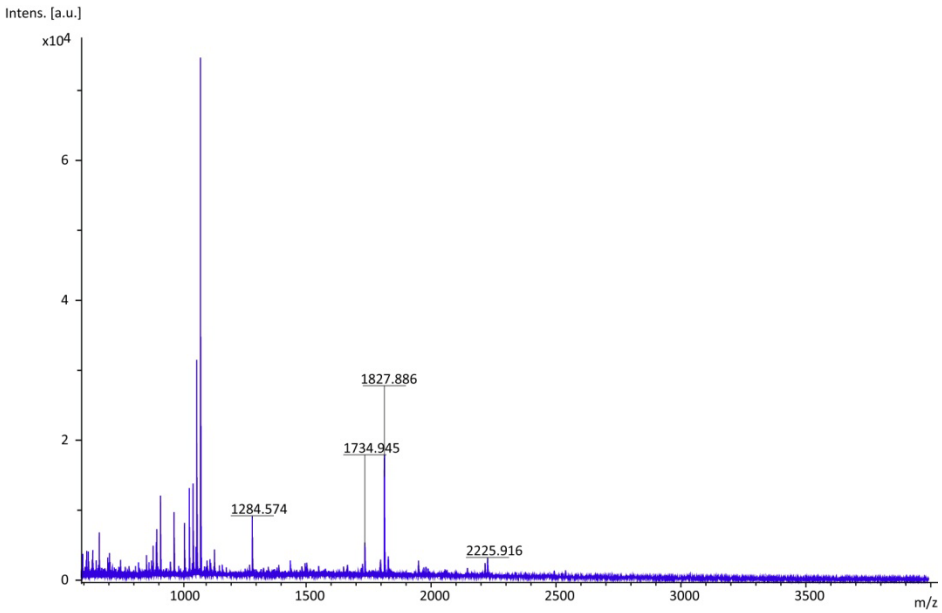


Figure 6.29 Positive ion reflector TOF - MALDI mass spectrum of 1_2_6

$[MH]^+$ 1284.574 Da	
Fragment masses	70,033; 84,057; 86,075; 98,071; 101,068; 104,108; 110,072; 112,088; 115,089; 120,091; 123,082; 129,105; 132,096; 136,081; 138,088; 141,098; 143,123; 145,070; 147,100; 154,095; 159,106; 163,106; 167,099; 169,107; 172,101; 175,127; 179,098; 181,112; 184,107; 186,111; 189,090; 193,095; 197,128; 201,122; 205,107; 207,098; 209,118; 212,127; 214,126; 216,125; 218,128; 221,113; 223,115; 226,126; 229,125; 231,115; 233,110; 235,122; 237,128; 239,129; 243,116; 246,126; 249,113; 251,124; 253,129; 255,129; 257,137; 259,106; 262,128; 264,125; 266,124; 268,138; 271,12; 9273,117; 276,137; 279,129; 282,130; 284,128; 286,130; 288,156; 292,124; 294,128; 297,122; 300,125; 303,139; 306,114; 313,133; 315,134; 326,135; 328,134; 331,141; 336,142; 339,134; 341,137; 343,143; 346,129; 358,141; 360,140; 372,128; 471,168; 504,187; 892,640; 908,545; 1081,527; 1085,703; 1087,820; 1089,881; 1091,989; 1098,242; 1145,039; 1182,574; 1232,077; 1234,338; 1237,764; 1240,906; 1254,869; 1256,919; 1259,061; 1261,279; 1263,376
T. atroviride	**Not related**
$[MH]^+$ 1734.945 Da	
Fragment masses	70,073; 84,078; 86,094; 98,108; 101,087; 110,083; 112,097; 115,107; 120,092; 129,118; 136,096; 140,121; 143,132; 147,108; 154,114; 157,124; 159,113; 167,109; 169,127; 171,128; 175,144; 181,131; 183,123; 185,130; 187,140; 195,127; 197,146; 199,143; 201,140; 204,153; 207,129; 209,134; 212,148; 215,154; 217,149; 227,152; 229,144; 231,131; 235,148; 240,153; 243,158; 252,163; 254,171; 258,147; 268,184; 270,179; 286,169; 344,169; 400,183; 428,190; 529,208; 547,269; 601,295; 619,319; 671,315; 748,351; 845,390; 890,429; 907,446; 987,512; 1032,355; 1116,542; 1147,591; 1190,612; 1218,696; 1289,819; 1418,873; 1532,158; 1607,226; 1660,536; 1665,488; 1683,499; 1691,165; 1708,367; 1711,438
T. atroviride	**Not related**
$[MH]^+$ 1827.886 Da	
Fragment masses	70,055; 84,074; 86,090; 101,079; 110,074; 112,094; 115,095; 120,089; 129,113; 136,085; 155,111; 157,115; 159,104; 167,102; 172,119; 175,133; 181,143; 185,126; 195,102; 197,132; 229,130; 289,190; 342,197; 559,283; 717,360; 832,386; 947,419; 959,468; 1176,525; 1484,835; 1632,309; 1649,400; 1723,746; 1741,782; 1753,499; 1756,633; 1760,917; 1765,397; 1770,242; 1776,862; 1779,629; 1783,120; 1795,081; 1812,025
T. atroviride	**Not related**

[MH]$^+$ 2225.916 Da	
Fragment masses	70,041; 84,079; 110,081; 112,095; 115,099; 129,118; 136,092; 167,121; 169,122; 175,138; 195,113; 319,213; 355,197; 546,300; 603,310; 624,243; 674,351; 720,438; 731,370; 787,341; 860,449; 888,471; 906,504; 975,469; 1003,503; 1021,489; 1032,505; 1131,577; 1149,534; 1221,580; 1317,662; 1446,772; 1507,678; 1606,847; 1861,701; 2023,883; 2049,385; 2167,843; 2171,460; 2182,288; 2196,624
T. atroviride	**Rossmann-fold NAD(P)$^+$ - binding proteins (NADP binding domain containing protein, 6-phosphogluconate dehydrogenase)** **K.SDGEACCEWVGDEGAGHYVK.M (significant)**

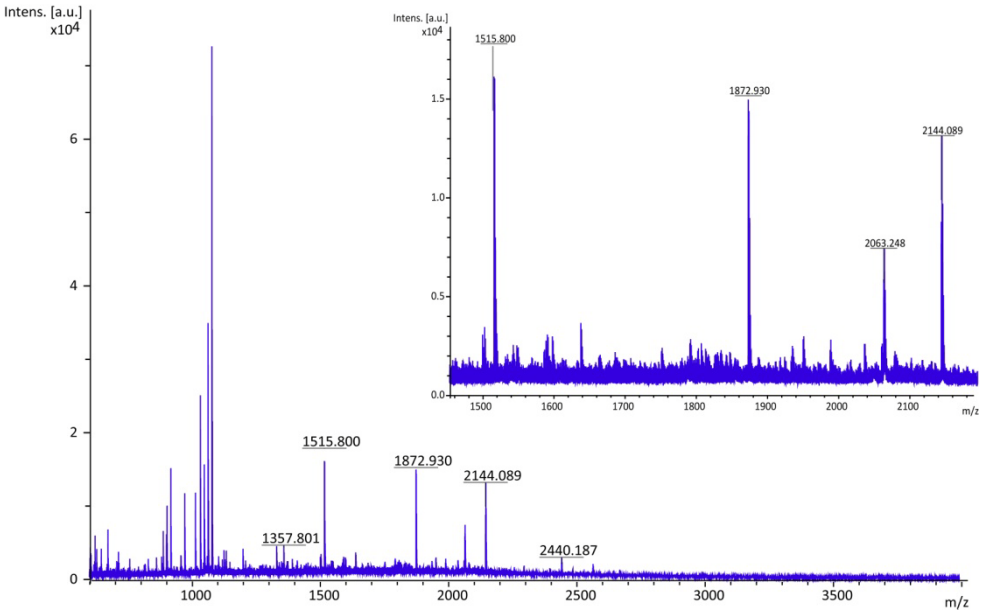


Figure 6.30 Positive ion reflector TOF - MALDI mass spectrum of 1_2_7

[MH]$^+$ 1357.801 Da	
Fragment masses	70,024; 84,055; 86,073; 110,069; 129,119; 136,099; 154,115; 175,154; 197,161; 209,146; 226,166; 308,205; 345,180; 366,163; 373,202; 473,195; 544,210; 589,265; 718,322; 742,306; 857,388; 1217,273; 1226,943; 1239,687; 1244,950; 1248,052; 1257,761; 1275,622; 1281,151; 1288,560; 1293,063; 1303,119; 1306,345; 1308,475; 1310,708; 1313,925; 1328,875; 1333,135; 1335,924
T. atroviride	**Not related**
[MH]$^+$ 1515.800 Da	
Fragment masses	70,039; 84,051; 86,073; 98,057; 102,049; 110,066; 113,076; 115,078; 120,078; 129,098; 133,082; 136,079; 138,075; 141,096; 143,089; 154,089; 157,103; 159,098; 167,101; 169,112; 172,106; 175,127; 183,124; 185,113; 188,118; 197,130; 201,116; 203,105; 205,101; 212,123; 215,125; 217,110; 219,106; 221,113; 225,120; 239,120; 275,122; 288,171; 295,148; 437,190; 508,233; 546,197; 574,206; 588,196; 623,198; 675,229; 694,236; 705,208; 841,307; 942,359; 981,171; 1015,168; 1062,410; 1079,586; 1104,287; 1152,740; 1228,491; 1270,050; 1287,942; 1302,000; 1350,339; 1388,136; 1403,938; 1407,148; 1413,589; 1421,948; 1431,667; 1445,314; 1450,633; 1464,382; 1466,622; 1468,790; 1472,068; 1483,765; 1488,090; 1490,249; 1493,465; 1496,920
T. atroviride	**Not related**
[MH]$^+$ 1872.930 Da	
Fragment masses	70,057; 84,088; 86,102; 100,110; 102,084; 110,098; 112,114; 115,116; 120,101; 129,140; 133,088; 136,116; 141,132; 143,142; 154,142; 157,157; 159,136; 167,142; 169,165; 171,157; 175,167; 181,165; 185,163; 195,166; 197,188;

	199,207; 201,186; 209,186; 212,168; 216,181; 227,211; 244,181; 262,196; 311,220; 398,247; 422,232; 535,251; 623,234; 641,267; 698,409; 754,364; 778,315; 865,412; 884,474; 964,475; 1032,569; 1061,561; 1095,616; 1158,557; 1175,609; 1304,695; 1338,754; 1418,805; 1512,483; 1661,502; 1690,235; 1759,442; 1762,709; 1764,782; 1775,495; 1793,553; 1803,075; 1810,278; 1815,447; 1826,137; 1837,054; 1848,836; 1854,375
T. atroviride	**Glycogen synthase kinase 3 K.ILVENEPNVSYICSR.Y + Phospho (significant)**
$[MH]^+$ 2063.248 Da	
Fragment masses	70,039; 84,059; 86,074; 101,059; 110,059; 112,074; 115,074; 120,075; 129,092; 136,067; 139,087; 141,074; 147,099; 154,071; 157,091; 159,079; 167,078; 169,103; 172,086; 175,105; 181,097; 183,103; 185,090; 187,082; 197,115; 200,112; 202,090; 209,093; 212,108; 214,112; 216,100; 219,110; 226,110; 229,109; 240,116; 244,113; 252,113; 258,121; 268,130; 270,127; 272,136; 296,158; 343,201; 382,159; 486,223; 614,300; 628,202; 638,338; 729,295; 766,433; 901,388; 1081,479; 1113,457; 1227,461; 1284,496; 1604,406; 1666,160; 1704,362; 1859,626; 1945,079; 1954,527; 1956,656; 1959,933; 1964,241; 2035,401; 2039,113; 2042,568; 2045,541
T. atroviride	**Not related**
$[MH]^+$ 2144.089 Da	
Fragment masses	70,047; 84,077; 102,056; 110,075; 112,091; 115,092; 120,090; 129,108; 136,084; 139,119; 141,095; 147,113; 157,105; 159,106; 165,109; 167,110; 169,134; 175,132; 181,117; 183,142; 185,118; 187,105; 197,139; 209,125; 212,139; 219,119; 226,142; 230,139; 240,148; 258,130; 266,158; 296,177; 325,199; 343,216; 379,206; 382,159; 424,259; 442,262; 638,380; 739,359; 766,485; 786,279; 895,508; 914,359; 1024,558; 1038,418; 1081,608; 1110,499; 1152,492; 1196,622; 1209,543; 1238,611; 1265,618; 1363,667; 1375,707; 1380,686; 1505,801; 1551,866; 1604,740; 1703,960; 1713,129; 1736,452; 1802,010; 1882,836; 1927,304; 1998,479; 2028,556; 2031,400; 2035,530; 2038,947; 2046,502; 2064,523; 2081,153; 2100,453; 2116,252; 2120,714; 2125,667
T. atroviride	**Elicitor protein R.FAYLGNDSDGEEKPVVPVK.T + Phospho (significant)**
$[MH]^+$ 2440.187 Da	
Fragment masses	70,016; 74,011; 84,052; 86,070; 101,059; 110,049; 113,061; 115,075; 129,083; 136,061; 138,058; 141,077; 155,072; 158,075; 167,068; 169,074; 175,095; 226,103; 232,110; 531,177; 657,170; 718,232; 832,270; 995,323; 1124,392; 1196,386; 1252,483; 1357,568; 1525,536; 2127,324; 2318,357; 2324,035; 2329,781; 2331,703; 2335,080; 2339,406; 2343,575; 2355,754; 2396,544; 2414,113; 2417,293
T. atroviride	**Glutamate ammonia ligase K.ALEPHHTECIKEYGEDNELR.L (NOT significant)**

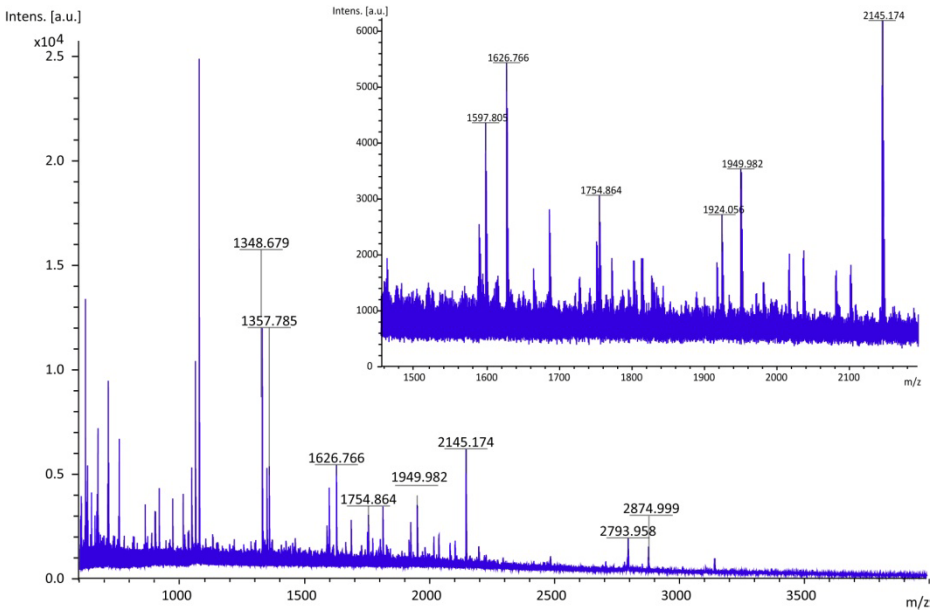


Figure 6.31 Positive ion reflector TOF - MALDI mass spectrum of 1_2_8

$[MH]^+$ 1348.679 Da	
Fragment masses	70,037; 72,037; 84,051; 86,080; 95,075; 98,064; 101,073; 110,069; 112,097; 115,094; 120,105; 129,115; 132,106; 136,095; 138,097; 141,112; 143,116; 146,100; 154,117; 157,133; 159,119; 169,136; 171,134; 175,143; 181,143; 183,142; 185,139; 195,130; 197,156; 201,146; 203,144; 209,139; 212,164; 214,145; 216,158; 218,170; 226,156; 230,152; 233,171; 235,141; 237,162; 239,164; 242,173; 244,153; 249,158; 251,162; 253,167; 255,172; 257,185; 260,183; 266,174; 268,187; 271,184; 273,172
T. atroviride	**Not related**
$[MH]^+$ 1357.785 Da	
Fragment masses	70,021; 72,050; 84,052; 86,067; 98,047; 100,072; 102,058; 110,061; 113,083; 115,081; 120,091; 125,094; 129,109; 132,094; 136,082; 139,100; 141,106; 143,102; 146,101; 154,105; 157,113; 159,093; 162,108; 164,108; 167,111; 169,125; 171,122; 175,136; 181,122; 185,133; 187,124; 189,116; 191,113; 195,114; 197,139; 201,135; 203,126; 209,131; 212,141; 214,160; 216,143; 218,153; 221,128; 226,146; 230,136; 235,145; 237,152; 239,149; 242,157; 244,145; 246,156; 249,148; 252,147; 254,147; 257,186; 260,177; 262,161; 266,160; 269,158; 271,163; 274,156; 276,157; 278,163; 280,163; 283,161; 286,161; 288,173; 290,170; 292,155; 295,154; 298,161; 301,156; 303,161; 305,154; 308,178; 311,167; 314,176; 317,156; 320,167; 322,175; 327,156; 329,173; 331,158; 340,172; 342,174; 345,157; 348,154; 354,165; 356,165; 362,174; 368,175; 370,159; 381,159; 473,171; 544,185; 676,259; 857,364; 1151,379; 1153,430; 1155,532; 1157,657; 1159,751; 1161,736; 1163,912; 1168,060; 1217,272; 1226,969; 1245,015; 1281,103; 1287,348; 1290,433; 1293,795; 1304,150; 1307,393; 1310,664; 1313,029; 1315,088; 1329,090; 1331,316; 1334,573
T. atroviride	**Not related**
$[MH]^+$ 1597.805 Da	
Fragment masses	110,067; 129,105; 175,121; 197,131; 287,148; 342,148; 415,198; 529,261; 612,223; 754,354; 840,307; 900,440; 977,326; 1032,413; 1078,540; 1112,447; 1155,513; 1347,546; 1440,413; 1457,450; 1460,983; 1532,688; 1536,031; 1540,163; 1545,383; 1548,559; 1552,921; 1555,231; 1557,342; 1567,988; 1571,223; 1574,436; 1577,542
T. atroviride	**Not related**
$[MH]^+$ 1626.766 Da	
Fragment masses	110,070; 129,105; 175,125; 197,131; 209,108; 253,103; 341,144; 343,152; 474,225; 569,233; 594,271; 611,310; 709,319; 726,346; 1040,541; 1268,710; 1280,366; 1452,835; 1549,118; 1558,690; 1562,911; 1566,123; 1575,431;

	1578,734; 1581,961; 1585,314; 1596,926; 1600,113; 1602,969; 1607,009
T. atroviride	**Transaldolase like protein K.EGGDIDSQVDHALDR.L (NOT significant)**
$[MH]^+$ 1754.864 Da	
Fragment masses	70,056; 84,083; 86,094; 98,065; 101,092; 110,079; 113,093; 115,097; 120,075; 129,116; 136,084; 139,101; 141,108; 143,103; 146,102; 150,104; 152,113; 155,116; 157,117; 167,121; 169,127; 175,133; 181,123; 185,138; 195,120; 197,145; 201,135; 209,118; 212,150; 214,144; 216,132; 218,140; 221,133; 226,140; 229,146; 243,156; 257,185; 266,168; 611,291; 726,315; 844,396; 981,445; 1040,526; 1268,734; 1497,869; 1581,091; 1636,002; 1678,310; 1683,571; 1690,027; 1693,258; 1698,385; 1701,497; 1704,663; 1706,840; 1710,061; 1725,567; 1727,821; 1732,640
T. atroviride	**Transaldolase like protein K.KEGGDIDSQVDHALDR.L (NOT significant)**
$[MH]^+$ 1924.056 Da	
Fragment masses	70,053; 84,086; 86,101; 101,093; 110,097; 113,105; 115,113; 129,137; 136,107; 139,128; 141,133; 155,138; 157,151; 167,143; 172,172; 175,164; 183,180; 186,158; 195,157; 197,182; 209,183; 368,280; 385,292; 415,238; 513,330; 570,416; 639,452; 668,454; 685,463; 996,663; 1111,706; 1295,939; 1363,767; 1416,807; 1752,532; 1804,217; 1851,638; 1863,408; 1869,561; 1873,825; 1877,046; 1880,286
T. atroviride	**Not related**
$[MH]^+$ 1949.982 Da	
Fragment masses	70,039; 84,059; 86,074; 101,063; 110,058; 112,074; 115,071; 129,090; 136,074; 155,072; 159,078; 167,094; 172,086; 175,099; 183,112; 195,066; 197,100; 202,089; 212,100; 226,114; 242,116; 259,098; 313,112; 368,172; 529,124; 570,346; 685,288; 996,324; 1295,125; 1440,714; 1634,837; 1882,993; 1899,592; 1902,847; 1922,785; 1926,319
T. atroviride	**Not related**
$[MH]^+$ 2154.174 Da	
Fragment masses	70,055; 84,088; 86,100; 101,074; 110,086; 113,102; 115,098; 129,121; 136,089; 141,110; 155,121; 157,121; 172,134; 175,134; 186,133; 195,112; 197,142; 209,121; 212,141; 217,141; 225,138; 242,149; 257,190; 266,161; 408,162; 558,276; 629,307; 835,375; 879,540; 895,445; 963,510; 982,480; 1035,611; 1052,610; 1081,629; 1110,556; 1147,648; 1163,709; 1238,670; 1250,767; 1360,893; 1375,751; 1387,842; 1446,850; 1490,803; 1517,015; 1618,142; 1646,069; 1674,086; 1733,229; 1806,202; 1870,309; 1933,081; 1998,548; 2046,457; 2081,316; 2090,342; 2093,705; 2097,119; 2100,164; 2115,785
T. atroviride	**Not related**
$[MH]^+$ 2793.958 Da	
Fragment masses	110,023; 112,059; 129,066; 169,077; 171,086; 175,100; 195,061; 201,070; 212,100; 229,073; 231,077; 239,113; 241,088; 254,102; 257,127; 259,090; 272,101; 274,143; 282,086; 284,113; 301,094; 311,127; 316,070; 328,138; 345,174; 385,156; 445,117; 474,203; 545,253; 643,220; 660,280; 789,304; 900,319; 918,361; 1029,333; 1047,398; 1162,414; 1346,422; 1403,414; 1663,507; 1877,744; 1992,951; 2705,820; 2712,259; 2717,394; 2721,647; 2731,173; 2735,389; 2743,488; 2748,551; 2774,616
T. atroviride	**Not related**
$[MH]^+$ 2874.999 Da	
Fragment masses	73,952; 110,030; 112,064; 129,100; 169,089; 175,117; 195,084; 229,118; 240,114; 257,133; 259,095; 272,107; 274,149; 301,124; 316,112; 345,189; 474,210; 545,253; 555,210; 625,244; 643,255; 660,284; 789,320; 900,362; 918,404; 981,547; 1029,440; 1047,446; 1114,462; 1127,456; 1144,473; 1162,474; 1242,442; 1259,550; 1277,530; 1346,540; 1403,619; 1550,622; 1663,781; 1681,665; 1761,813; 1877,885; 1975,783; 1992,822; 2108,126; 2223,116; 2609,713; 2759,801; 2777,750; 2789,707; 2792,737; 2795,770; 2853,070
T. atroviride	**Elongation factor 1 beta (EF1B) K.APAAEDDDDVDLFGSDDEEEDAEAVR.I + Phospho (significant)**

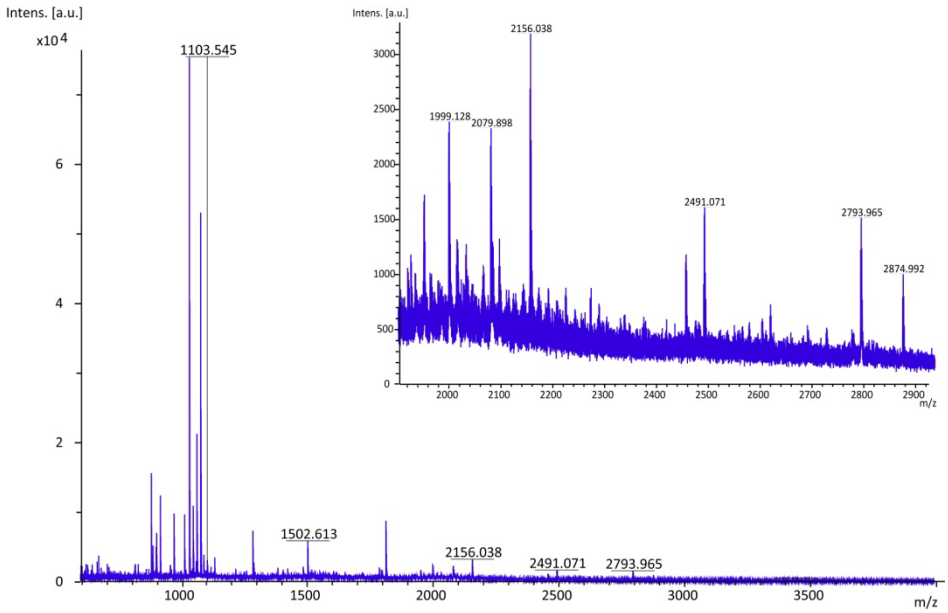


Figure 6.32 Positive ion reflector TOF - MALDI mass spectrum of 1_2_9

$[MH]^+$ 1103.545 Da	
Fragment masses	58,036; 70,069; 72,088; 84,098; 86,116; 89,095; 100,102; 102,085; 110,114; 112,135; 115,129; 129,156; 133,139; 136,126; 141,152; 143,167; 147,124; 154,144; 156,151; 158,151; 167,155; 171,159; 175,177; 181,160; 183,182; 185,174; 187,159; 195,162; 197,181; 199,181; 201,162; 203,171; 205,172; 209,177; 211,184; 213,169; 216,171; 226,191; 232,198; 235,168; 243,188; 245,186; 247,194; 249,196; 253,181; 258,186; 262,190; 268,211; 284,185; 294,184; 311,183; 321,209; 339,208; 508,325; 549,161; 596,347; 666,087; 719,987; 731,210; 741,407; 759,246; 892,615; 909,002; 935,199; 941,177; 949,167; 983,316; 990,120; 999,285; 1015,088; 1018,320; 1031,216; 1039,115; 1041,818; 1056,849; 1059,916; 1063,247; 1069,812; 1074,641; 1076,680; 1079,517
T. atroviride	**Nuclear pore complex protein R.KMVSKGTTR.D + Phospho (NOT significant)**
$[MH]^+$ 1502.613 Da	
Fragment masses	70,048; 84,069; 86,085; 89,054; 110,078; 112,094; 115,088; 129,119; 133,094; 136,096; 141,101; 155,108; 158,112; 167,109; 172,125; 175,141; 181,117; 183,146; 187,102; 195,112; 197,137; 203,115; 211,141; 215,138; 221,127; 227,141; 232,160; 237,124; 242,157; 247,126; 249,139; 253,132; 257,140; 259,125; 272,153; 277,154; 279,130; 284,124; 286,156; 288,165; 290,149; 294,150; 301,163; 310,143; 345,217; 355,184; 369,166; 397,163; 411,155; 508,256; 522,243; 525,172; 588,225; 606,223; 623,249; 688,211; 942,191; 1015,296; 1032,438; 1040,222; 1152,314; 1284,710; 1288,621; 1302,671; 1361,780; 1387,926; 1392,062; 1404,920; 1422,973; 1451,319; 1458,939; 1466,799; 1474,037; 1477,206; 1484,053
T. atroviride	**Ca^{2+} dependent lipid binding protein (containing C2 domain) R.QTALKMYADGGLR.A (not significant)**
$[MH]^+$ 1999.128 Da	
Fragment masses	70,037; 86,082; 102,040; 110,060; 112,071; 115,082; 129,094; 133,073; 136,066; 138,084; 143,064; 153,095; 155,077; 172,082; 175,110; 181,090; 185,089; 187,085; 193,112; 195,091; 198,094; 201,103; 211,123; 213,080; 221,115; 233,096; 250,109; 256,110; 266,157; 269,126; 278,102; 284,108; 294,154; 300,119; 302,102; 346,135; 363,162; 369,158; 391,167; 397,168; 425,117; 443,109; 473,132; 496,149; 522,240; 581,198; 599,182; 637,246; 681,201; 696,227; 765,190; 782,185; 811,223; 829,200; 882,251; 899,280; 924,269; 928,302; 960,284; 964,287; 974,287; 992,281; 995,308; 1012,322; 1022,268; 1032,355; 1040,265; 1056,280; 1089,367; 1152,325; 1235,333; 1315,371;

	1491,510; 1847,989; 1869,088; 1889,318; 1894,747; 1899,059; 1915,657; 1933,883; 1951,892; 1963,718; 1975,604
T. atroviride	**Not related**
$[MH]^+$ 2079.898 Da	
Fragment masses	70,056; 86,095; 129,112; 155,092; 175,116; 181,099; 211,148; 221,132; 284,135; 294,134; 397,127; 494,201; 522,251; 581,205; 659,292; 681,238; 696,268; 794,252; 812,276; 830,273; 882,340; 899,347; 906,371; 909,302; 924,369; 927,343; 942,376; 955,688; 960,378; 964,394; 972,649; 974,377; 977,395; 995,405; 1012,419; 1016,000; 1022,381; 1025,462; 1040,374; 1055,429; 1125,533; 1134,459; 1152,480; 1164,331; 1194,451; 1235,532; 1250,466; 1283,507; 1315,479; 1323,505; 1333,522; 1381,532; 1436,679; 1491,725; 1505,714; 1620,898; 1851,039; 1861,856; 1869,113; 1878,527; 1916,073; 1933,880; 1938,862; 1947,490; 1950,691; 1953,827; 1964,360; 1967,294; 1971,379; 1980,105; 1982,310; 2000,341
T. atroviride	**Not related**
$[MH]^+$ 2156.038 Da	
Fragment masses	70,067; 84,077; 86,100; 110,086; 112,103; 115,113; 129,124; 133,097; 153,115; 155,117; 175,155; 181,136; 197,132; 211,174; 244,178; 284,174; 301,193; 397,292; 409,173; 494,335; 516,284; 539,301; 587,332; 799,441; 811,405; 876,414; 892,359; 894,429; 910,370; 924,499; 942,494; 956,383; 960,498; 1022,472; 1040,464; 1056,475; 1077,323; 1092,508; 1104,526; 1120,479; 1125,669; 1134,580; 1152,599; 1164,711; 1232,550; 1250,562; 1283,589; 1299,641; 1337,732; 1381,550; 1387,586; 1397,591; 1438,768; 1511,684; 1569,873; 1812,257; 1981,330; 2027,421; 2028,915; 2031,341; 2035,003; 2041,796; 2044,199; 2046,498; 2049,688; 2051,894; 2062,870; 2079,633; 2096,005; 2113,469
T. atroviride	**Heme binding peroxidase R.DNDAAACTPDGRLPDASQGPK.H (NOT significant)**
$[MH]^+$ 2491.071 Da	
Fragment masses	74,047; 110,063; 112,077; 129,093; 175,114; 195,087; 212,125; 255,128; 272,144; 373,160; 381,119; 386,175; 412,190; 430,176; 456,184; 499,188; 527,226; 545,193; 584,228; 616,241; 654,146; 687,351; 715,314; 727,254; 736,272; 753,293; 766,310; 792,378; 810,314; 879,339; 907,332; 925,349; 1012,385; 1073,365; 1112,419; 1138,481; 1156,446; 1225,499; 1253,522; 1271,482; 1358,546; 1484,530; 1502,627; 1571,612; 1589,731; 1617,637; 2063,481; 2204,341; 2365,593; 2387,178; 2391,544; 2412,881; 2430,781; 2447,532; 2461,512; 2465,941
T. atroviride	**Not related**
$[MH]^+$ 2793.965 Da	
Fragment masses	112,058; 129,072; 158,068; 169,084; 175,102; 185,082; 187,064; 201,069; 222,100; 227,072; 229,101; 240,116; 257,134; 272,109; 274,154; 298,092; 300,112; 311,137; 316,095; 328,151; 330,104; 345,178; 369,123; 374,075; 387,124; 440,150; 445,114; 461,124; 474,208; 484,177; 486,120; 504,153; 545,262; 555,195; 560,142; 615,177; 625,217; 643,232; 660,281; 714,213; 789,326; 829,238; 900,291; 918,392; 1012,431; 1029,340; 1043,335; 1047,437; 1114,432; 1127,400; 1145,399; 1162,432; 1196,534; 1260,437; 1277,447; 1346,415; 1403,515; 1550,325; 1663,554; 1877,507; 1992,452; 2108,381; 2222,725; 2681,116; 2758,010; 2766,753; 2769,801; 2775,184
T. atroviride	**Not related**
$[MH]^+$ 2874.992 Da	
Fragment masses	112,105; 169,108; 175,124; 240,134; 257,176; 272,132; 274,168; 311,164; 328,185; 345,212; 369,151; 387,161; 440,175; 445,134; 457,219; 474,234; 484,209; 527,276; 545,273; 555,252; 625,266; 643,271; 660,297; 670,321; 771,384; 789,370; 799,343; 829,314; 900,354; 918,429; 928,383; 1029,497; 1043,425; 1047,490; 1057,464; 1114,474; 1127,495; 1144,496; 1162,532; 1242,528; 1260,570; 1277,563; 1346,629; 1403,636; 1550,704; 1663,839; 1675,370; 1681,794; 1761,784; 1877,933; 1975,658; 1992,934; 2108,033; 2178,295; 2206,018; 2223,200; 2321,266; 2609,661; 2622,474; 2707,433; 2741,731; 2746,271; 2749,8862759,896 2777,945 2795,041 2798,063
T. atroviride	**Elongation factor 1 beta (EF1B) K.APAAEDDDDVDLFGSDDEEEDAEAVR.I + Phospho (significant)**

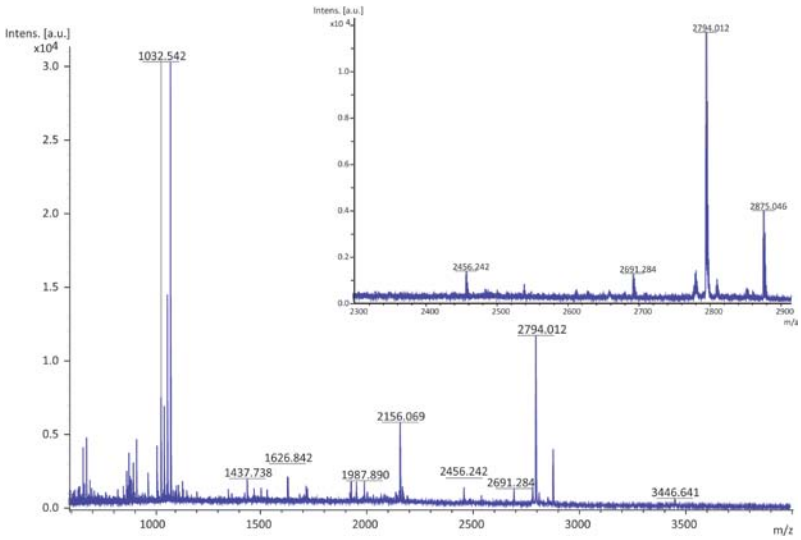


Figure 6.33 Positive ion reflector TOF - MALDI mass spectrum of 1_2_10

$[MH]^+$ 1032.542 Da	
Fragment masses	58,040; 70,071; 72,073; 86,107; 100,100; 102,091; 110,097; 112,115; 115,118; 120,094; 125,120; 129,133; 136,104; 139,103; 141,116; 143,149; 147,105; 154,115; 158,117; 167,119; 172,120; 175,145; 181,123; 185,129; 188,130; 195,121; 197,141; 199,130; 201,124; 205,128; 207,108; 209,131; 215,140; 226,143; 228,136; 232,163; 235,127; 242,145; 244,147; 249,165; 253,130; 257,155; 259,142; 270,158; 272,156; 279,141; 284,145; 288,185; 294,131; 296,155; 311,123; 345,232; 382,203; 410,193; 416,190; 473,198; 508,322; 525,250; 585,157; 606,339; 623,330; 651,107; 660,336; 681,756; 688,337; 698,003; 731,145; 743,408; 801,431; 817,557; 833,769; 839,003; 841,101; 843,210; 918,849; 924,276; 935,550; 960,928; 985,308; 988,754; 992,058; 997,564
T. atroviride	FAD/FMN containing dehydrogenases R.NTGHDYLGR.S (NOT significant)
$[MH]^+$ 1437.738 Da	
Fragment masses	70,081; 72,084; 84,078; 86,087; 110,096; 112,119; 115,115; 120,107; 126,101; 129,144; 136,123; 139,127; 141,143; 143,141; 154,136; 159,154; 167,145; 169,159; 171,170; 175,175; 185,184; 187,146; 195,167; 197,188; 201,162; 215,188; 218,166; 221,169; 225,180; 227,200; 229,185; 232,195; 235,196; 237,199; 240,212; 244,204; 252,210; 254,187; 257,226; 259,175; 266,208; 268,214; 274,239; 278,230; 286,231; 288,237; 296,230; 298,218; 300,233; 312,219; 314,230; 316,194; 330,204; 345,266; 365,261; 369,257; 373,241; 508,331; 545,316; 772,360; 866,532; 995,549; 1032,626; 1242,037; 1245,144; 1371,684; 1389,881; 1395,095; 1403,384; 1415,957
T. atroviride	**Not related**
$[MH]^+$ 1626.842 Da	
Fragment masses	70,058; 84,050; 86,076; 110,065; 112,083; 115,088; 120,078; 129,103; 136,087; 141,107; 143,100; 154,079; 159,092; 167,093; 169,096; 171,105; 175,116; 181,105; 185,110; 187,091; 195,100; 197,123; 200,110; 209,106; 216,109; 226,129; 229,112; 232,118; 235,113; 244,127; 253,113; 257,146; 259,109; 266,133; 271,149; 273,129; 288,160; 294,161; 298,128; 324,137; 327,130; 344,122; 359,121; 383,179; 400,183; 435,207; 474,212; 564,256; 611,293; 664,291; 778,378; 1032,390; 1040,519; 1268,626; 1514,161; 1521,423; 1530,014; 1553,154; 1559,636; 1574,228; 1579,689; 1582,905; 1604,017
T. atroviride	**Transaldolase like protein K.EGGDIDSQVDHALDR.L (NOT significant)**
$[MH]^+$ 1987.890 Da	
Fragment masses	70,055; 84,069; 86,084; 101,066; 110,066; 112,090; 115,084; 120,075; 129,107; 136,081; 154,080; 158,102; 167,088; 169,115; 171,077; 175,115; 183,099; 185,123; 187,071; 195,097; 197,095; 199,098; 201,108; 212,097; 227,099; 232,092; 240,112; 244,108; 259,063; 272,134; 282,117; 288,183; 329,173; 345,157; 388,079; 545,231; 586,268; 645,190; 712,221; 774,228; 903,282;

	1018,276; 1147,332; 1225,576; 1267,522; 1276,389; 1333,416; 1452,583; 1480,603; 1537,681; 1594,788; 1707,875; 1855,029; 1873,479; 1877,348; 1880,355; 1882,692; 1886,830; 1890,226; 1900,656; 1908,299; 1939,888
T. atroviride	**60s Acidic ribosomal protein K.KEEEEEEDEEGFGGLFD.- (significant)**
$[MH]^+$ 2156.069 Da	
Fragment masses	70,071; 84,065; 86,098; 110,086; 112,103; 115,111; 129,119; 136,104; 155,114; 158,105; 175,145; 185,114; 197,150; 214,151; 244,182; 272,175; 284,161; 287,154; 301,174; 345,163; 371,188; 384,177; 409,202; 412,247; 416,169; 426,203; 429,247; 487,190; 494,275; 499,258; 516,278; 522,280; 539,325; 558,250; 587,351; 605,354; 644,298; 687,448; 701,355; 799,447; 814,472; 892,517; 912,505; 924,499; 942,459; 997,587; 1012,586; 1022,540; 1040,453; 1077,330; 1108,653; 1120,485; 1125,689; 1152,630; 1171,613; 1223,676; 1244,622; 1250,591; 1320,747; 1329,667; 1337,770; 1438,801; 1569,906; 1812,279; 2027,449; 2029,763; 2041,509; 2045,635; 2049,704; 2055,250; 2058,432; 2062,981; 2096,405; 2112,379; 2125,294
T. atroviride	**Heme binding peroxidase R.DNDAAACTPDGRLPDASQGPK.H (significant)**
$[MH]^+$ 2456.242 Da	
Fragment masses	74,043; 110,067; 112,074; 129,098; 175,116; 197,102; 232,132; 345,208; 414,170; 430,201; 442,224; 523,285; 545,252; 558,165; 687,259; 794,257; 855,392; 954,476; 1018,370; 1070,460; 1141,396; 1285,638; 1511,713; 1582,581; 1711,659; 1738,822; 1886,033; 2015,114; 2143,734; 2265,269; 2337,000; 2340,472; 2346,361; 2353,077; 2358,571; 2435,549
T. atroviride	**Ran-binding domain containing domain R.DAKGDEEEAPESEDVHFEPVVK.L (NOT significant)**
$[MH]^+$ 2691.284 Da	
Fragment masses	74,019; 84,050; 110,079; 112,088; 129,116; 158,113; 169,122; 175,141; 226,180; 240,180; 254,177; 257,193; 274,212; 298,177; 316,155; 328,186; 342,218; 345,242; 369,184; 427,198; 474,225; 484,254; 545,326; 556,244; 642,315; 644,322; 652,305; 660,366; 687,346; 715,326; 781,388; 789,363; 843,444; 918,406; 1011,517; 1047,534; 1068,539; 1140,537; 1162,556; 1207,643; 1269,675; 1293,719; 1398,711; 1512,769; 1551,895; 1623,896; 1849,036; 1921,117; 2050,288; 2218,404; 2575,363; 2579,353; 2591,385; 2592,763; 2594,821; 2609,061
T. atroviride	**14-3-3 like protein K.KEEGEAAKPAEEEPKPAEEPAPEAAS.- (significant)**
$[MH]^+$ 2794.012 Da	
Fragment masses	69,986; 72,032; 86,054; 102,022; 112,054; 115,067; 120,061; 129,080; 133,076; 141,077; 158,072; 169,074; 171,092; 175,100; 185,059; 187,058; 195,084; 201,067; 205,085; 215,095; 222,095; 229,093; 231,045; 240,106; 245,047; 257,131; 272,093; 274,151; 283,127; 298,079; 300,083; 303,157; 311,128; 316,079; 328,153; 345,181; 357,083; 360,066; 369,137; 374,084; 387,108; 399,124; 407,108; 417,121; 427,103; 429,106; 440,158; 445,108; 457,152; 461,082; 468,120; 474,215; 484,161; 486,122; 504,110; 514,132; 516,144; 542,132; 545,259; 555,199; 558,150; 560,140; 572,130; 574,152; 587,133; 590,128; 597,148; 599,176; 615,167; 618,167; 625,223; 633,150; 643,228; 660,273; 670,232; 675,168; 687,201; 689,161; 714,195; 732,207; 744,194; 762,206; 771,289; 785,218; 789,304; 799,285; 804,216; 811,244; 829,231; 841,221; 859,214; 875,239; 882,247; 900,282; 918,345; 928,284; 1006,252; 1025,292; 1029,363; 1043,310; 1047,387; 1057,276; 1059,215; 1096,303; 1114,343; 1127,366; 1145,402; 1162,407; 1242,375; 1260,416; 1277,404; 1346,446; 1403,447; 1550,467; 1645,513; 1663,495; 1681,660; 1761,484; 1778,569; 1877,500; 1895,849; 1975,503; 1988,083; 1992,463; 2079,540; 2090,413; 2107,483; 2175,873; 2222,484; 2275,331; 2608,801; 2683,415; 2687,811; 2704,205; 2731,610; 2740,194; 2746,646; 2748,355; 2757,910; 2774,884
T. atroviride	**Not related**
$[MH]^+$ 2875.046 Da	
Fragment masses	70,016; 71,997; 74,003; 102,023; 112,078; 129,110; 141,100; 158,094; 169,100; 175,126; 195,110; 201,096; 215,125; 222,122; 229,117; 231,080; 240,135; 245,075; 257,165; 274,175; 284,162; 300,130; 311,157; 316,104; 328,191; 345,203; 355,177; 357,092; 369,170; 374,110; 387,142; 399,174; 412,189; 427,126; 429,155; 440,195; 445,150; 456,226; 461,115; 474,238; 484,201; 499,237; 503,168; 510,230; 527,256;

	545,275; 555,255; 558,182; 560,171; 572,184; 574,191; 581,236; 590,171; 599,231; 615,201; 618,239; 625,263; 633,219; 643,268; 660,300; 670,286; 675,187; 689,233; 714,250; 732,262; 744,256; 762,262; 771,352; 785,298; 789,356; 799,345; 804,264; 829,293; 859,268; 875,321; 882,332; 900,370; 918,420; 928,393; 972,420; 988,397; 999,425; 1006,361; 1029,474; 1043,425; 1047,486; 1057,463; 1096,442; 1114,460; 1127,483; 1144,520; 1162,523; 1172,500; 1227,501; 1242,517; 1259,567; 1277,560; 1287,514; 1328,585; 1346,599; 1359,657; 1385,614; 1403,621; 1416,431; 1421,628; 1426,588; 1444,536; 1501,558; 1550,715; 1562,742; 1568,688; 1647,680; 1663,799; 1675,333; 1681,797; 1743,720; 1761,773; 1778,882; 1839,336; 1859,835; 1877,929; 1888,560; 1895,911; 1975,836; 1989,852; 1992,891; 2003,302; 2010,966; 2081,768; 2090,941; 2107,705; 2117,881; 2126,121; 2178,166; 2206,014; 2223,198; 2232,630; 2241,191; 2277,843; 2321,188; 2338,286; 2379,262; 2538,694; 2557,747 2609,679; 2617,823; 2623,698; 2628,341; 2707,559; 2741,864; 2749,175 2759,854; 2763,080; 2777,918; 2795,940; 2855,900
T. atroviride	**Elongation factor 1 beta (EF1B) K.APAAEDDDDVDLFGSDDEEEDAEAVR.I + Phospho (significant)**
$[MH]^+$ 3446.641 Da	
Fragment masses	110,036; 175,157; 244,146; 253,156; 272,190; 284,160; 289,203; 324,156; 342,183; 381,159; 397,176; 411,181; 418,194; 443,194; 496,187; 512,231; 515,202; 532,219; 569,189; 627,255; 629,235; 646,251; 717,296; 797,327; 807,349; 814,340; 831,330; 928,390; 938,399; 945,414; 958,423; 985,410; 988,324; 1002,451; 1005,460; 1028,459; 1071,504; 1082,434; 1099,506; 1117,514; 1144,578; 1174,540; 1273,614; 1360,666; 1497,747; 1550,750; 1553,890; 1568,809; 1648,883; 1665,789; 1683,831; 1894,154; 1911,969; 2447,264; 2494,406; 2511,467; 2892,961; 3332,244; 3350,134; 3387,246; 3420,496
T. atroviride	**Not related**

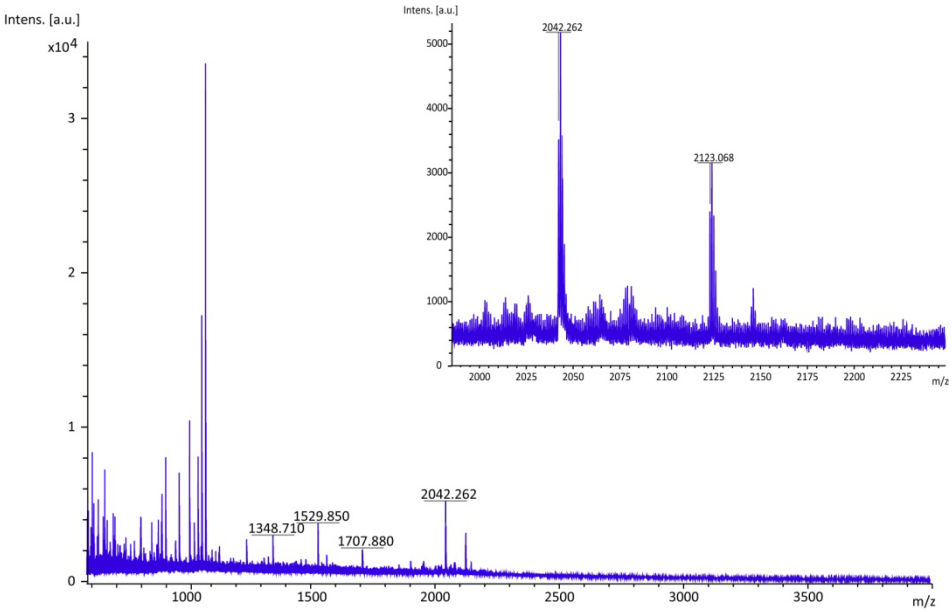


Figure 6.34 Positive ion reflector TOF - MALDI mass spectrum of 1_2_11

$[MH]^+$ 1348.710 Da	
Fragment masses	57,987; 70,024; 72,045; 84,057; 86,062; 98,054; 101,074; 110,070; 112,087; 115,087; 129,113; 136,092; 143,119; 146,096; 151,095; 154,113; 157,115; 159,115; 165,095; 167,116; 169,125; 171,133; 175,140; 183,140; 186,140; 188,142; 190,146; 192,145; 197,154; 201,141; 203,138; 207,126; 209,140; 211,157; 213,150; 216,154; 218,175; 221,141; 226,149; 230,156; 232,160; 235,150; 237,162; 239,163; 244,146; 248,168; 251,162; 254,169; 257,192; 259,154; 261,154; 264,160; 266,165; 268,168; 270,167; 272,178; 274,170;

	276,168; 278,168; 280,158; 282,170; 284,174; 286,181; 288,194; 290,179; 292,181; 294,151; 296,168; 298,169; 301,172; 303,183; 306,161; 308,160; 310,173; 312,159; 314,180; 317,174; 327,162; 329,172; 331,194; 333,194; 338,176; 340,175; 342,171; 345,169; 356,185; 358,178; 360,179; 362,172; 455,183; 473,179; 475,159; 503,236; 544,209; 574,205; 645,224 676,294; 744,248; 758,192; 845,306; 916,388; 962,675; 1144,438; 1147,541; 1150,671; 1153,844; 1157,013; 1160,153; 1217,944; 1281,738; 1297,302; 1300,272; 1317,785; 1320,997; 1324,266; 1328,736; 1330,636
T. atroviride	**Not related**
$[MH]^+$ 1529.850 Da	
Fragment masses	70,065; 84,071; 86,083; 110,067; 112,086; 115,085; 120,074; 129,110; 136,082; 141,094; 143,100; 146,083; 154,089; 158,105; 167,097; 169,118; 171,118; 175,129; 181,111; 183,123; 185,120; 187,106; 190,118; 195,096; 197,133; 199,116; 201,111; 205,106; 207,102; 209,127; 212,131; 214,127; 218,143; 221,110; 223,117; 227,131; 229,127; 232,138; 235,113; 237,128; 240,136; 242,159; 244,128; 246,151; 248,132; 252,133; 254,147; 258,133; 260,143; 262,146; 266,136; 268,150; 270,145; 273,138; 275,133; 277,128; 283,139; 286,145; 288,148; 292,142; 301,136; 304,144; 310,133; 312,143; 314,153; 316,156; 327,133; 333,160; 343,168; 345,152; 353,152; 355,151; 371,166; 381,157; 399,167; 461,193; 512,213; 574,205; 590,224; 645,213; 699,258; 831,381; 960,406; 1032,307; 1333,681; 1415,112; 1459,362; 1476,220; 1479,543; 1485,006; 1500,992; 1504,137; 1506,428; 1510,406
T. atroviride	**Cyclophilin K.DGKPTAEIKEQTGR.I (significant)**
$[MH]^+$ 1707.880 Da	
Fragment masses	70,076; 86,096; 101,084; 110,063; 112,085; 115,074; 129,099; 136,071; 147,074; 154,095; 157,099; 159,091; 167,096; 171,106; 175,121; 181,107; 186,115; 192,104; 195,099; 197,123; 200,108; 212,115; 218,128; 226,121; 240,131; 242,160; 244,118; 266,136; 327,121; 345,125; 544,193; 598,286; 667,324; 719,284; 1304,497; 1322,781; 1494,790; 1559,034; 1577,096; 1593,287; 1611,263; 1629,196; 1655,400; 1658,694; 1661,752; 1687,032; 1690,066
T. atroviride	**Not related**
$[MH]^+$ 2042.262 Da	
Fragment masses	70,050; 84,065; 86,077; 110,075; 112,092; 115,086; 129,109; 155,107; 175,120; 181,107; 195,109; 197,131; 201,095; 218,123; 226,143; 244,177; 272,151; 284,147; 316,155; 341,155; 357,254; 415,209; 456,305; 470,195; 571,326; 583,280; 601,268; 632,338; 672,398; 712,305; 730,304; 771,455; 825,364; 875,427; 942,412; 954,353; 957,468; 964,393; 992,391; 1072,504; 1118,413; 1137,391; 1155,359; 1200,494; 1236,460; 1418,418; 1689,108; 1916,555; 1934,566; 1951,560; 1954,876; 1967,432; 1996,129; 2000,463; 2011,947; 2018,140; 2023,489
T. atroviride	**Not related**
$[MH]^+$ 2123.068 Da	
Fragment masses	74,195; 84,062; 86,073; 110,060; 112,065; 129,086; 175,110; 195,081; 226,102; 244,125; 316,086; 341,016; 357,191; 415,145; 442,159; 456,196; 470,103; 514,187; 529,180; 555,190; 571,240; 583,159; 601,212; 616,169; 654,240; 672,297; 681,142; 694,211; 712,216; 745,236; 771,375; 807,305; 810,199; 825,297; 844,295; 858,326; 870,454; 923,297; 936,324; 939,474; 954,323; 957,481; 1068,410; 1071,523; 1119,435; 1137,423; 1149,448; 1155,416; 1200,564; 1236,488; 1238,545; 1253,346; 1313,688; 1353,581; 1442,768; 1555,878; 1764,049; 1781,843; 1799,167; 1914,272; 1997,680; 2008,449; 2012,725; 2025,418; 2043,407
T. atroviride	**Not related**

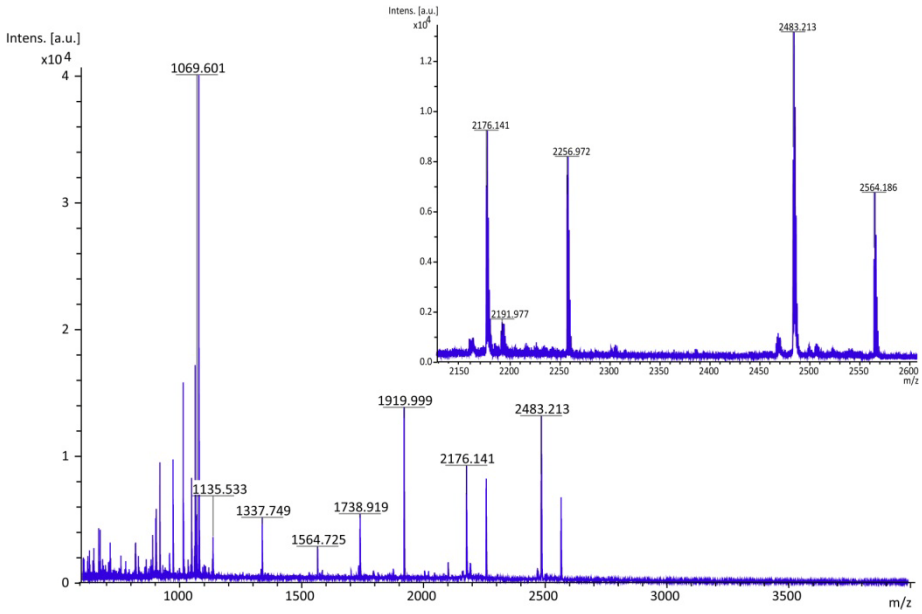


Figure 6.35 Positive ion reflector TOF - MALDI mass spectrum of 1_2_12

$[MH]^+$ 1069.601 Da	
Fragment masses	58,008; 70,038; 72,069; 84,069; 86,076; 102,073; 110,080; 113,081; 115,098; 120,090; 129,107; 131,096; 136,087; 138,091; 141,099; 143,109; 155,105; 158,105; 167,106; 172,105; 175,133; 179,106; 181,092; 184,105; 186,114; 191,096; 197,133; 200,132; 205,107; 207,095; 212,120; 214,118; 216,119; 227,119; 231,138; 234,066; 240,126; 242,145; 244,140; 247,138; 249,117; 252,148; 258,121; 266,141; 275,137; 288,163; 295,141; 311,100; 348,164; 391,149; 432,200; 487,071; 489,088; 569,132; 585,101; 593,244; 603,067; 651,044; 681,835; 687,981; 712,963; 730,971; 767,223; 870,741; 877,033; 881,112; 886,124; 895,032; 897,015; 904,138; 923,973; 934,208; 960,938; 967,645; 974,878; 976,891; 978,889; 982,053; 987,343; 996,852; 1000,132; 1003,325; 1018,092; 1023,908; 1027,054; 1040,712; 1043,234
T. atroviride	**Not related**
$[MH]^+$ 1135.533 Da	
Fragment masses	58,030; 70,075; 72,093; 84,105; 86,118; 101,123; 104,148; 110,122; 112,139; 115,143; 120,138; 123,141; 125,135; 129,159; 136,137; 138,154; 141,155; 143,150; 154,152; 158,158; 161,163; 167,157; 169,161; 175,189; 181,169; 183,181; 185,175; 187,148; 192,183; 197,205; 202,179; 205,182; 213,191; 216,185; 223,191; 227,194; 229,213; 231,195; 234,158; 240,203; 242,196; 244,218; 252,212; 254,213; 258,212; 260,213; 266,221; 269,217; 274,203; 285,222; 287,229; 302,206; 304,247; 311,223; 314,253; 316,227; 327,227; 339,231; 359,237; 398,289; 432,313; 488,296; 502,336; 519,377; 575,367; 617,381; 648,467; 759,276; 834,630; 930,700; 941,040; 943,259; 947,380; 1015,305; 1017,588; 1020,980; 1024,251; 1039,542; 1044,232; 1069,551; 1079,723; 1083,152; 1086,481; 1092,013; 1095,216; 1097,513; 1114,774
T. atroviride	**40S ribosomal protein S12 K.DWGEESQER.S (NOT significant)**
$[MH]^+$ 1337.749 Da	
Fragment masses	70,052; 72,051; 84,085; 86,093; 110,088; 112,104; 115,112; 129,133; 135,128; 138,099; 141,131; 143,147; 148,113; 154,128; 157,146; 167,129; 169,143; 172,154; 175,163; 179,143; 181,151; 185,162; 187,154; 192,156; 197,176; 200,174; 202,163; 212,169; 214,171; 217,155; 223,205; 227,166; 229,168; 235,178; 240,188; 244,184; 251,206; 254,198; 257,213; 266,183; 271,210; 275,184; 280,179; 288,227; 292,183; 296,197; 304,192; 313,239; 315,186; 326,185; 330,237; 351,218; 356,208; 361,235; 364,252; 373,201; 379,245; 471,257; 484,260; 488,277; 501,266; 587,344; 636,303; 685,335; 702,358; 751,436; 822,485; 850,537; 959,604; 982,450; 1135,649; 1176,562; 1202,398;

	1211,279; 1271,629; 1273,809; 1286,347; 1289,521; 1291,737; 1294,015; 1296,258; 1298,581; 1314,225; 1318,706
T. atroviride	**Not related**
$[MH]^+$ 1564.725 Da	
Fragment masses	70,063; 72,088; 84,068; 86,076; 110,077; 112,099; 115,096; 129,115; 136,093; 147,110; 154,102; 159,112; 167,099; 172,131; 175,134; 187,116; 192,125; 197,148; 212,141; 217,113; 221,113; 229,135; 231,129; 235,129; 240,134; 244,150; 262,158; 270,168; 272,160; 275,145; 288,185; 298,151; 304,157; 316,161; 326,161; 333,171; 369,175; 371,170; 385,171; 403,162; 448,182; 470,213; 573,321; 668,320; 683,268; 726,260; 783,293; 817,370; 884,372; 1383,442; 1401,514; 1450,001; 1498,705; 1515,596; 1518,920; 1521,022; 1539,250; 1544,807
T. atroviride	**Not related**
$[MH]^+$ 1738.919 Da	
Fragment masses	70,056; 84,069; 86,096; 101,067; 110,077; 115,089; 129,109; 136,079; 138,078; 141,101; 147,105; 154,099; 157,119; 167,115; 172,104; 175,129; 186,103; 197,138; 200,120; 202,127; 209,136; 216,122; 218,130; 227,128; 229,101; 237,130; 244,153; 257,173; 259,125; 275,153; 285,132; 288,151; 294,126; 303,178; 315,156; 357,182; 389,173; 400,181; 409,166; 457,202; 494,245; 517,239; 522,235; 570,253; 579,258; 588,261; 611,264; 693,306; 703,286; 778,380; 797,311; 804,344; 806,360; 819,385; 915,387; 925,364; 933,387; 935,410; 1036,491; 1046,496; 1088,385; 1122,514; 1151,549; 1160,512; 1187,419; 1217,592; 1222,569; 1330,730; 1350,718; 1407,814; 1502,938; 1522,987; 1586,657; 1592,991; 1602,134; 1605,610; 1611,171; 1674,051; 1684,241; 1687,506; 1691,813; 1695,178; 1712,009; 1714,239; 1720,428
T. atroviride	**Copper/Zinc superoxid dismutase R.HVGDLGNEITDAQGNAK.G (significant)**
$[MH]^+$ 1919.999 Da	
Fragment masses	70,054; 84,086; 101,089; 110,097; 112,110; 115,117; 120,109; 129,130; 136,122; 141,158; 155,131; 158,134; 169,131; 172,158; 175,152; 186,150; 197,173; 226,153; 244,169; 272,298; 284,157; 297,180; 315,186; 322,195; 373,209; 431,230; 443,263; 502,272; 530,302; 547,320; 601,370; 618,378; 687,359; 765,486; 844,447; 872,486; 1031,587; 1048,645; 1095,705; 1119,669; 1176,716; 1233,794; 1548,123; 1752,004; 1805,460; 1815,952; 1858,430; 1864,503; 1868,793; 1873,078; 1876,359; 1889,593
T. atroviride	**40S ribosomal protein S10 R.DAGEGKEGGAPGEFAPQFR.G (significant)**
$[MH]^+$ 2176.141 Da	
Fragment masses	70,056; 84,087; 101,100; 110,094; 112,105; 115,107; 129,129; 136,101; 140,114; 157,149; 175,129; 186,145; 200,150; 233,186; 240,187; 244,183; 258,199; 260,161; 275,215; 278,167; 286,188; 303,199; 320,241; 338,235; 349,228; 421,284; 432,296; 449,297; 467,299; 475,329; 492,319; 547,322; 564,340; 648,398; 665,408; 676,398; 693,401; 710,437; 804,480; 821,531; 904,558; 914,511; 921,514; 932,564; 949,555; 975,570; 992,578; 1003,585; 1020,580; 1084,683; 1138,606; 1155,618; 1166,654; 1183,640; 1200,686; 1226,707; 1280,661; 1298,648; 1340,710; 1385,660; 1411,725; 1466,729; 1483,70; 61564,914; 1856,077; 2054,100; 2071,075; 2074,170; 2089,761; 2097,492; 2113,187; 2124,981; 2129,169; 2141,269; 2149,301; 2158,155
T. atroviride	**HMG box protein K.RYEDEKQAYNADQEDESS.- (significant)**
$[MH]^+$ 2191.977 Da	
Fragment masses	70,051; 84,079; 101,091; 110,093; 112,111; 115,111; 129,134; 136,109; 157,142; 172,166; 175,160; 186,151; 195,139; 201,143; 209,161; 212,171; 229,157; 240,193; 244,158; 255,164; 258,189; 260,207; 275,224; 293,173; 303,224; 320,253; 408,253; 421,314; 432,319; 449,334; 466,354; 475,337; 483,266; 492,381; 547,376; 564,404; 665,431; 676,403; 693,457; 710,465; 804,522; 821,541; 904,557; 921,566; 932,559; 975,570; 992,595; 995,599; 1003,566; 1020,590; 1084,707; 1138,671; 1155,646; 1166,624; 1183,703; 1189,703; 1200,671; 1280,638; 1298,660; 1304,730; 1385,689; 1411,794; 1466,591; 1483,633 ;1577,797; 1648,834; 1785,727; 1855,648; 1917,351; 2072,210; 2080,753; 2084,571; 2089,283; 2099,561; 2114,488; 2124,730; 2141,062;

	2144,036; 2148,504; 2158,553; 2165,711
T. atroviride	**Not related**
$[MH]^+$ 2256.972 Da	
Fragment masses	70,074; 84,096; 87,099; 101,099; 112,117; 115,114; 129,136; 136,111; 141,134; 157,139; 175,137; 186,141; 200,142; 233,158; 240,169; 245,149; 275,180; 292,192; 303,196; 320,192; 338,190; 421,252; 432,244; 449,240; 459,284; 466,257; 492,308; 547,275; 564,268; 665,331; 676,340; 693,332; 710,388; 804,453; 821,455; 904,523; 914,521; 921,552; 932,539; 949,523; 967,509; 975,591; 979,460; 992,590; 996,382; 1003,587; 1020,573; 1038,578; 1138,676; 1155,699; 1166,669; 1183,658; 1200,718; 1269,742; 1280,736; 1298,732; 1340,794; 1351,737; 1368,783; 1385,834; 1411,826; 1466,837; 1469,708; 1483,877; 1565,534; 1595,916; 1611,939; 1693,953; 1741,125; 1758,243; 1839,235; 1856,268; 1868,515; 1883,559; 1985,388; 2037,498; 2054,498; 2062,562; 2072,511; 2080,281; 2097,614; 2115,306; 2121,185; 2124,714; 2127,872; 2131,734; 2135,031; 2141,815; 2144,831; 2149,013; 2159,647; 2177,687; 2188,340
T. atroviride	**HMG box protein K.RYEDEKQAYNADQEDESS.- + Phospho (significant)**
$[MH]^+$ 2483.213 Da	
Fragment masses	110,068; 147,102; 169,084; 199,119; 227,098; 229,118; 244,166; 259,109; 280,144; 298,158; 301,115; 308,150; 315,210; 326,167; 331,136; 344,141; 358,175; 373,168; 397,248; 407,263; 412,178; 425,247; 430,220; 439,200; 455,207; 457,227; 469,191; 473,160; 487,245; 496,269; 509,205; 511,254; 526,252; 536,219; 554,297; 558,234; 568,252; 574,301; 584,252; 587,276; 625,298; 640,274; 655,295; 665,285; 673,366; 683,334; 698,278; 754,355; 764,395; 767,327; 782,380; 785,332; 795,307; 802,387; 812,318; 830,256; 838,299; 848,344; 853,412; 866,319; 883,345; 886,390; 893,361; 901,398; 911,419; 964,364; 967,406; 982,411; 1010,432; 1012,439; 1030,468; 1074,391; 1081,428; 1092,394; 1097,466; 1109,420; 1141,493; 1159,478; 1191,370; 1210,442; 1240,523; 1258,542; 1269,491; 1340,518; 1357,560; 1565,664; 1583,630; 1654,651; 1768,564; 1882,957; 2239,497; 2432,103; 2436,330; 2448,428; 2463,989
T. atroviride	**Not related**
$[MH]^+$ 2564.186 Da	
Fragment masses	70,035; 72,056; 110,055; 129,085; 147,109; 169,095; 187,115; 199,112; 201,117; 227,102; 244,165; 259,075; 280,130; 298,147; 300,122; 308,152; 310,151; 315,193; 326,159; 331,121; 340,136; 344,168; 358,144; 369,199; 373,143; 397,198; 407,188; 412,181; 425,230; 430,191; 439,206; 455,169; 458,195; 469,188; 473,152; 487,210; 496,231; 509,209; 511,232; 526,226; 536,263; 541,196; 554,253; 558,221; 568,242; 574,245; 584,200; 586,236; 610,245; 625,288; 638,266; 655,301; 658,257; 665,274; 673,309; 683,295; 698,252; 724,327; 736,314; 739,312; 754,338; 764,360; 767,291; 772,299; 782,353; 785,328; 795,268; 802,362; 812,292; 830,284; 838,324; 848,338; 853,385; 866,318; 883,334; 893,398; 901,426; 911,409; 916,353; 926,911; 964,374; 967,436; 981,316; 984,365; 992,470; 1010,486; 1013,480; 1030,492; 1063,513; 1074,420; 1079,509; 1081,511; 1092,422; 1097,518; 1109,444; 1112,468; 1123,503; 1141,536; 1159,550; 1169,546; 1191,490; 1208,508; 1210,528; 1222,562; 1240,635; 1251,585; 1258,624; 1269,591; 1290,513; 1307,551; 1322,609; 1340,641; 1357,709; 1468,796; 1486,788; 1547,789; 1565,822; 1583,857; 1636,861; 1654,909; 1704,134; 1751,018; 1756,995; 1769,002; 1847,544; 1866,029; 1883,153; 1943,615; 1994,258; 2012,220; 2056,152; 2141,405; 2240,479; 2260,253; 2355,662; 2429,153; 2432,655; 2437,893; 2440,140; 2448,993; 2452,597; 2466,775; 2484,793; 2504,482
T. atroviride	**Not related**

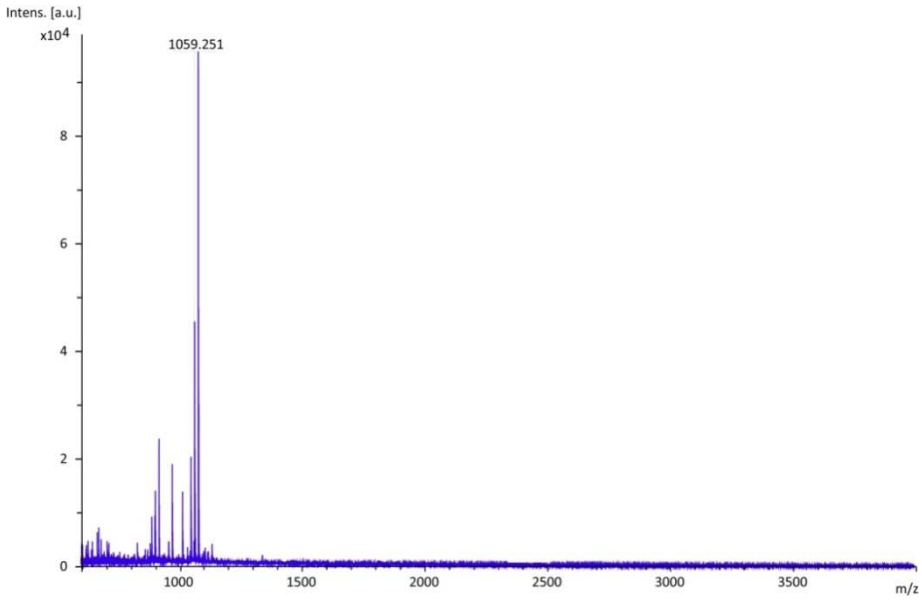


Figure 6.36 Positive ion reflector TOF - MALDI mass spectrum of 1_2_13

$[MH]^+$ 1059.251 Da	
Fragment masses	58,020; 70,055; 72,065; 84,062; 86,081; 98,060; 100,065; 102,073; 107,054; 110,068; 113,083; 123,077; 127,094; 130,098; 136,070; 138,073; 141,093; 143,110; 147,065; 154,078; 157,095; 167,077; 170,096; 172,070; 175,103; 184,120; 186,092; 188,100; 190,078; 197,108; 200,093; 207,095; 212,099; 226,121; 231,119; 247,116; 267,065; 311,085; 348,154; 379,118; 391,146; 471,106; 487,100; 489,122; 521,166; 569,184; 585,206; 603,155; 651,211; 665,156; 682,015; 691,967; 713,159; 719,831; 731,226; 766,305; 862,838; 864,914; 870,150; 881,531; 888,896; 895,505; 913,526; 924,509; 933,187; 943,407; 961,620; 975,360; 977,476; 979,580; 997,534; 1007,026; 1009,163; 1011,456; 1014,806; 1016,966; 1019,187; 1023,590; 1026,343; 1028,484; 1030,643; 1032,781; 1035,055; 1040,727
T. atroviride	**Not related**

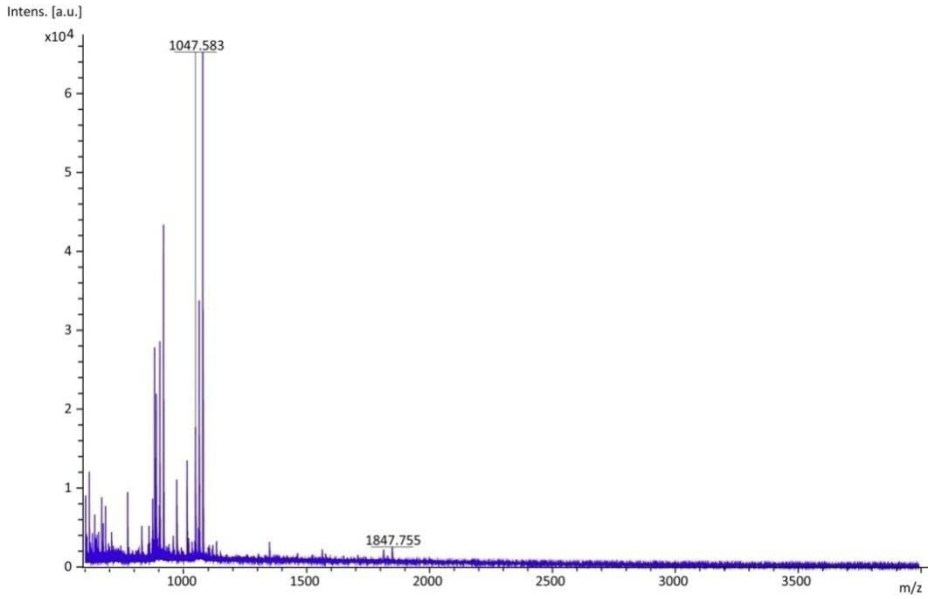


Figure 6.37 Positive ion reflector TOF - MALDI mass spectrum of 1_2_14

$[MH]^+$ 1047.583 Da	
Fragment masses	58,008; 70,040; 72,047; 84,042; 86,062; 107,030; 110,049; 112,064; 115,068; 129,075; 136,064; 138,049; 141,070; 143,084; 147,042; 154,067; 157,083; 169,061; 172,055; 175,087; 181,065; 184,062; 187,071; 197,092; 200,086; 207,055; 209,079; 211,081; 213,075; 216,066; 227,089; 231,094; 234,039; 240,090; 244,085; 250,034; 252,083; 254,100; 268,078; 271,117; 286,102; 288,112; 311,051; 391,099; 489,047; 585,088; 649,062; 651,065; 665,924; 703,675; 713,012; 731,032; 855,014; 881,136; 895,081; 924,079; 943,038; 961,038; 996,128; 999,080; 1002,656; 1006,031; 1009,288; 1014,297; 1016,395; 1019,645; 1022,797; 1026,625
T. atroviride	**Not related**
$[MH]^+$ 1847.755 Da	
Fragment masses	70,060; 110,090; 112,107; 115,108; 129,133; 175,162; 197,145; 226,103; 285,308; 313,129; 331,157; 425,210; 442,248; 470,231; 580,284; 598,287; 684,367; 695,424; 712,454; 720,438; 737,471; 754,490; 1006,536; 1451,568; 1460,912; 1640,991; 1673,983; 1779,965; 1786,280; 1789,338; 1794,624; 1797,786; 1799,953; 1802,150; 1805,515; 1813,991; 1822,497; 1829,939
T. atroviride	**Not related**

6.2.3 *Trichoderma atroviride* $_{wt}$ vs. *Rhizoctonia solani* (induced mycoparasitism)

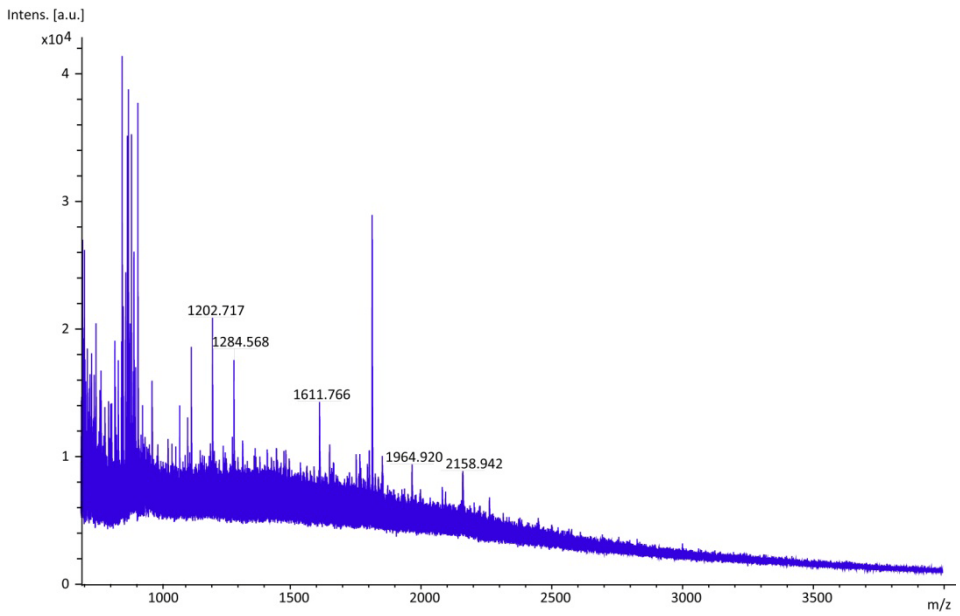


Figure 6.38 Positive ion reflector TOF - MALDI mass spectrum of 2_1_1

$[MH]^+$ 1202.717 Da	
Fragement masses	70,051; 84,07; 110,082; 112,099; 115,099; 129,108; 136,092; 139,098; 154,093; 157,11; 167,108; 172,095; 175,117; 186,117; 197,125; 200,119; 202,111; 205,098; 212,138; 214,118; 221,112; 223,113; 226,14; 228,123; 230,104; 234,055; 237,116; 240,111; 242,133; 245,102; 251,105; 254,123; 257,151; 259,126; 262,125; 270,138; 272,149; 280,138; 285,14; 288,168; 297,147; 299,134; 304,144; 314,153; 324,128; 326,144; 331,146; 343,145; 770,526; 1007,86; 1010,995; 1028,878; 1046,866; 1136,326; 1139,582; 1142,846; 1147,955; 1151,175; 1153,357; 1155,468; 1158,929; 1161,109; 1177,078,

	1179,603
T. atroviride	**Not related**
[MH]+ 1284.568 Da	
Fragment masses	70,07; 84,086; 86,107; 102,085; 110,096; 112,11; 115,114; 129,132; 132,136; 136,107; 154,125; 157,138; 159,131; 169,14; 172,129; 175,144; 183,137; 185,16; 187,15; 190,116; 197,164; 201,161; 203,13; 205,153; 209,141; 211,159; 213,155; 216,157; 218,155; 226,175; 229,167; 231,155; 237,169; 240,171; 243,162; 245,156; 253,191; 257,182; 259,164; 261,16; 263,171; 266,169; 268,183; 270,196; 272,166; 275,186; 279,181; 286,188; 288,208; 292,194; 294,173; 303,192; 309,199; 311,195; 313,202; 315,193; 342,185; 351,197; 946,925; 1087,904; 1090,003; 1092,044; 1218,656; 1221,658; 1232,325; 1235,584; 1238,838; 1241,045; 1243,203; 1254,973; 1257,032; 1259,353; 1262,518
T. atroviride	**Not related**
$[MH]^+$ 1611.766 Da	
Fragment masses	70,055; 84,079; 110,088; 112,104; 115,099; 129,13; 136,104; 154,114; 167,123; 172,131; 175,148; 181,142; 185,135; 195,133; 197,15; 209,142; 212,158; 229,142; 243,154; 254,161; 268,182; 384,199; 708,389; 871,45; 904,453; 1032,512; 1139,633; 1280,822; 1410,688; 1415,97; 1528,935; 1542,629; 1545,894; 1559,384; 1562,639; 1565,873; 1569,153; 1585,863
T. atroviride	**Not related**
$[MH]^+$ 1694.920 Da	
Fragment masses	110,084; 112,092; 115,104; 129,121; 136,1; 172,107; 195,123; 197,139; 513,262; 1853,535; 1909,505; 1918,143; 1921,436; 1935,652; 1943,741
T. atroviride	**Not related**
$[MH]^+$ 2158.942 Da	
Fragment masses	110,072; 112,086; 115,088; 129,097; 136,088; 599,276; 691,256; 785,333; 1447,528; 1809,022; 2089,703; 2098,562; 2103,563; 2107,726; 2112,263; 2115,325; 2117,593
T. atroviride	**Not related**

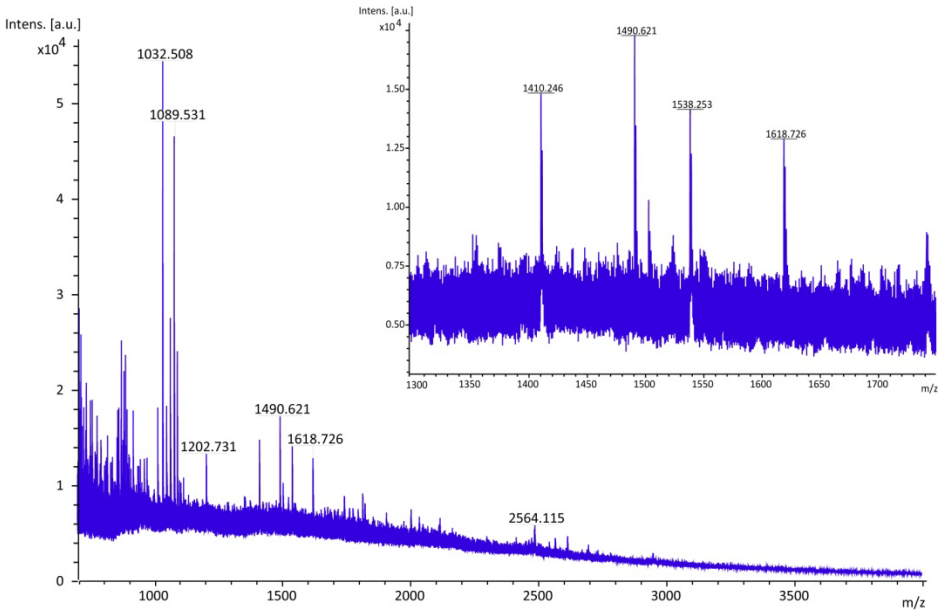


Figure 6.39 Positive ion reflector TOF - MALDI mass spectrum of 2_1_2

$[MH]^+$ 1032.508 Da	
Fragment masses	58,043; 70,069; 72,079; 84,085; 86,11; 95,085; 100,107; 102,106; 107,098; 110,097; 112,114; 115,107; 123,132; 129,123; 132,113; 136,107; 140,114; 143,112; 147,094; 150,123; 154,113; 157,126; 159,134; 167,117; 172,107; 175,147; 181,124; 184,137; 186,136; 190,122; 195,117; 197,136; 200,142;

	202,141; 207,121; 216,134; 227,131; 232,16; 235,140; 239,145; 241,150; 245,134; 253,127; 271,161; 279,142; 288,166; 292,152; 294,123; 296,158; 310,148; 345,233; 382,198; 410,209; 508,341; 525,262; 623,355; 651,027; 660,371; 681,732; 688,434; 833,832; 837,012; 839,095; 841,178; 924,434; 962,142; 966,358; 980,167; 982,223; 985,547; 988,996; 1005,000; 1007,170; 1010,864
T. atroviride	**FAD/FMN containing dehydrogenases R.NTGHDYLGR.S (NOTsignificant)**
$[MH]^+$ 1089.532 Da	
Fragement masses	70,086; 81,105; 84,11; 86,119; 95,114; 98,118; 100,125; 102,125; 107,114; 110,121; 112,138; 115,136; 123,162; 129,154; 131,147; 133,134; 136,142; 139,15; 141,143; 143,153; 149,150; 151,135; 154,153; 157,160; 159,157; 161,154; 167,162; 172,144; 175,184; 179,161; 181,161; 183,165; 185,181; 187,175; 190,169; 195,183; 197,196; 200,185; 202,185; 205,163; 207,168; 209,186; 212,183; 214,197; 216,189; 218,195; 221,175; 224,194; 227,197; 229,202; 232,21; 234,137; 237,194; 240,212; 243,193; 245,201; 247,204; 250,143; 252,197; 255,214; 258,206; 260,216; 268,215; 271,206; 276,210; 282,214; 284,228; 288,251; 294,189; 298,227; 301,214; 311,193; 314,227; 329,228; 439,300; 508,396; 549,178; 582,378; 650,135; 682,025; 704,015; 731,056; 768,209; 871,078; 886,816; 893,054; 897,212; 961,041; 967,982; 997,017; 1024,421; 1026,635; 1031,393; 1044,143; 1048,266; 1050,672; 1052,673; 1058,780; 1061,914; 1065,619; 1067,887
T. atroviride	**Not related**
$[MH]^+$ 1202.731 Da	
Fragment masses	70,045; 84,084; 86,087; 98,077; 101,078; 107,073; 110,084; 112,101; 115,095; 123,111; 129,119; 133,108; 136,093; 141,108; 143,108; 154,107; 157,116; 159,121; 161,131; 167,113; 169,11; 172,104; 175,135; 184,135; 186,112; 189,104; 195,118; 197,134; 200,124; 202,134; 207,107; 209,112; 211,135; 213,132; 216,124; 218,133; 221,119; 223,117; 225,105; 227,123; 229,144; 231,119; 235,124; 238,121; 240,141; 243,131; 245,126; 250,083; 253,132; 255,142; 258,135; 261,124; 263,128; 266,101; 268,147; 270,157; 272,152; 275,136; 278,142; 285,141; 288,166; 294,112; 297,141; 301,14; 312,155; 314,141; 1011,107; 1144,810; 1150,182; 1153,464; 1156,849; 1159,033; 1161,293; 1176,101; 1179,241; 1181,894
T. atroviride	**Not related**
$[MH]^+$ 1410.246 Da	
Fragment masses	70,069; 84,105; 86,122; 102,117; 104,174; 110,132; 112,147; 115,149; 120,149; 129,18; 136,166; 154,185; 157,212; 167,2; 169,213; 172,189; 175,224; 181,219; 183,226; 185,212; 187,205; 195,212; 197,236; 202,231; 209,244; 212,243; 214,244; 216,226; 227,249; 232,255; 235,251; 243,241; 245,246; 257,272; 259,253; 262,276; 266,275; 268,267; 270,283; 272,285; 284,279; 288,297; 290,289; 294,288; 298,293; 301,275; 314,302; 316,287; 326,311; 343,328; 427,349; 455,353; 508,398; 902,422; 1032,652; 1211,099; 1214,144; 1279,345; 1306,858; 1354,4; 1358,738; 1362,027; 1379,211; 1386,361
T. atroviride	**Not related**
$[MH]^+$ 1490.621 Da	
Fragment masses	70,052; 84,069; 110,083; 112,108; 115,111; 129,134; 154,118; 157,137; 167,143; 169,13; 172,132; 175,163; 187,146; 197,172; 200,167; 202,142; 209,172; 214,167; 221,146; 226,175; 232,185; 237,162; 243,173; 245,183; 250,156; 257,203; 259,166; 268,197; 270,204; 272,187; 275,174; 277,166; 286,196; 288,214; 298,182; 300,191; 313,208; 315,203; 326,186; 339,197; 343,211; 345,247; 472,233; 508,294; 571,292; 787,383; 902,472; 1032,443; 1146,654; 1261,877; 1279,86; 1288,561; 1376,075; 1393,059; 1411,096; 1440,524; 1443,836; 1462,149; 1464,431; 1467,312
T. atroviride	**Elongation factor 3 (EF-3) K.RGEEVFSDEDDL.- + Phospho (significant)**
$[MH]^+$ 1538.253 Da	
Fragment masses	70,069; 84,098; 86,123; 101,125; 110,112; 112,13; 115,136; 120,13; 129,152; 136,133; 143,138; 154,141; 157,15; 167,163; 172,156; 175,187; 181,165; 185,176; 187,162; 195,171; 197,194; 212,179; 214,196; 216,195; 227,19;

	229,191; 232,202; 235,191; 246,215; 250,196; 252,206; 254,206; 257,226; 268,245; 272,237; 286,229; 288,248; 292,22; 298,234; 316,198; 343,267; 508,359; 1151,898; 1340,896; 1432,592; 1450,58; 1489,692; 1512,339; 1514,816; 1519,652
T. atroviride	**Not related**
$[MH]^+$ 1618.726 Da	
Fragment masses	70,074; 84,098; 110,09; 112,107; 115,107; 120,107; 129,129; 136,113; 141,143; 143,13; 147,118; 154,123; 157,146; 159,115; 172,131; 175,162; 181,128; 185,151; 187,134; 197,155; 202,146; 226,172; 228,172; 230,168; 244,159; 255,182; 259,185; 268,196; 272,187; 285,213; 288,231; 471,282; 508,326; 600,35; 915,543; 1032,491; 1274,808; 1389,96; 1401,418; 1408,049; 1417,698; 1503,196; 1505,462; 1510,524; 1512,755; 1521,194; 1539,237; 1562,265; 1568,739; 1584,887; 1590,089; 1597,177
T. atroviride	**Elongation factor 3 (EF-3) R.KRGEEVFSDEDDL.- + Phospho (NOT significant)**
$[MH]^+$ 2564.1165 Da	
Fragment masses	112,09; 175,156; 197,125; 232,178; 386,192; 725,369; 858,525; 935,483; 1050,537; 1087,695; 1179,592; 1365,817; 1627,978; 1888,882; 2395,309; 2448,779; 2458,362; 2463,635; 2466,979; 2485,724; 2521,3; 2523,138
T. atroviride	**Not related**

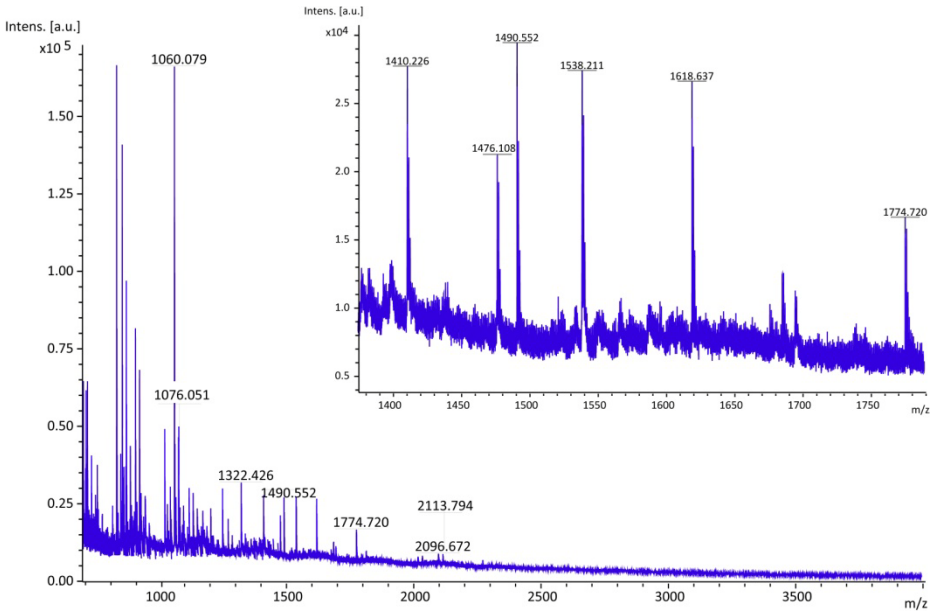


Figure 6.40 Positive ion reflector TOF - MALDI mass spectrum of 2_1_3

$[MH]^+$ 1060.079 Da	
Fragment masses	70,075; 102,128; 110,130; 112,140; 115,141; 127,138; 129,167; 136,139; 141,137; 154,162; 167,162; 175,201; 184,244; 187,192; 197,204; 209,186; 215,201; 227,198; 231,218; 250,200; 288,264; 311,185; 385,329; 585,308; 638,078; 644,055; 651,257; 665,947; 676,022; 682,120; 698,549; 703,921; 719,982; 731,298; 783,268; 821,015; 827,333; 831,551; 858,875; 860,972; 863,058; 865,109; 871,386; 908,994; 959,909; 963,255; 1003,908; 1016,595; 1032,376
T. atroviride	**Not related**
$[MH]^+$ 1076.051 Da	
Fragment masses	70,086; 81,103; 86,122; 95,118; 107,111; 110,128; 112,137; 115,129; 129,151; 136,134; 143,157; 154,144; 157,137; 167,164; 169,154; 172,140; 175,182; 185,178; 190,136; 195,170; 197,190; 201,195; 209,171; 211,196; 221,185; 231,204; 234,115; 311,187; 577,923; 593,936; 599,283; 637,887; 644,034; 665,972; 675,723; 681,878; 685,933; 687,989; 698,421; 703,596; 707,937;

	709,995; 719,743; 731,057; 760,746; 782,820; 820,665; 826,800; 831,029; 837,160; 841,361; 843,385; 845,557; 855,015; 864,672; 870,787; 873,887; 877,006; 881,158; 887,447; 892,661; 908,433; 925,065; 959,546; 963,429; 976,349; 1003,508; 1015,650; 1019,877; 1032,687; 1041,907; 1053,067
T. atroviride	**Cytochrome P450 K.MLNYRR.E + Phospho (not significant)**
$[MH]^+$ 1322.426 Da	
Fragment masses	70,042; 110,094; 112,110; 115,122; 129,146; 147,116; 154,131; 157,127; 175,168; 195,148; 197,175; 226,192; 252,177; 257,214; 264,178; 266,216; 268,204; 288,240; 760,455; 804,560; 820,476; 864,390; 892,486; 908,389; 914,439; 924,597; 928,700; 930,780; 950,685; 1003,129; 1007,558; 1069,579; 1075,774; 1079,909; 1091,156; 1097,297; 1103,356; 1107,410; 1113,559; 1119,813; 1123,918; 1130,228; 1136,621; 1186,306; 1286,188; 1296,502; 1302,325; 1305,262
T. atroviride	**Not related**
$[MH]^+$ 1410.226 Da	
Fragment masses	70,080; 110,142; 112,164; 115,154; 120,175; 129,190; 154,201; 157,229; 172,200; 175,234; 181,234; 197,248; 211,282; 214,245; 239,269; 245,264; 257,321; 259,273; 277,323; 288,314; 298,319; 316,311; 326,330; 427,367; 455,391; 472,401; 908,825; 930,212; 1027,244; 1097,719; 1113,996; 1119,914; 1135,584; 1206,915; 1216,335; 1369,372
T. atroviride	**Not related**
$[MH]^+$ 1476.108 Da	
Fragment masses	110,122; 112,152; 129,181; 154,170; 175,214; 197,219; 343,288; 385,298; 865,199; 909,159; 931,037; 1092,139; 1098,296; 1117,181; 1136,106; 1281,172; 1287,476; 1375,008; 1378,129; 1392,631; 1416,665; 1425,506; 1432,824; 1441,097; 1449,218
T. atroviride	**Not related**
$[MH]^+$ 1490.552 Da	
Fragment masses	110,092; 112,108; 129,140; 154,136; 175,185; 197,175; 214,192; 286,201; 288,231; 326,221; 343,226; 444,268; 455,258; 472,267; 543,327; 571,317; 690,415; 718,422; 787,450; 902,518; 908,808; 931,030; 1031,589; 1097,711; 1103,885; 1107,970; 1114,173; 1116,747; 1135,631; 1146,734; 1151,862; 1261,820; 1279,883; 1286,563; 1289,744; 1292,849; 1297,049; 1303,386; 1376,102; 1393,054; 1411,075; 1440,447; 1443,669; 1448,967; 1464,564
T. atroviride	**Elongation factor 3 (EF-3) K.RGEEVFSDEDDL.- + Phospho (significant)**
$[MH]^+$ 1538.211 Da	
Fragment masses	84,113; 110,118; 112,125; 115,132; 120,130; 129,153; 154,163; 175,204; 185,184; 187,153; 197,209; 209,206; 226,234; 240,237; 246,248; 268,270; 285,280; 288,256; 316,237; 572,410; 583,410; 600,433; 654,438; 1031,556; 1135,622; 1141,709; 1151,949; 1154,709; 1158,141; 1170,718; 1176,830; 1324,601; 1328,631; 1330,730; 1335,792; 1341,026; 1347,317; 1489,554; 1497,270; 1512,534
T. atroviride	**Not related**
$[MH]^+$ 1618.637Da	
Fragment masses	84,096; 110,093; 112,116; 129,128; 175,177; 197,187; 268,221; 285,229; 342,260; 471,319; 572,376; 583,376; 600,400; 671,481; 682,429; 699,486; 846,568; 915,618; 933,564; 1030,680; 1274,908; 1324,660; 1390,000; 1408,025; 1417,616; 1421,070; 1504,251; 1512,674; 1521,197; 1539,192; 1561,798; 1569,603; 1577,249; 1584,971; 1593,373
T. atroviride	**Elongation factor 3 (EF-3) R.KRGEEVFSDEDDL.- + Phospho (NOT significant)**
$[MH]^+$ 1774.720 Da	
Fragment masses	110,098; 112,146; 129,160; 197,201; 1362,550; 1378,893; 1385,079; 1551,217; 1556,594; 1567,877; 1573,997; 1635,585; 1660,509; 1677,465; 1695,492; 1729,149; 1753,566
T. atroviride	**Not related**
$[MH]^+$ 2096.672 Da	
Fragment masses	110,087; 129,137; 347,207; 639,362; 768,502; 997,559; 1066,618; 1999,519; 2017,545; 2040,970; 2049,006; 2065,057
T. atroviride	**Not related**
$[MH]^+$ 2113.794 Da	
Fragment masses	74,092; 110,082; 112,099; 347,222; 528,408; 639,312; 768,440; 997,499; 1066,536; 1084,638; 1164,575; 1535,989; 1724,977; 1998,453; 2010,151;

	2016,536; 2034,629; 2065,337
T. atroviride	**Mannosyl oligosaccharide glucosidase R.YNGAGNEEDSGGDEYETRA.- + Phospho (NOT significant)**

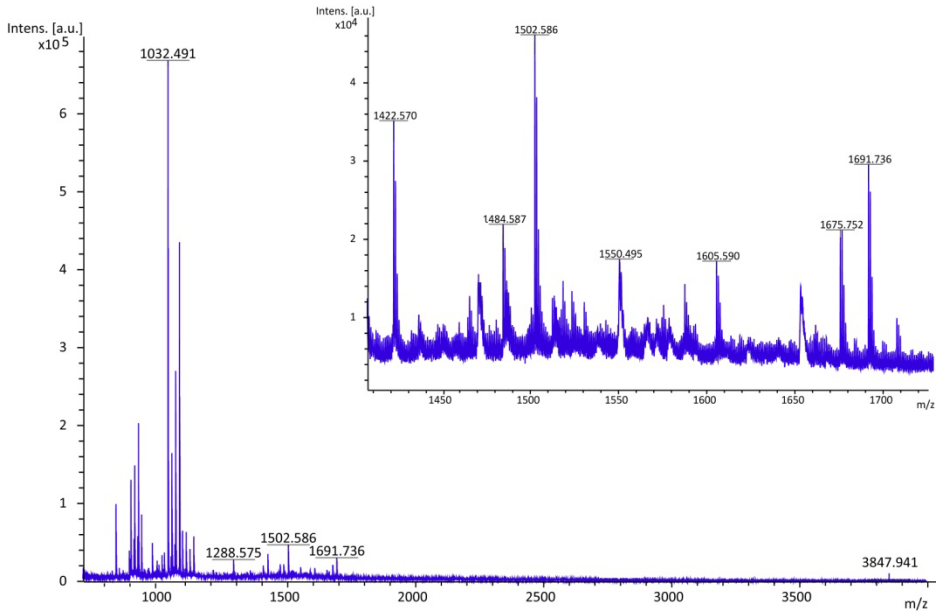


Figure 6.41 Positive ion reflector TOF - MALDI mass spectrum of 2_1_4

$[MH]^+$ 1032.491 Da	
Fragment masses	60,045; 70,076; 86,110; 110,092; 113,095; 129,130; 136,094; 151,075; 155,103; 158,110; 167,107; 172,110; 175,136; 181,113; 188,119; 190,121; 195,102; 198,098; 207,102; 215,125; 225,109; 232,149; 238,129; 249,166; 253,102; 268,137; 270,129; 273,123; 279,108; 296,139; 306,124; 310,126; 313,120; 324,129; 328,197; 345,230; 355,185; 365,146; 377,123; 382,189; 386,402; 388,156; 393,156; 398,147; 403,130; 410,190; 416,169; 421,147; 445,167; 449,142; 453,196; 473,190; 481,172; 491,190; 508,315; 525,238; 529,236; 574,255; 585,058; 606,327; 623,396; 643,270; 650,993; 660,343; 671,299; 688,371; 700,779; 730,959; 743,475; 760,548; 773,545; 801,569; 817,626; 918,870; 934,911; 953,762; 960,961; 971,932; 983,044; 988,922; 997,677; 1006,922; 1009,208; 1013,892
T. atroviride	**FAD/FMN containing dehydrogenases R,NTGHDYLGR.S (significant)**
$[MH]^+$ 1288.575 Da	
Fragment masses	70,038; 84,068; 86,081; 102,067; 104,115; 110,076; 112,092; 115,088; 123,093; 129,113; 133,080; 136,086; 141,109; 143,097; 145,079; 147,093; 151,085; 154,103; 158,104; 161,086; 163,091; 167,103; 172,102; 175,131; 179,101; 181,103; 185,108; 191,080; 195,110; 197,137; 201,115; 203,098; 205,094; 207,114; 209,133; 212,125; 215,121; 219,089; 221,100; 227,134; 229,125; 232,146; 235,111; 239,118; 241,124; 243,124; 245,119; 249,108; 251,121; 253,115; 255,125; 257,108; 259,111; 262,110; 264,124; 271,131; 273,122; 275,110; 277,135; 279,114; 286,132; 288,153; 294,111; 296,134; 299,129; 301,127; 310,124; 314,152; 326,148; 328,159; 345,190; 349,143; 508,288; 525,152; 709,286; 781,314; 916,447; 1031,158; 1092,862; 1220,455; 1236,264; 1238,400; 1240,595; 1243,885; 1246,075; 1248,400; 1259,996; 1262,083; 1264,043; 1266,983
T. atroviride	**cAMP regulated phosphoproteins family protein IgO1 R.KEDSLKIYGR.L + Phospho (NOT significant)**
$[MH]^+$ 1422.570 Da	
Fragment masses	70,078; 86,123; 104,136; 110,117; 112,138; 115,128; 127,110; 129,162; 136,145; 141,134; 145,117; 147,137; 155,169; 167,171; 175,198; 195,183; 197,211; 201,162; 209,187; 215,197; 219,183; 232,219; 253,208; 262,221; 275,198; 289,205; 293,192; 296,240; 311,203; 339,271; 345,314; 373,192; 382,275; 387,193; 391,208; 440,302; 473,297; 508,379; 518,344; 525,311; 588,356;

	606,364; 623,393; 688,353; 801,438; 988,602; 1015,638; 1032,697; 1222,823; 1250,307; 1307,145; 1309,322; 1317,547; 1325,085; 1343,131; 1369,495; 1373,779; 1379,105; 1386,972; 1393,010; 1396,841
T. atroviride	**Not related**
$[MH]^+$ 1484.587 Da	
Fragment masses	70,082; 84,069; 110,090; 112,105; 115,102; 129,123; 136,109; 167,123; 172,130; 175,156; 195,129; 197,144; 199,124; 216,151; 219,153; 232,176; 240,154; 244,153; 249,165; 253,140; 260,146; 272,169; 299,178; 301,164; 310,150; 313,183; 345,246; 355,192; 365,183; 410,176; 508,283; 518,239; 525,209; 588,255; 606,254; 623,295; 688,224; 774,301; 918,368; 1015,396; 1032,463; 1089,436; 1302,900; 1378,459; 1381,583; 1387,000; 1399,574; 1404,915; 1415,510; 1422,657; 1432,386; 1435,606; 1441,025; 1458,331; 1466,236
T. atroviride	**Not related**
$[MH]^+$ 1502.586 Da	
Fragment masses	70,073; 86,110; 110,089; 112,109; 115,113; 129,133; 136,112; 158,131; 167,134; 175,159; 181,137; 195,134; 197,159; 213,176; 215,153; 227,153; 232,179; 253,150; 255,159; 287,172; 301,170; 310,166; 314,185; 323,168; 345,244; 355,217; 371,204; 508,294; 518,267; 525,209; 588,273; 606,278; 623,306; 688,240; 1015,324; 1032,509; 1285,646; 1288,603; 1302,788; 1318,714; 1388,068; 1392,104; 1395,394; 1405,025; 1423,040; 1450,317; 1457,937; 1467,707; 1477,300; 1484,174
T. atroviride	**Not related**
$[MH]^+$ 1550.495 Da	
Fragment masses	141,120; 158,134; 167,133; 172,134; 175,161; 195,138; 197,166; 209,150; 213,179; 232,183; 253,177; 268,193; 310,181; 316,217; 345,266; 508,322; 525,234; 588,292; 623,322; 688,297; 817,317; 988,461; 1015,437; 1032,475; 1089,434; 1432,851; 1447,729; 1450,897; 1465,604; 1495,066; 1500,575; 1503,869; 1512,598; 1525,522; 1529,868
T. atroviride	**Kinesin motor domain containing protein R.TASVASTSTIGR.R + Phospho (NOT significant)**
$[MH]^+$ 1605.590 Da	
Fragment masses	86,115; 110,093; 112,103; 129,130; 158,128; 172,135; 175,151; 232,171; 345,248; 355,201; 466,173; 483,162; 508,312; 525,242; 528,159; 546,159; 588,250; 606,302; 623,321; 688,314; 801,365; 817,396; 858,383; 988,464; 997,364; 1015,458; 1032,529; 1044,448; 1103,402; 1361,636; 1403,876; 1499,428; 1502,684; 1507,986; 1511,988; 1526,011; 1538,754; 1561,777; 1586,851
T. atroviride	**Not related**
$[MH]^+$ 1675.752 Da	
Fragment masses	86,098; 102,070; 110,075; 112,099; 115,099; 129,116; 154,110; 158,107; 175,132; 197,145; 212,147; 227,126; 232,154; 255,143; 272,165; 276,096; 289,152; 366,181; 389,176; 415,198; 474,228; 508,298; 589,278; 641,306; 659,257; 676,267; 774,363; 887,421; 1000,583; 1014,288; 1032,397; 1088,521; 1104,623; 1202,644; 1431,959; 1483,725; 1501,949; 1519,990; 1569,484; 1572,690; 1577,006; 1585,116; 1616,155; 1625,459; 1633,098; 1636,296; 1641,056
T. atroviride	**Heat shock 70 kDa protein R.EDRCDIIANDQGNR.T (NOT significant)**
$[MH]^+$ 1691.736 Da	
Fragment masses	110,078; 112,099; 129,117; 175,142; 211,137; 239,124; 251,147; 255,149; 259,126; 272,155; 289,144; 404,184; 411,191; 474,311; 508,280; 533,228; 551,241; 589,300; 624,285; 642,299; 652,293; 666,258; 670,292; 676,296; 783,405; 909,361; 1000,471; 1014,406; 1032,364; 1159,592; 1260,657; 1403,859; 1484,593; 1585,062; 1588,565; 1591,866; 1633,720; 1648,020; 1657,514
T. atroviride	**Heat shoch 70 kDa protein STAGDTHLGGEDFDNR.L (NOT significant)**
$[MH]^+$ 3847.941 Da	
Fragment masses	74,303; 206,925; 460,197; 636,217; 1032,401; 2289,413; 2389,112; 2508,957; 3212,681
T. atroviride	**Short chain dehydrogenase/reductase family protein K.SRGSIINTASVVALVGAATPQLAYTASKGAVLALTR.E + Phospho (NOT significant)**

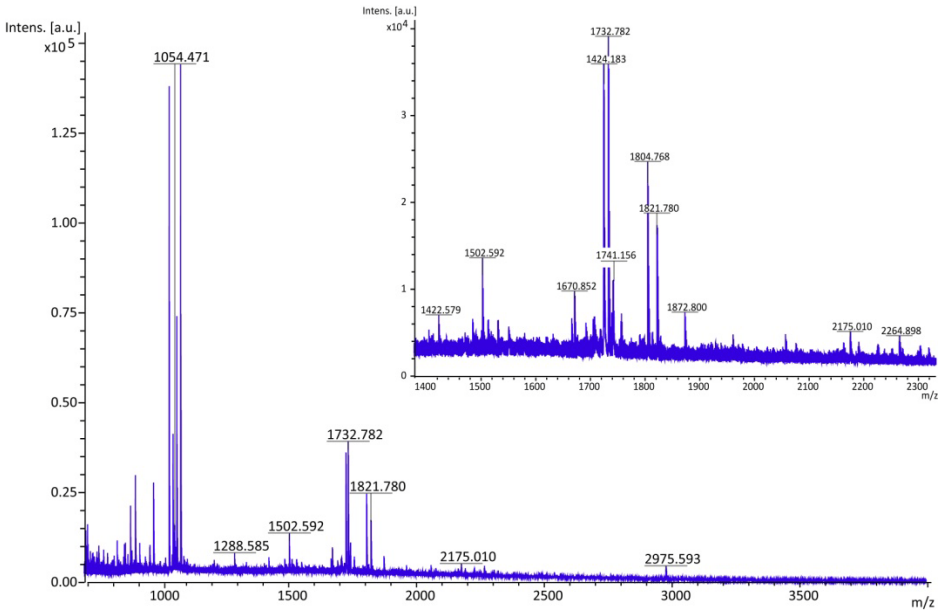


Figure 6.42 Positive ion reflector TOF - MALDI mass spectrum of 2_1_5

$[MH]^+$ 1054.471 Da	
Fragment masses	70,090; 84,117; 86,132; 102,130; 107,109; 110,130; 112,145; 115,134; 123,173; 129,166; 136,146; 147,162; 154,163; 158,172; 167,175; 175,200; 184,209; 186,173; 195,178; 197,207; 216,205; 232,236; 253,198; 268,238; 279,209; 311,196; 382,281; 410,280; 489,218; 508,267; 525,286; 585,269; 649,204; 651,210; 688,412; 713,072; 731,174; 851,811; 854,986; 857,031; 859,092; 861,210; 864,380; 924,239; 961,216; 997,053; 999,119; 1005,569; 1007,757; 1015,554; 1026,980; 1031,757
T. atroviride	**FAD/FMN containing dehydrogenases R.NTGHDYYGK.S (NOT significant)**
$[MH]^+$ 1288.585 Da	
Fragment masses	70,039; 84,065; 86,084; 102,078; 104,119; 110,078; 112,101; 115,098; 129,119; 136,102; 141,101; 154,113; 158,120; 169,133; 172,100; 175,139; 185,120; 187,115; 195,120; 197,142; 201,120; 207,115; 209,147; 212,164; 215,148; 226,154; 229,157; 232,156; 235,132; 237,142; 240,157; 244,137; 249,148; 251,124; 253,129; 255,153; 257,129; 259,144; 264,173; 266,156; 272,167; 276,164; 279,142; 286,158; 288,175; 294,136; 304,180; 327,176; 508,316; 763,338; 1031,339; 1082,549; 1087,744; 1089,705; 1091,845; 1095,038; 1098,201; 1236,337; 1239,636; 1242,896; 1247,265; 1262,252; 1264,927; 1268,207
T. atroviride	**Not related**
$[MH]^+$ 1422.579 Da	
Fragment masses	70,072; 84,106; 86,126; 104,164; 110,121; 112,141; 115,152; 129,170; 136,152; 147,164; 167,172; 172,199; 175,211; 181,198; 195,218; 197,229; 199,205; 212,222; 232,241; 245,222; 253,240; 272,288; 293,242; 326,297; 328,281; 508,425; 1032,769; 1217,713; 1221,898; 1224,996; 1228,113; 1231,232; 1234,604; 1307,340; 1316,599; 1319,841; 1325,210; 1343,240; 1369,464; 1372,738; 1392,342; 1397,031
T. atroviride	**Not related**
$[MH]^+$ 1502.592 Da	
Fragment masses	70,053; 84,076; 86,113; 110,096; 112,125; 115,109; 129,151; 136,115; 154,131; 172,158; 175,176; 195,157; 197,168; 201,162; 215,178; 232,196; 244,193; 270,191; 272,228; 286,212; 345,272; 508,337; 525,263; 1032,614; 1302,865; 1392,291; 1399,709; 1405,108; 1423,142; 1441,368; 1456,932; 1464,911; 1484,493
T. atroviride	**Not related**
$[MH]^+$ 1670.852 Da	

Fragment masses	70,073; 84,083; 86,092; 101,098; 110,086; 112,108; 115,107; 129,130; 175,153; 195,150; 197,165; 272,194; 759,422; 1032,541; 1324,985; 1563,691; 1573,336; 1609,341; 1617,575; 1621,845; 1633,247
T. atroviride	**Not related**
$[MH]^+$ 1724.183 Da	
Fragment masses	70,062; 74,205; 84,084; 86,102; 101,087; 110,090; 112,105; 115,107; 120,102; 129,123; 136,099; 147,130; 157,131; 167,137; 175,146; 186,149; 195,134; 197,162; 200,149; 213,168; 217,140; 221,174; 226,164; 231,133; 235,163; 240,164; 242,176; 244,153; 249,168; 255,151; 259,168; 267,150; 270,184; 272,184; 276,161; 305,225; 318,206; 345,202; 370,210; 482,229; 546,297; 562,317; 568,299; 611,288; 633,385; 797,374; 816,377; 833,366; 925,428; 1030,560; 1032,498; 1145,542; 1578,476; 1615,733; 1617,831; 1619,877; 1651,671; 1656,131; 1662,610; 1681,152; 1706,573
T. atroviride	**Ribosome associated chaperon zuotin R.TFSEDDRIQAQESAK.K (NOT significant)**
$[MH]^+$ 1732.782 Da	
Fragment masses	70,063; 84,085; 101,091; 110,090; 112,107; 115,103; 120,091; 129,123; 136,103; 147,135; 155,130; 157,129; 172,136; 175,155; 200,149; 217,153; 221,167; 242,185; 249,154; 255,165; 259,173; 267,133; 271,186; 276,190; 305,212; 345,199; 370,241; 454,241; 482,225; 489,269; 546,318; 581,286; 611,284; 645,381; 668,310; 744,395; 769,389; 797,377; 808,483; 814,441; 843,439; 897,454; 919,523; 925,455; 936,567; 1030,618; 1032,571; 1060,579; 1088,566; 1099,556; 1122,711; 1145,635; 1187,657; 1244,747; 1251,784; 1358,882; 1388,976; 1458,066; 1587,157; 1596,783; 1605,075; 1618,211; 1627,805; 1631,915; 1680,745; 1689,226; 1706,337
T. atroviride	**Rossmann-fold $NAD(P)^+$- binding proteins (FAD-binding containing protein, FAD-Monooxygenase) R.DTQHEGEQYVGNVEK.H (significant)**
$[MH]^+$ 1741.159 Da	
Fragment masses	70,066; 84,081; 86,102; 101,086; 110,088; 113,087; 115,098; 120,092; 129,126; 136,098; 147,124; 157,127; 172,132; 175,156; 200,145; 217,143; 221,156; 244,148; 249,164; 255,160; 259,181; 267,160; 276,202; 315,183; 345,200; 370,244; 454,276; 482,289; 546,393; 581,335; 611,356; 645,453; 668,358; 744,415; 769,385; 797,418; 808,524; 814,434; 843,447; 897,452; 919,538; 925,455; 936,579; 946,418; 1030,541; 1032,529; 1060,528; 1063,631; 1065,560; 1088,505; 1099,639; 1122,616; 1145,516; 1159,603; 1187,573; 1244,600; 1251,634; 1358,653; 1388,706; 1457,684; 1586,681; 1604,647; 1617,746; 1641,235; 1645,528; 1680,569; 1689,717; 1698,549; 1705,961; 1715,111; 1724,159
T. atroviride	**Not related**
$[MH]^+$ 1804.768 Da	
Fragment masses	70,091; 84,108; 86,137; 101,111; 110,118; 112,139; 115,130; 129,158; 147,159; 154,158; 157,175; 167,168; 175,192; 244,224; 259,213; 329,359; 633,458; 761,537; 816,544; 833,542; 1030,781; 1033,637; 1110,804; 1128,828; 1145,877; 1216,622; 1260,984; 1390,120; 1447,760; 1579,315; 1590,365; 1596,448; 1663,556; 1667,042; 1671,470; 1676,599; 1679,946; 1689,575; 1692,807; 1695,981; 1699,049; 1701,265; 1707,562; 1725,598; 1742,198; 1752,910; 1761,306; 1777,512
T. atroviride	**Ribosome associated chaperon zuotin R.TFSEDDRIQAQESAK.K + Phospho (NOT significant)**
$[MH]^+$ 1821.780 Da	
Fragment masses	70,093; 86,114; 110,116; 112,132; 120,123; 129,152; 175,196; 259,203; 329,301; 373,296; 656,392; 687,456; 705,452; 785,446; 1030,744; 1032,689; 1037,690; 1145,729; 1578,707; 1589,652; 1596,395; 1613,606; 1689,593; 1694,009; 1697,862; 1706,588; 1713,828; 1717,109; 1724,570; 1742,601; 1754,191; 1771,972; 1777,208; 1795,225
T. atroviride	**Not related**
$[MH]^+$ 1872.800 Da	
Fragment masses	70,071; 84,108; 86,131; 110,126; 112,140; 115,147; 129,172; 175,216; 250,244; 262,244; 448,312; 563,354; 775,541; 874,584; 1032,735; 1118,755; 1432,781; 1512,746; 1515,815; 1761,796; 1768,142; 1773,531; 1803,037; 1825,373; 1849,238; 1853,313
T. atroviride	**Ribosome associated chaperon zuotin R.SFEYLDEDVPDDGESR.D**

	(NOT significant)
$[MH]^+$ 2175.010 Da	
Fragment masses	70,070; 110,107; 112,124; 115,128; 129,151; 167,155; 175,184; 195,188; 197,168; 272,233; 475,455; 605,493; 687,427; 1032,676; 1118,736; 1199,769; 1734,627; 2049,018; 2060,795; 2065,122; 2068,177; 2077,980; 2151,825
T. atroviride	**Not related**
$[MH]^+$ 2264.898 Da	
Fragment masses	110,102; 112,114; 129,137; 136,118; 175,170; 272,246; 605,499; 709,543; 789,554; 804,654; 918,626; 1032,657; 1118,725; 1162,742; 1277,777; 1392,929; 1560,814; 1837,107; 2059,289; 2139,281; 2154,092; 2157,100; 2159,116; 2162,584; 2173,296; 2176,494; 2184,712; 2233,660; 2240,539
T. atroviride	**Ankyrin repeat containing protein K.TLSLSSDQITVYSLAKTSNR.W + Phospho (NOT significant)**
$[MH]^+$ 2975.593 Da	
Fragment masses	74,851; 175,124; 226,133; 313,156; 355,174; 396,187; 414,226; 825,411; 972,587; 1034,571; 1051,585; 1069,683; 1122,616; 1209,658; 1296,763; 1383,689; 1608,970; 1680,039; 1935,630; 2517,083; 2733,240; 2858,088; 2875,484; 2904,952; 2931,405; 2944,388; 2947,192; 2951,298; 2955,380
T. atroviride	**Dihydrolipoamide acetyltransferase component K.KDSEPAPQSTPASAPQSSSAPEQYSSQGR.I (significant)**

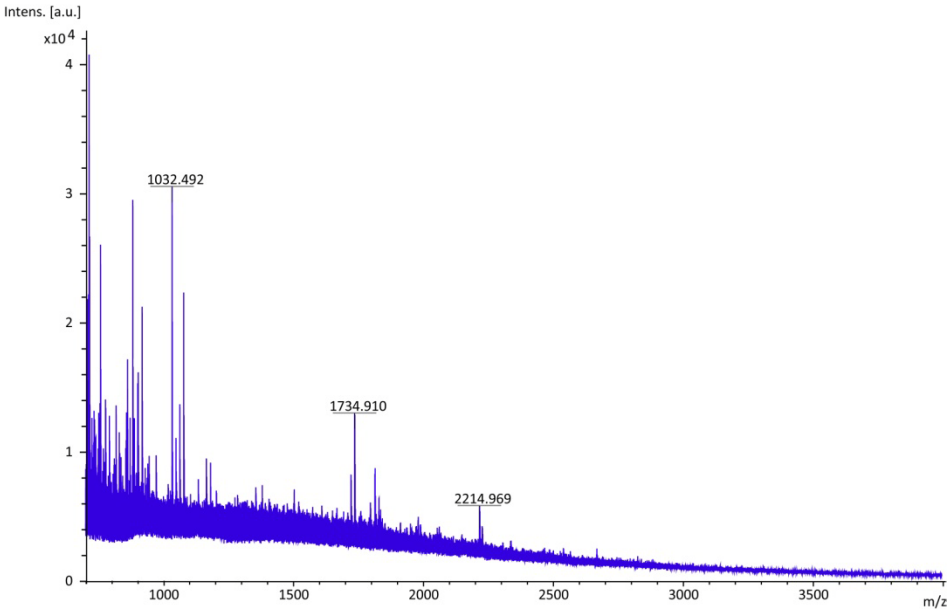


Figure 6.43 Positive ion reflector TOF - MALDI mass spectrum of 2_1_6

$[MH]^+$ 1032.492 Da	
Fragment masses	70,063; 84,083; 86,097; 95,092; 98,081; 100,090; 102,091; 104,123; 107,081; 110,090; 112,107; 115,101; 121,087; 123,122; 125,112; 129,119; 133,104; 136,097; 139,101; 141,109; 143,105; 146,095; 148,088; 154,102; 158,107; 163,107; 166,125; 169,119; 172,109; 175,134; 179,111; 181,108; 184,119; 186,117; 188,127; 190,114; 192,125; 195,114; 197,138; 200,128; 202,114; 205,114; 207,120; 209,122; 212,126; 215,138; 218,135; 228,137; 232,146; 235,122; 240,150; 243,125; 245,140; 249,123; 251,124; 253,119; 255,137; 258,140; 260,134; 262,140; 264,140; 268,151; 271,149; 279,123; 285,170; 288,170; 294,111; 301,137; 310,135; 313,157; 345,204; 382,164; 411,185; 508,302; 525,229; 623,296; 660,308; 681,683; 688,332; 834,815; 836,991; 839,081; 841,127; 843,223; 924,320; 970,627; 978,966; 981,163; 983,253; 985,538; 988,876; 1006,008; 1008,232; 1011,266
T. atroviride	**FAD/FMN containing dehydrogenases R.NTGHDYLGR.S (NOT significant)**
$[MH]^+$ 1734.910 Da	
Fragment masses	84,097; 86,121; 98,125; 101,097; 104,137; 110,097; 112,109; 115,114; 129,136;

	136,114; 143,148; 147,120; 154,128; 157,126; 167,138; 172,157; 175,165; 187,174; 197,178; 213,169; 215,180; 229,185; 240,185; 244,173; 258,192; 344,217; 405,223; 529,299; 588,373; 601,361; 619,417; 748,455; 845,498; 907,550; 987,609; 1116,674; 1147,730; 1204,564; 1218,799; 1289,916; 1392,094; 1419,006; 1521,263; 1532,250; 1589,247; 1607,244; 1660,665; 1663,767; 1669,097; 1680,363; 1684,750; 1689,141; 1704,529; 1708,067; 1711,403
T. atroviride	**RNA polymerase II subunit R.RKSYLQYEVSLIR.D + Phospho (NOT significant)**
$[MH]^+$ 2214.969 Da	
Fragment masses	70,064; 74,136; 110,108; 112,116; 115,120; 129,144; 136,116; 155,147; 175,184; 197,197; 226,213; 355,233; 720,417; 888,571; 906,522; 1021,578; 1032,641; 1131,670; 1149,692; 2110,711; 2139,642; 2154,604; 2161,834; 2185,823; 2191,187
T. atroviride	**Not related**

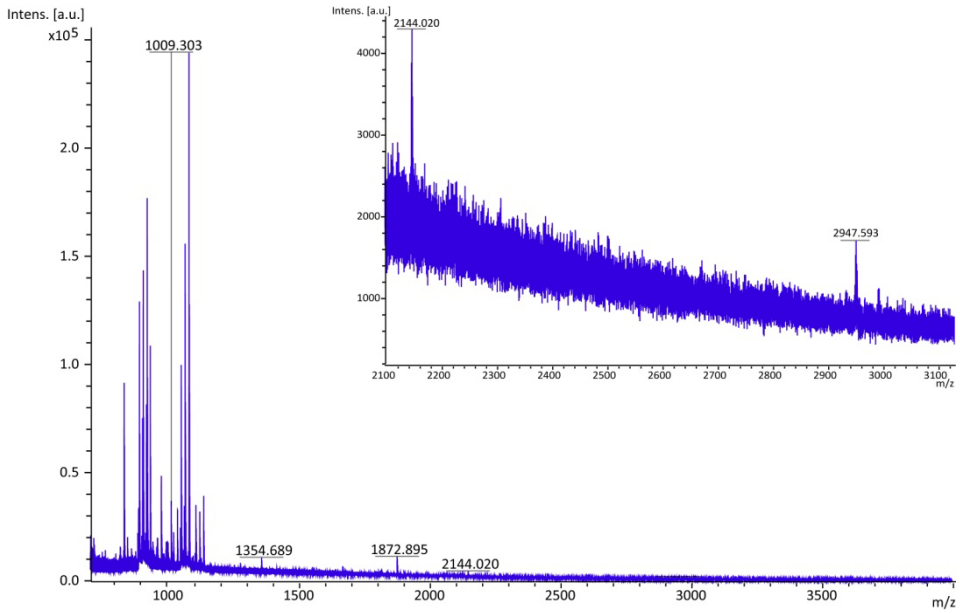


Figure 6.44 Positive ion reflector TOF - MALDI mass spectrum of 2_1_7

$[MH]^+$ 1009.303 Da	
Fragment masses	58,073; 70,098; 73,088; 81,098; 84,110; 86,123; 89,108; 95,114; 98,116; 100,118; 102,125; 104,161; 107,109; 110,113; 112,134; 114,123; 121,104; 123,140; 125,128; 127,126; 129,145; 131,132; 133,124; 137,117; 141,135; 143,134; 146,127; 151,111; 154,144; 156,140; 158,145; 161,127; 163,123; 165,134; 167,132; 169,145; 175,142; 177,132; 179,130; 181,135; 184,139; 187,146; 189,136; 191,131; 193,139; 195,140; 197,166; 199,154; 201,152; 203,146; 205,147; 207,147; 209,156; 211,152; 213,159; 215,166; 218,175; 221,151; 223,163; 225,160; 227,162; 231,175; 234,154; 237,167; 240,173; 243,184; 245,159; 247,178; 250,162; 253,172; 255,166; 257,171; 259,164; 263,164; 267,144; 269,170; 271,166; 273,178; 279,169; 281,153; 283,167; 285,169; 287,167; 289,174; 295,168; 297,175; 299,164; 311,149; 315,180; 321,167; 323,168; 325,166; 327,173; 329,164; 331,187; 339,176; 353,176; 585,134; 645,156; 651,046; 663,182; 731,009; 759,076; 812,116; 875,399; 882,189; 893,934; 917,047; 919,019; 934,991; 937,125; 939,175; 952,958; 955,825; 958,171; 960,822; 964,051; 967,169; 969,405; 973,786; 978,759; 982,958; 985,213; 987,787; 990,031
T. atroviride	**Not related**
$[MH]^+$ 1354.689 Da	
Fragment masses	70,035; 72,066; 84,069; 86,083; 89,072; 95,072; 100,093; 102,096; 104,133; 110,099; 112,110; 115,115; 120,117; 123,128; 125,128; 129,139; 133,121; 137,111; 143,136; 151,104; 154,145; 158,149; 161,129; 163,136; 165,142; 167,143; 169,160; 171,153; 175,174; 179,155; 181,161; 184,162; 186,178; 189,161; 191,145; 193,160; 195,157; 197,188; 199,176; 201,171; 203,161; 205,156; 207,171; 209,181; 212,190; 214,184; 216,185; 218,193; 221,177; 223,201; 225,192; 227,188; 229,207; 231,206; 233,183; 235,192; 237,195; 240,199; 243,203; 245,191; 247,203; 249,195; 251,197; 253,201;

	255,191; 257,223; 259,195; 261,209; 264,205; 267,198; 269,206; 271,204; 273,204; 276,212; 278,200; 285,210; 287,210; 289,217; 292,214; 294,208 297,195 299,199; 301,212; 303,232; 309,199; 311,196; 313,207; 315,204; 317,221 321,203; 323,201; 325,198; 327,213; 329,211; 331,219; 333,224; 335,217; 337,212; 339,217; 341,211; 343,215; 351,212; 353,210; 355,228; 357,234; 369,223; 373,232; 1151,616; 1154,835; 1157,987; 1240,267; 1248,482; 1282,385; 1285,469; 1293,941; 1297,207; 1299,258; 1301,553; 1303,618; 1305,868; 1309,048; 1311,190; 1321,892; 1325,058; 1327,248; 1330,692; 1332,666
T. atroviride	**Not related**
$[MH]^+$ 1872.895 Da	
Fragment masses	70,078; 84,093; 86,118; 102,111; 104,158; 112,132; 115,131; 129,164; 137,138; 151,137; 175,187; 212,210; 227,245; 262,235; 311,254; 422,236; 535,321; 698,446; 754,521; 865,499; 964,632; 1061,648; 1095,783; 1158,740; 1175,762; 1419,012; 1775,830; 1793,777; 1821,016; 1825,165; 1847,071; 1850,197; 1854,596
T. atroviride	**Glycogen synthase kinase 3 K.ILVENEPNVSYICSR.Y + Phospho (significant)**
$[MH]^+$ 2244.020 Da	
Fragment masses	74,128; 110,093; 112,109; 129,124; 136,106; 175,156; 343,244; 382,145; 638,455; 766,539; 1081,743; 1363,695; 1704,983; 1736,781; 2046,864; 2064,939; 2089,673; 2113,830; 2120,479; 2125,013
T. atroviride	**Elicitor protein R.FAYLGNDSDGEEKPVVPVK.T + Phospho (NOT significant)**
$[MH]^+$ 2047.593 Da	
Fragment masses	74,083; 175,132; 463,206; 499,215; 602,232; 757,392; 774,347; 1093,585; 1278,696; 1392,766; 1809,117; 2905,180; 2920,939; 2924,940; 2928,281
T. atroviride	**Elastinolytic metalloprotease K.GNDLVIVNAQGSGTNNANFATPVDGSSGR.M (NOT significant)**

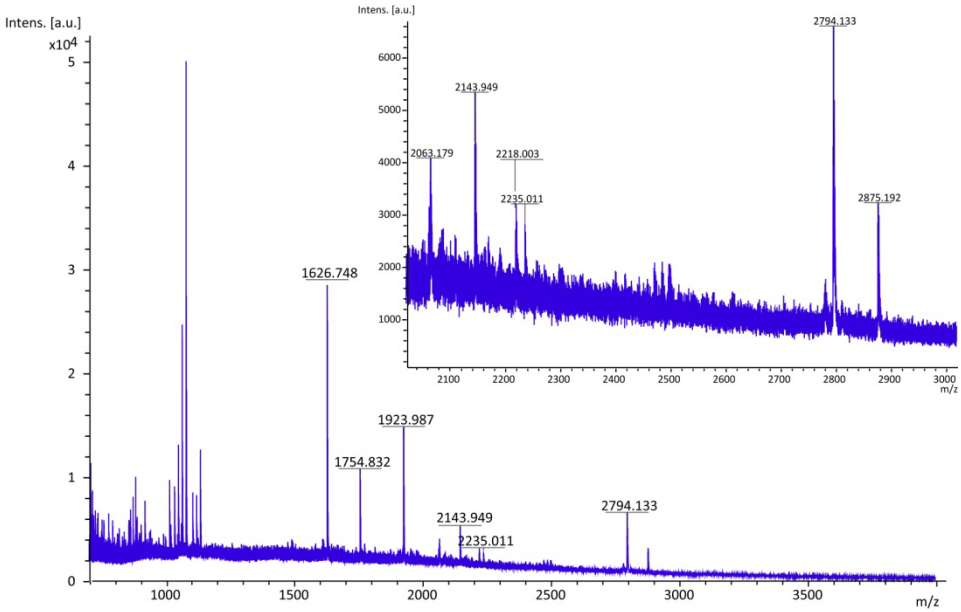


Figure 6.45 Positive ion reflector TOF - MALDI mass spectrum of 2_1_8

$[MH]^+$ 1626.748 Da	
Fragment masses	70,079; 86,110; 101,093; 110,097; 113,108; 115,102; 129,134; 136,112; 141,123; 155,127; 157,149; 159,132; 172,132; 175,157; 181,149; 185,148; 187,139; 195,155; 197,172; 199,141; 201,156; 203,140; 209,146; 216,140; 225,147; 229,168; 244,180; 246,197; 253,139; 258,180; 273,163; 286,203; 288,225; 290,177; 304,203; 313,188; 315,211; 324,173; 331,192; 341,175; 343,215; 352,186; 359,164; 365,248; 403,254; 413,255; 423,248; 426,266; 437,254; 444,256; 454,268; 474,305; 552,306; 567,326; 569,309; 587,291; 594,350; 611,384; 638,365; 691,363; 709,406; 726,423; 825,502; 866,523; 953,649;

	1040,690; 1268,948; 1422,703; 1426,818; 1453,097; 1498,227; 1520,682; 1573,668; 1577,910; 1603,481; 1608,295
T. atroviride	**Transaldolase like protein K.EGGDIDSQVDHALDR.L (significant)**
$[MH]^+$ 1754.832 Da	
Fragment masses	84,096; 86,117; 110,097; 113,097; 115,111; 129,137; 136,111; 155,150; 172,146; 175,162; 181,161; 197,180; 209,139; 253,132; 324,191; 474,296; 611,355; 709,398; 715,375; 726,384; 930,515; 1040,657; 1144,618; 1268,863; 1362,820; 1404,793; 1551,923; 1581,384; 1680,798; 1704,831; 1728,710
T. atroviride	**Transaldolase like protein K.KEGGDIDSQVDHALDR.L (NOT significant)**
$[MH]^+$ 1923.987 Da	
Fragment masses	69,884; 83,890; 85,908; 109,877; 111,891; 114,894; 128,898; 174,892; 182,916; 185,876; 300,836; 367,891; 384,885; 414,827; 512,874; 569,907; 638,892; 667,881; 684,908; 783,970; 996,040; 1093,055; 1295,230; 1751,817; 1874,974; 1891,768
T. atroviride	**Not related**
$[MH]^+$ 2063.179 Da	
Fragment masses	70,045; 110,075; 112,090; 115,086; 129,113; 136,104; 172,116; 175,142; 197,155; 212,160; 343,246; 570,342; 614,368; 628,297; 729,407; 901,466; 1113,616; 1285,660; 1818,717; 1964,655; 1992,161; 2002,136; 2017,176; 2040,519; 2045,461
T. atroviride	**Pentatricopeptide repeat domain-containing protein R.SSVVSRIATGMVPGRPRHR.A (not significant)**
$[MH]^+$ 2143.949 Da	
Fragment masses	86,106; 110,091; 112,110; 129,135; 136,106; 175,155; 197,159; 296,231; 343,264; 382,210; 424,326; 638,468; 739,485; 766,604; 895,687; 914,507; 1081,789; 1196,821; 1209,730; 1265,869; 1363,849; 1506,855; 1704,289; 1802,335; 2028,838; 2046,892; 2064,894; 2089,832; 2113,401; 2121,440
T. atroviride	**Elicitor protein R.FAYLGNDSDGEEKPVVPVK.T + Phospho (NOT significant)**
$[MH]^+$ 2218.003 Da	
Fragment masses	110,083; 112,108; 175,150; 445,201; 583,277; 629,382; 853,543; 968,609; 1636,201; 2014,635; 2107,641; 2137,074; 2161,330; 2164,670; 2184,690; 2192,834
T. atroviride	**F-actin capping protein R.QVEQDLPVENDDSHIANVGR.L (significant)**
$[MH]^+$ 2235.011 Da	
Fragment masses	110,090; 112,098; 115,102; 129,121; 136,093; 175,159; 197,170; 583,436; 766,570; 853,612; 968,641; 1083,642; 1197,738; 1635,799; 2162,310; 2184,516; 2209,005
T. atroviride	**F-actin capping protein R.QVEQDLPVENDDSHIANVGR.L (significant)**
$[MH]^+$ 2794.133 Da	
Fragment masses	112,071; 129,099; 158,077; 169,092; 175,114; 201,073; 240,126; 245,075; 257,154; 272,122; 274,164; 311,173; 316,109; 328,190; 330,107; 345,211; 357,107; 369,154; 374,094; 387,157; 427,127; 440,208; 445,147; 461,090; 474,232; 484,165; 486,151; 545,296; 555,234; 560,204; 599,250; 615,224; 625,252; 643,267; 660,307; 670,311; 714,300; 785,265; 789,383; 829,268; 900,341; 918,435; 1029,427; 1043,378; 1047,471; 1114,461; 1127,458; 1145,488; 1162,498; 1242,516; 1260,478; 1277,505; 1346,569; 1403,587; 1663,691; 1877,649; 1992,392; 2737,225; 2759,577; 2776,057
T. atroviride	**Not related**
$[MH]^+$ 2875.192 Da	
Fragment masses	112,089; 175,138; 240,152; 257,189; 272,139; 274,200; 311,184; 316,146; 328,220; 345,241; 369,221; 387,176; 440,257; 445,209; 456,254; 474,265; 484,253; 527,248; 545,311; 555,278; 599,264; 625,310; 643,331; 660,359; 714,334; 771,400; 789,407; 799,416; 829,392; 900,444; 918,486; 928,468; 981,647; 1029,557; 1043,524; 1047,572; 1057,580; 1114,537; 1127,554; 1144,593; 1162,616; 1242,620; 1260,677; 1277,652; 1346,693; 1403,724; 1550,793; 1663,995; 1675,420; 1682,003; 1761,939; 1779,031; 1878,050; 1976,116; 1989,218; 1993,121; 2081,568; 2091,164; 2108,402; 2178,048; 2206,095; 2223,498; 2277,926; 2610,176; 2623,320; 2707,202; 2742,685; 2749,618; 2760,298; 2778,356; 2796,340

T. atroviride	**Elongation factor 1 beta (EF1B) K.APAAEDDDDVDLFGSDDEEEDAEAVR.I + Phospho (significant)**

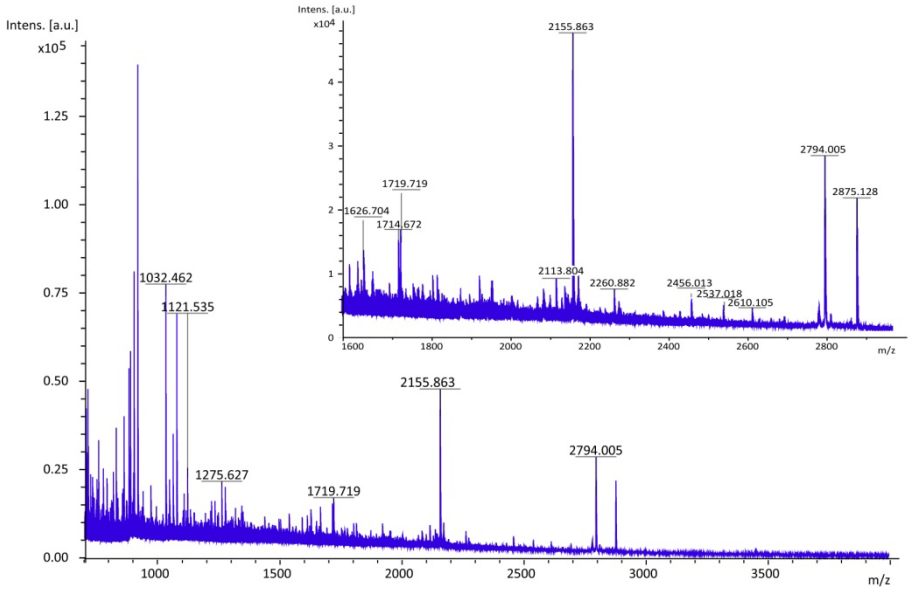


Figure 6.46 Positive ion reflector TOF - MALDI mass spectrum of 2_1_9

$[MH]^+$ 1032.462 Da	
Fragment masses	70,062; 72,071; 81,068; 84,079; 86,107; 95,077; 102,085; 107,072; 110,094; 112,106; 115,103; 121,090; 123,119; 125,093; 129,121; 133,110; 136,093; 141,111; 143,108; 149,112; 154,104; 157,122; 159,107; 161,121; 167,117; 169,106; 172,088; 175,138; 184,125; 186,126; 190,100; 195,114; 197,135; 201,126; 203,120; 207,106; 209,123; 212,133; 215,142; 218,137; 221,116; 223,125; 225,132; 227,123; 232,151; 235,133; 237,147; 240,150; 242,158; 250,119; 253,127; 261,132; 277,135; 279,127; 294,116; 310,140; 345,217; 382,196; 411,177; 508,321; 525,246; 688,389; 697,989; 836,054; 839,151; 841,213; 843,294; 980,140; 982,245; 984,362; 986,492; 988,928; 1006,505; 1009,653; 1011,942
T. atroviride	**FAD/FMN containing dehydrogenase R.NTGHDYLGR.S (NOT significant)**
$[MH]^+$ 1121.535 Da	
Fragment masses	70,092; 84,128; 86,142; 95,140; 100,141; 102,135; 107,130; 110,145; 112,163; 115,167; 121,145; 123,178; 125,166; 129,188; 136,163; 143,196; 147,175; 154,187; 157,199; 159,199; 167,202; 169,199; 172,188; 175,224; 185,213; 187,198; 190,207; 195,217; 197,233; 200,224; 203,214; 205,222; 212,245; 214,250; 216,238; 222,247; 224,253; 226,252; 228,251; 231,247; 234,214; 244,234; 248,257; 251,261; 253,283; 255,253; 257,263; 259,245; 267,277; 269,271; 272,270; 276,264; 286,281; 288,294; 293,252; 301,290; 303,301; 311,279; 339,268; 407,314; 536,403; 682,177; 736,055; 759,300; 874,886; 881,060; 885,223; 908,688; 919,924; 921,938; 925,046; 929,202; 931,356; 933,445; 994,040; 1015,207; 1039,375; 1070,453; 1073,639; 1078,291; 1080,458; 1093,955; 1096,696; 1099,423
T. atroviride	**Not related**
$[MH]^+$ 1261.614 Da	
Fragment masses	70,056; 84,088; 86,106; 95,100; 101,104; 107,095; 110,103; 112,121; 115,119; 120,130; 129,143; 136,128; 141,135; 143,132; 147,130; 154,134; 158,149; 164,141; 169,145; 172,142; 175,173; 183,159; 185,162; 187,163; 195,155; 197,174; 201,165; 203,159; 205,152; 207,142; 209,162; 211,172; 213,165; 216,165; 218,170; 221,164; 223,163; 226,180; 229,183; 231,164; 235,174; 237,177; 240,192; 243,189; 245,169; 247,173; 249,164; 252,177; 254,184; 257,190; 259,169; 262,185; 268,206; 270,198; 272,191; 274,185; 276,193; 279,181; 281,179; 286,194; 288,214; 294,166; 300,187; 303,209; 312,203; 314,195; 326,208; 328,194; 343,203; 354,222; 1059,662; 1061,751; 1066,015; 1069,112; 1157,569; 1212,610; 1214,741; 1235,371; 1237,526;

	1240,035; 1242,168
T. atroviride	**Not related**
$[MH]^+$ 1275.627 Da	
Fragment masses	70,045; 84,073; 86,094; 101,080; 110,082; 112,102; 115,100; 129,118; 136,100; 143,114; 147,104; 154,113; 157,136; 159,101; 167,130; 169,124; 175,141; 181,108; 183,136; 185,143; 187,138; 189,121; 195,123; 197,145; 202,123; 207,124; 209,125; 212,134; 214,154; 216,127; 218,143; 221,127; 226,153; 229,142; 232,145; 235,143; 237,133; 241,141; 244,136; 246,153; 248,145; 253,166; 255,157; 258,149; 264,142; 266,157; 268,151; 270,170; 272,140; 276,155; 280,155; 282,148; 284,150; 286,163; 288,181; 290,170; 294,130; 303,177; 311,162; 316,161; 341,177; 355,168; 690,312; 892,957; 1075,666; 1077,788; 1079,919; 1081,997; 1085,239; 1225,404; 1248,155; 1253,759
T. atroviride	**Not related**
$[MH]^+$ 1626.704 Da	
Fragment masses	86,105; 110,089; 112,106; 115,103; 129,125; 136,116; 154,115; 157,114; 167,134; 172,147; 175,151; 185,127; 195,133; 197,161; 209,145; 212,166; 214,161; 229,144; 244,159; 259,147; 611,362; 708,434; 1032,455; 1170,315; 1238,493; 1295,141; 1427,572; 1520,549; 1538,519; 1556,636; 1559,690; 1575,492; 1579,809; 1584,287
T. atroviride	**CorA-like Mg^{2+} transporter protein R.IKMMGGERPRLSR.G + Phospho (NOT significant)**
$[MH]^+$ 1714.668 Da	
Fragment masses	110,066; 112,091; 115,092; 129,111; 175,129; 195,119; 197,132; 209,141; 226,130; 268,158; 440,204; 457,224; 978,528; 1207,692; 1322,412; 1517,716; 1680,999
T. atroviride	**Not related**
$[MH]^+$ 1719.719 Da	
Fragment masses	110,087; 112,097; 129,126; 175,146; 185,134; 197,147; 226,164; 440,284; 457,260; 544,288; 691,387; 708,385; 798,357; 826,402; 978,530; 1032,572; 1093,551; 1160,733; 1207,602; 1656,012; 1670,782; 1681,284
T. atroviride	**Not related**
$[MH]^+$ 2113.804 Da	
Fragment masses	110,063; 112,085; 129,113; 175,115; 369,191; 498,235; 626,271; 685,307; 754,367; 756,364; 772,365; 786,344; 826,397; 882,389; 885,445; 900,441; 915,395; 954,462; 971,476; 1014,491; 1100,520; 1125,562; 1143,542; 1196,569; 1214,560; 1229,598; 1231,584; 1324,643; 1342,672; 1358,636; 1429,644; 1510,776; 1557,791; 1711,066; 1998,990; 2016,446; 2040,938; 2065,558; 2088,979
T. atroviride	**40S ribosomal protein S3 R.VAEQEGAAEEEAQPAAEEQQ.- (significant)**
$[MH]^+$ 2155.863 Da	
Fragment masses	70,045; 110,086; 112,095; 129,119; 175,139; 197,139; 244,156; 301,171; 409,183; 412,247; 487,194; 516,316; 587,289; 799,415; 912,507; 997,604; 1125,690; 1337,767; 1438,747; 1569,957; 1812,366; 2028,508; 2041,611; 2045,879; 2049,088; 2064,192; 2113,334; 2135,727
T. atroviride	**Heme binding peroxidase R.DNDAAACTPDGRLPDASQGPK.H (significant)**
$[MH]^+$ 2260.882 Da	
Fragment masses	110,100; 112,111; 175,159; 272,202; 605,445; 1118,657; 2064,547; 2158,350; 2162,602; 2185,313; 2209,302; 2233,040
T. atroviride	**Not related**
$[MH]^+$ 2610.105 Da	
Fragment masses	523,397; 545,243; 621,364; 636,487; 734,382; 922,518; 937,611; 1035,691; 1397,739; 1885,604; 2061,236; 2448,564; 2510,536; 2514,860; 2521,876; 2546,371; 2569,000; 2572,285
T. atroviride	**Not related**
$[MH]^+$ 2794.005 Da	
Fragment masses	112,061; 169,087; 171,102; 175,113; 201,083; 240,120; 245,061; 257,146; 272,123; 274,163; 311,165; 316,091; 328,174; 330,115; 345,205; 357,096; 369,148; 374,100; 387,144; 429,138; 440,204; 443,132; 445,115; 461,126; 474,235; 484,177; 486,137; 504,160; 528,222; 545,290; 555,250; 560,142;

	599,239; 615,173; 625,253; 643,253; 660,307; 714,221; 789,356; 829,283; 900,329; 918,400; 1029,363; 1043,367; 1047,473; 1114,404; 1127,474; 1145,487; 1162,488; 1242,524; 1260,525; 1277,551; 1346,493; 1403,523; 1550,690; 1663,668; 1681,824; 1762,608; 1778,864; 1877,704; 1992,650; 2109,062; 2223,903; 2633,376; 2758,834; 2775,928
T. atroviride	**Not related**
$[MH]^+$ 2875.128 Da	
Fragment masses	112,094; 169,085; 175,132; 201,088; 240,150; 257,172; 272,134; 274,186; 311,156; 316,139; 328,175; 345,212; 369,169; 387,152; 399,221; 440,198; 445,182; 474,264; 484,204; 504,154; 527,265; 545,299; 555,267; 599,257; 615,200; 625,285; 643,290; 660,325; 670,289; 714,278; 771,372; 789,385; 799,350; 829,302; 882,366; 900,420; 918,477; 928,442; 972,487; 1029,518; 1043,452; 1047,529; 1114,497; 1127,535; 1144,578; 1162,576; 1242,597; 1260,643; 1277,623; 1346,644; 1403,688; 1444,651; 1501,828; 1550,777; 1645,840; 1663,903; 1675,482; 1681,849; 1761,850; 1778,773; 1878,045; 1896,055; 1975,940; 1989,295; 1993,005; 2081,507; 2089,773; 2108,208; 2178,284; 2205,533; 2223,346; 2278,295; 2321,597; 2609,842; 2618,011; 2623,475; 2708,535; 2739,882; 2743,375; 2749,260; 2757,272; 2760,147; 2766,387; 2796,126
T. atroviride	**Elongation factor 1 beta (EF1B) K.APAAEDDDDVDLFGSDDEEEDAEAVR.I + Phospho (significant)**

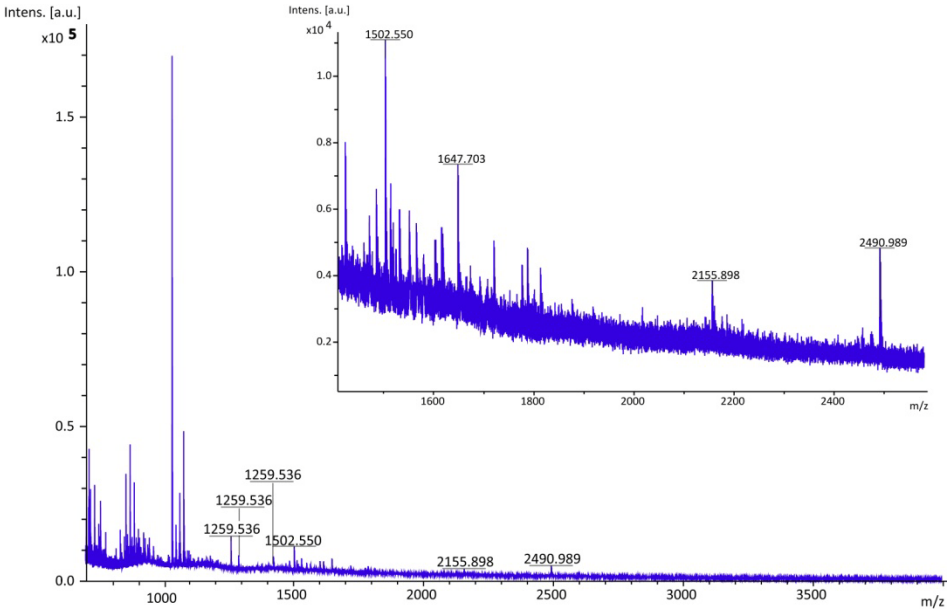


Figure 6.47 Positive ion reflector TOF - MALDI mass spectrum of 2_1_10

$[MH]^+$ 1259.536 Da	
Fragment masses	110,097; 112,115; 129,131; 154,123; 167,116; 171,141; 175,151; 197,157; 213,141; 219,120; 221,154; 223,182; 232,129; 234,065; 243,161; 250,070; 253,149; 255,160; 257,194; 288,206; 508,254; 681,942; 688,042; 773,022; 814,648; 864,771; 870,899; 877,065; 881,215; 908,710; 924,742; 1059,859; 1062,960; 1066,154; 1069,261; 1120,042; 1123,542; 1145,108; 1162,075; 1232,387; 1234,898; 1237,954; 1240,695; 1242,857
T. atroviride	**MedA like protein R.NHHSPPQSSLR.I (NOT significant)**
$[MH]^+$ 1288.544 Da	
Fragment masses	70,058; 72,049; 110,097; 112,103; 115,119; 129,129; 136,105; 154,123; 172,115; 175,154; 197,159; 221,127; 230,133; 232,168; 249,152; 251,153; 257,178; 259,145; 288,206; 345,241; 508,360; 892,714; 896,745; 903,022; 909,162; 940,699; 946,914; 1031,464; 1085,753; 1087,804; 1095,121; 1098,275; 1238,529; 1240,669; 1266,58
T. atroviride	**Not related**
$[MH]^+$ 1422.532 Da	

Fragment masses	110,125; 112,147; 129,173; 154,168; 172,189; 175,221; 197,229; 232,256; 257,258; 288,312; 293,222; 373,242; 508,422; 525,348; 1032,805; 1217,796; 1222,017; 1225,150; 1317,789; 1325,210; 1343,282; 1393,016; 1400,978
T. atroviride	**Not related**
$[MH]^+$ 1502.550 Da	
Fragment masses	110,102; 112,130; 129,151; 154,143; 175,189; 197,196; 232,208; 257,224; 286,214; 288,259; 345,290; 355,223; 508,353; 588,319; 623,343; 908,602; 931,053; 962,739; 1015,818; 1032,655; 1059,942; 1113,881; 1120,081; 1151,752; 1299,798; 1302,908; 1305,976; 1309,140; 1311,225; 1313,405; 1405,099; 1423,134; 1465,486; 1484,531
T. atroviride	**Not related**
$[MH]^+$ 1647.703 Da	
Fragment masses	110,088; 112,111; 129,129; 154,122; 169,126; 175,144; 197,166; 508,349; 543,293; 618,394; 1032,567; 1231,827; 1265,033; 1404,887; 1448,881; 1533,211; 1608,806
T. atroviride	**Not related**
$[MH]^+$ 2155.898 Da	
Fragment masses	112,116; 691,255; 799,484; 910,382; 942,556; 1032,604; 1040,523; 1120,592; 1125,775; 1152,710; 1250,701; 1337,819; 1517,201; 1683,163; 1767,680; 1796,795; 1812,347; 2091,114; 2113,422
T. atroviride	**Not related**
$[MH]^+$ 2490.989 Da	
Fragment masses	255,169; 272,187; 386,253; 430,246; 499,275; 527,309; 545,296; 766,451; 792,443; 810,439; 879,460; 907,434; 925,483; 1138,571; 1156,628; 1271,737; 1502,870; 2104,767; 2425,992; 2450,782
T. atroviride	**Not related**

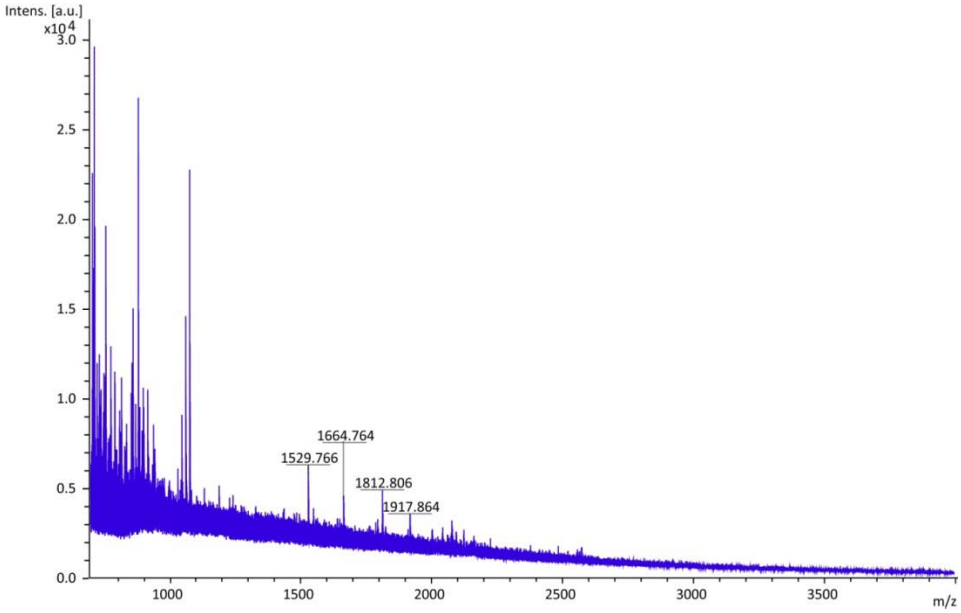


Figure 6.48 Positive ion reflector TOF - MALDI mass spectrum of 2_1_11

$[MH]^+$ 1529.766 Da	
Fragment masses	84,078; 110,080; 112,098; 129,129; 154,124; 175,157; 197,163; 288,237; 399,212; 484,277; 1032,524; 1135,616; 1324,667; 1329,824; 1332,994; 1415,320; 1463,813; 1474,367; 1478,693; 1482,045; 1485,242; 1500,124; 1503,249; 1505,941; 1509,407; 1512,393
T. atroviride	**Fungal specific transcription factor K.KGMYPFTLIR.A (NOT significant)**
$[MH]^+$ 1664.764 Da	
Fragment masses	86,097; 110,102; 129,142; 154,142; 175,181; 197,189; 226,201; 372,210;

	471,318; 1080,624; 1205,820; 1464,955; 1606,344; 1609,636; 1611,858; 1614,978; 1632,465; 1636,496; 1640,027; 1642,486; 1645,254
T. atroviride	**Not related**
$[MH]^+$ 1812.806 Da	
Fragment masses	70,065; 86,096; 110,092; 112,108; 115,105; 129,128; 136,111; 154,127; 172,140; 175,161; 197,167; 1707,052; 1752,326; 1754,388; 1760,947; 1764,208; 1777,548; 1789,056; 1793,615
T. atroviride	**Not related**
$[MH]^+$ 1917.864 Da	
Fragment masses	70,079; 74,184; 84,100; 110,119; 112,132; 115,133; 129,166; 197,228; 1866,111; 1873,369
T. atroviride	**Not related**

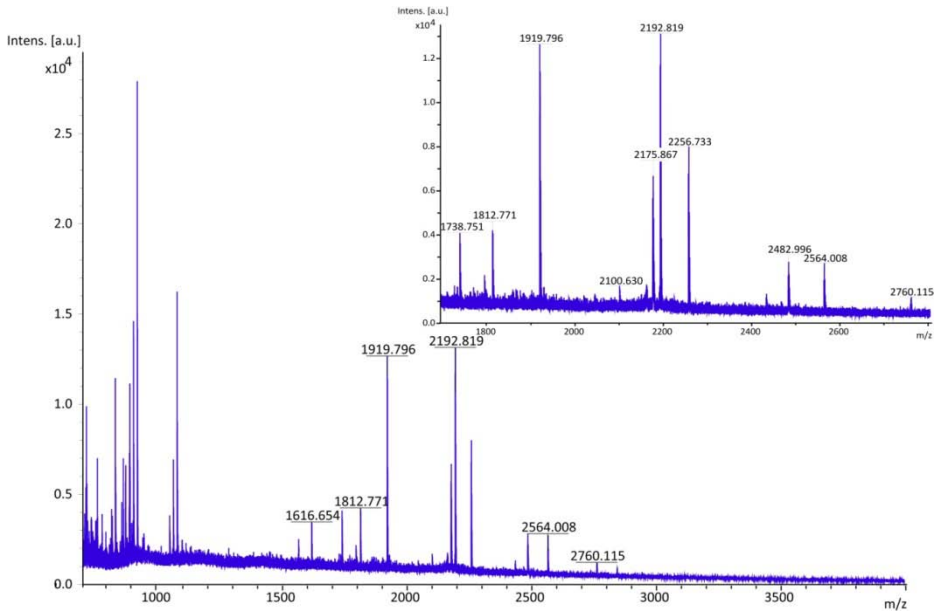


Figure 6.49 Positive ion reflector TOF - MALDI mass spectrum of 2_1_12

$[MH]^+$ 1616.654 Da	
Fragment masses	84,074; 110,087; 112,106; 115,106; 129,124; 136,105; 154,121; 167,119; 171,136; 175,145; 186,146; 197,159; 200,167; 226,177; 244,150; 288,219; 315,186; 502,253; 687,342; 745,404; 816,385; 844,429; 872,426; 1155,687; 1244,615; 1281,656; 1373,836; 1408,462; 1521,321; 1584,838
T. atroviride	**Not related**
$[MH]^+$ 1738.751 Da	
Fragment masses	110,103; 112,122; 129,146; 154,134; 197,178; 209,210; 237,183; 522,291; 588,359; 693,439; 778,493; 804,534; 806,532; 933,572; 935,593; 1151,754; 1222,803; 1350,989; 1503,225; 1545,095; 1681,439; 1688,745; 1696,772; 1704,724
T. atroviride	**Copper/Zinc superoxid dismutase R.HVGDLGNIETDAQGNAK.G (significant)**
$[MH]^+$ 1812.771 Da	
Fragment masses	110,093; 112,101; 115,111; 129,131; 154,122; 197,170; 227,155; 713,424; 970,600; 1007,558; 1044,490; 1320,650; 1378,684; 1425,774; 1611,993; 1706,890; 1752,727; 1760,707; 1777,500; 1785,237
T. atroviride	**Not related**
$[MH]^+$ 1919.796 Da	
Fragment masses	70,073; 84,104; 101,112; 110,121; 112,137; 115,139; 129,160; 136,131; 154,169; 172,179; 175,180; 186,190; 197,237; 226,216; 244,196; 284,239; 373,245; 431,214; 502,352; 530,389; 547,402; 618,448; 687,461; 765,586; 872,564; 1031,781; 1048,762; 1119,823; 1176,907; 1233,942; 1548,334; 1805,683; 1873,952; 1896,990

T. atroviride	**Plectin/S10 domain containing protein R.DAGEGKEGGAPGEFAPQFR.G (significant)**
$[MH]^+$ 2100.630 Da	
Fragment masses	110,067; 129,104; 155,120; 793,368; 864,409; 1027,490; 1141,605; 1327,658; 1986,403; 2003,366; 2041,837; 2049,533; 2057,680; 2065,317
T. atroviride	**HMG box protein R.YEDEKQAYNADQEESS.- + Phospho (NOT significant)**
$[MH]^+$ 2175.867 Da	
Fragment masses	70,045; 74,093; 84,075; 101,084; 110,083; 112,097; 115,095; 129,116; 136,093; 157,132; 186,127; 201,148; 229,162; 240,182; 255,128; 275,202; 303,156; 449,273; 466,299; 483,258; 492,318; 547,303; 564,329; 676,380; 693,401; 710,458; 727,473; 804,462; 821,485; 904,505; 921,533; 932,496; 975,552; 992,576; 1003,540; 1027,671; 1084,550; 1138,634; 1155,616; 1200,648; 1298,670; 1385,640; 1411,734; 1466,707; 1483,760; 1856,287; 2071,894; 2113,670; 2124,971; 2131,397; 2140,928; 2158,960
T. atroviride	**Not related**
$[MH]^+$ 2192.819 Da	
Fragment masses	101,079; 110,087; 112,096; 115,093; 129,112; 136,089; 157,128; 201,113; 229,127; 255,127; 259,146; 275,187; 344,129; 368,186; 385,181; 449,276; 466,246; 483,208; 500,224; 547,314; 564,354; 568,275; 585,299; 596,322; 667,339; 684,385; 693,406; 710,376; 804,456; 812,428; 821,507; 932,504; 1084,708; 1186,764; 1214,708; 1414,818; 1483,607; 1543,969; 1673,000; 1850,321; 1917,376; 1948,358; 2064,660; 2078,637; 2132,463; 2137,641; 2143,346; 2149,576; 2159,267; 2176,210
T. atroviride	**40S ribosomal protein S19 R.DLDRIAQTTAEAEEEEDEE.- (NOT significant)**
$[MH]^+$ 2256.733 Da	
Fragment masses	70,088; 84,108; 110,113; 112,133; 115,130; 129,155; 136,128; 275,237; 320,251; 421,300; 449,299; 466,331; 492,357; 547,345; 564,332; 665,439; 676,413; 693,429; 710,469; 804,513; 821,538; 921,650; 932,615; 949,598; 975,632; 992,713; 1003,645; 1020,723; 1138,716; 1155,806; 1166,755; 1183,838; 1200,815; 1280,813; 1297,888; 1340,875; 1368,971; 1385,980; 1467,008; 1484,040; 1565,328; 1741,311; 1758,348; 1838,415; 1856,455; 1884,336; 2054,695; 2072,640; 2097,794; 2114,644; 2124,883; 2132,005; 2140,061; 2142,860; 2150,270; 2159,907; 2177,948
T. atroviride	**HMG box protein K.RYEDEKQAYNADQEDESS.- + Phospho (significant)**
$[MH]^+$ 2482.996 Da	
Fragment masses	227,117; 244,200; 326,224; 425,291; 487,283; 554,320; 574,370; 584,338; 673,457; 683,396; 782,551; 802,522; 812,416; 866,464; 883,493; 901,495; 911,520; 1030,595; 1159,678; 1258,745; 1357,844; 1583,981; 1769,181; 1981,324; 2106,285; 2145,313; 2354,667; 2402,088; 2410,413; 2417,996; 2426,153; 2433,335; 2436,454; 2441,603; 2449,355
T. atroviride	**Not related**
$[MH]^+$ 2564.008 Da	
Fragment masses	227,149; 244,214; 315,265; 326,211; 425,322; 455,256; 487,296; 554,367; 574,358; 584,360; 625,371; 655,445; 673,442; 683,437; 698,414; 754,478; 782,498; 795,410; 802,536; 812,464; 853,540; 866,500; 883,506; 901,607; 911,579; 981,541; 1010,677; 1030,682; 1080,728; 1092,628; 1097,688; 1141,768; 1159,774; 1258,836; 1269,832; 1340,878; 1357,932; 1486,944; 1566,010; 1584,128; 1655,160; 1769,291; 1884,714; 2012,419; 2241,955; 2450,060; 2467,065; 2485,078; 2498,194; 2507,576; 2513,444; 2521,785
T. atroviride	**DEAD like helicases containing protein K.LTATMAVVLTWMDEAPDDKILSK.F (NOT significant)**
$[MH]^+$ 2760.115 Da	
Fragment masses	257,191; 1148,625; 2665,188; 2691,090; 2697,916; 2713,796
T. atroviride	**Not related**

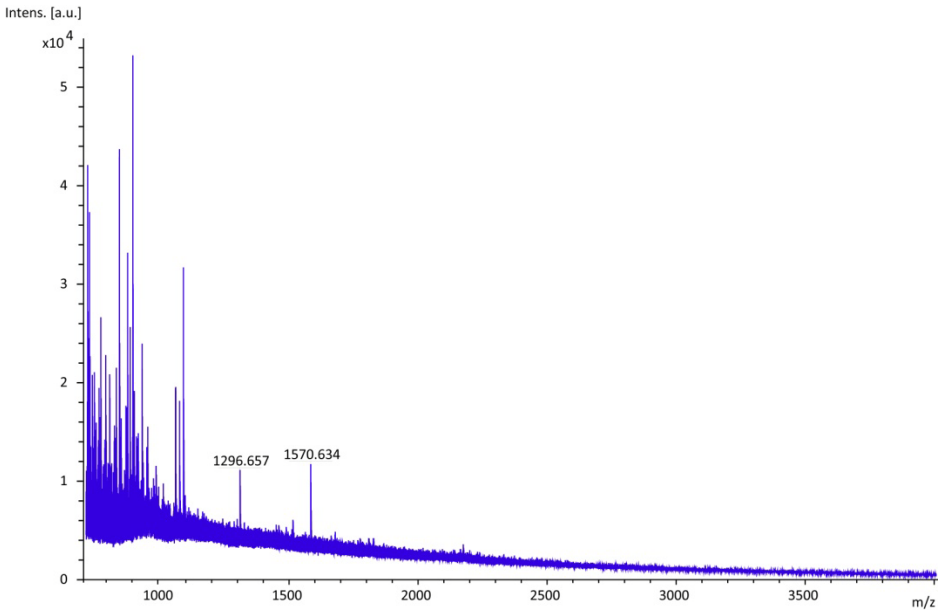


Figure 6.50 Positive ion reflector TOF - MALDI mass spectrum of 2_1_13

$[MH]^+$ 1296.657 Da	
Fragment masses	70,038; 72,054; 81,045; 84,070; 86,083; 95,077; 98,069; 100,089; 102,081; 104,125; 107,079; 110,085; 112,098; 115,105; 121,089; 123,129; 126,106; 129,122; 135,142; 137,127; 139,113; 141,117; 143,125; 149,111; 154,119; 157,126; 159,136; 167,129; 171,138; 175,148; 179,125; 181,137; 183,137; 185,142; 187,139; 197,163; 200,146; 202,155; 207,142; 209,156; 211,159; 213,150; 215,164; 217,155; 219,158; 221,155; 226,164; 229,153; 235,153; 237,158; 240,184; 243,150; 245,164; 247,164; 249,161; 251,167; 254,176; 257,170; 259,153; 262,166; 269,189; 271,183; 273,160; 275,164; 277,160; 283,193; 288,209; 294,151; 311,181; 354,196; 855,014; 908,865; 915,104; 928,815; 946,663; 1082,276; 1091,617; 1097,861; 1102,069; 1104,197; 1245,524; 1249,498; 1267,182; 1270,603; 1273,839; 1277,172; 1279,705
T. atroviride	**Not related**
$[MH]^+$ 1570.634 Da	
Fragment masses	84,088; 86,108; 100,108; 104,157; 110,100; 112,122; 115,117; 120,125; 129,143; 136,121; 141,124; 143,143; 154,143; 157,163; 169,144; 172,152; 175,182; 184,174; 186,174; 190,165; 192,177; 197,188; 200,204; 202,186; 205,176; 207,171; 209,180; 212,203; 214,205; 217,178; 219,182; 221,175; 223,208; 226,209; 229,187; 231,194; 233,191; 235,195; 240,224; 243,197; 246,204; 252,203; 254,218; 257,231; 259,213; 262,208; 268,225; 270,241; 272,214; 275,204; 277,207; 286,228; 288,250; 292,228; 294,228; 298,233; 312,241; 314,238; 316,231; 333,255; 684,415; 813,455; 885,419; 917,436; 1056,672; 1173,653; 1325,758; 1362,598; 1365,674; 1367,786; 1369,807; 1371,881; 1377,155; 1379,198; 1513,364; 1519,788; 1535,889; 1538,055; 1547,102; 1550,915
T. atroviride	**Not related**

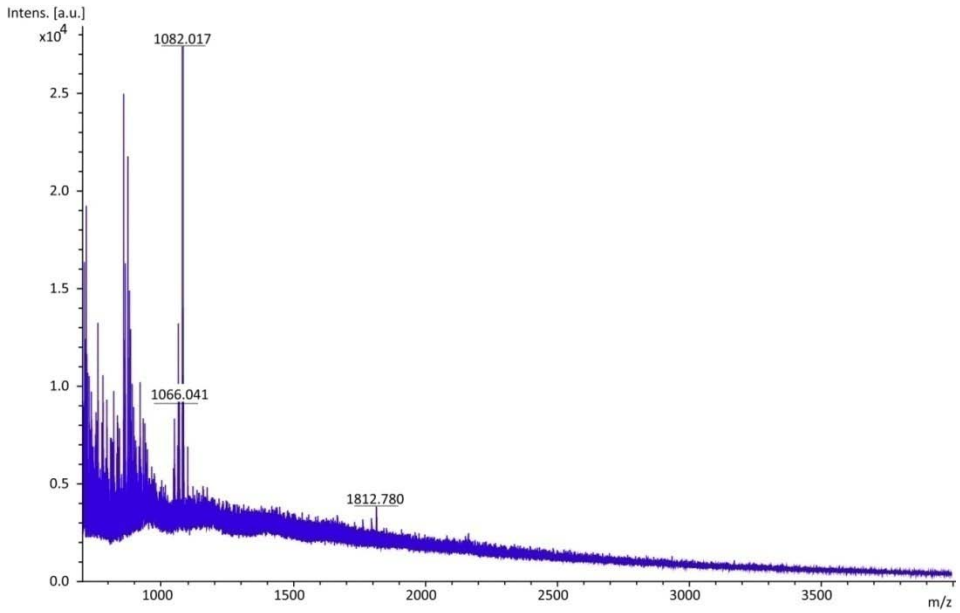


Figure 6.51 Positive ion reflector TOF - MALDI mass spectrum of 2_1_14

$[MH]^+$ 1066.041 Da	
Fragment masses	70,093; 72,051; 86,131; 95,119; 98,117; 100,124; 102,128; 107,120; 110,125; 112,137; 115,136; 129,158; 136,140; 154,160; 171,176; 175,183; 185,177; 197,204; 231,212; 234,117; 245,196; 250,126; 257,216; 294,203; 311,184; 585,238; 638,025; 649,153; 651,189; 666,102; 675,894; 682,028; 688,158; 698,601; 703,974; 709,873; 719,857; 731,175; 783,085; 820,863; 827,104; 831,324; 845,690; 855,413; 864,863; 871,093; 877,426; 908,780; 961,302; 1003,623; 1016,142; 1041,114
T. atroviride	**Not related**
$[MH]^+$ 1082.017 Da	
Fragment masses	70,091; 72,091; 84,111; 86,125; 95,117; 98,133; 100,131; 102,121; 104,168; 107,118; 110,134; 112,145; 115,150; 121,148; 125,151; 127,154; 129,167; 131,147; 133,161; 136,163; 141,157; 143,174; 151,147; 154,168; 157,181; 159,176; 167,178; 171,191; 175,186; 177,188; 184,189; 186,189; 188,209; 190,158; 192,185; 197,216; 201,196; 203,207; 209,211; 213,215; 215,210; 218,222; 223,204; 225,208; 227,215; 229,223; 231,212; 234,124; 238,219; 240,220; 242,245; 245,220; 247,222; 252,230; 254,231; 257,235; 259,218; 261,218; 266,216; 268,236; 270,272; 273,245; 277,234; 286,253; 288,277; 294,215; 301,233; 311,201; 314,243; 585,258; 644,074; 650,145; 665,969; 681,867; 687,902; 691,971; 698,037; 704,134; 719,875; 725,714; 731,176; 767,431; 820,652; 836,902; 843,123; 847,331; 854,843; 864,607; 870,621; 876,809; 880,897; 887,101; 893,422; 924,672; 961,431; 968,311; 977,461; 979,627; 981,937; 997,460; 1015,522; 1024,723; 1026,943; 1032,228; 1041,405; 1058,236; 1059,829
T. atroviride	**Not related**
$[MH]^+$ 1812.780 Da	
Fragment masses	110,083; 112,100; 115,101; 129,124; 154,120; 172,138; 197,165; 1753,511; 1777,222
T. atroviride	**Not related**

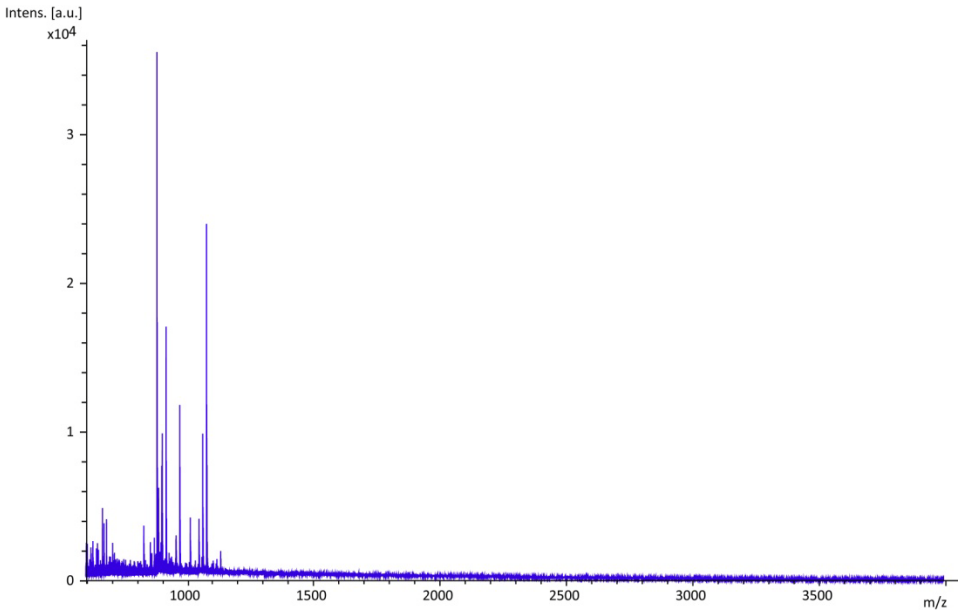


Figure 6.52 Positive ion reflector TOF - MALDI mass spectrum of 2_2_1

No relevant Peaks for PSD analysis

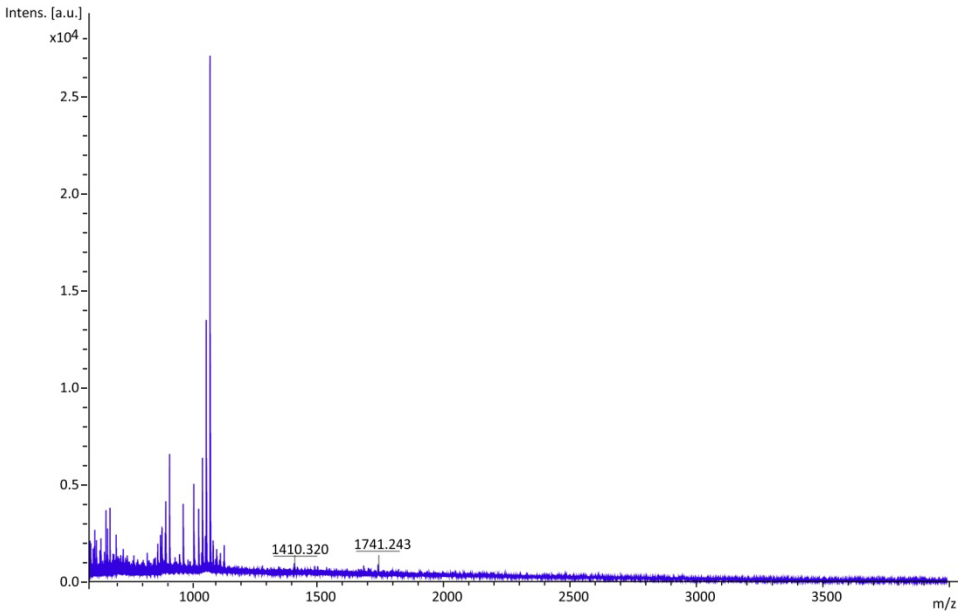


Figure 6.53 Positive ion reflector TOF - MALDI mass spectrum of 2_2_2

$[MH]^+$ 1410.320 Da	
Fragment masses	70,062; 86,105; 104,152; 110,103; 112,124; 115,122; 120,129; 129,148; 136,139; 154,152; 157,179; 167,152; 169,183; 171,176; 175,188; 184,166; 186,203; 197,192; 201,178; 212,210; 214,202; 216,187; 227,195; 230,208; 232,235; 235,206; 245,184; 247,189; 255,204; 258,212; 261,215; 268,228; 270,220; 272,232; 284,208; 286,221; 288,233; 298,228; 311,223; 314,227; 316,236; 325,245; 327,223; 330,232; 343,233; 427,265; 455,272; 508,308; 902,341; 1023,916; 1032,449; 1211,873; 1217,107; 1306,629; 1357,333; 1360,589; 1362,757
T. atroviride	**Not related**
$[MH]^+$ 1741.243 Da	
Fragment masses	70,046; 84,060; 86,080; 101,059; 110,055; 112,076; 115,079; 129,099; 136,069;

	154,092; 167,077; 172,102; 175,117; 187,088; 195,090; 197,125; 212,098; 230,109; 255,140; 272,156; 345,146; 398,168; 495,296; 528,308; 608,307; 854,359; 872,327; 925,296; 1032,330; 1122,366; 1187,367; 1252,325; 1380,340; 1458,510; 1631,283; 1634,441; 1636,527; 1641,973; 1687,367; 1690,528; 1711,832; 1715,019; 1722,323
T. atroviride	**Not related**

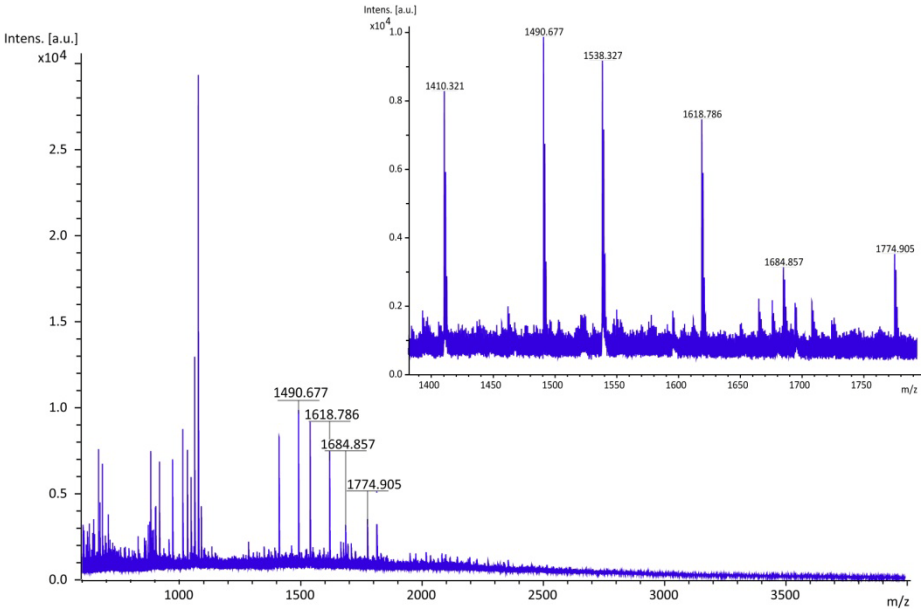


Figure 6.54 Positive ion reflector TOF - MALDI mass spectrum of 2_2_3

$[MH]^+$ 1410.321 Da	
Fragment masses	70,060; 72,076; 84,085; 86,117; 102,084; 104,130; 110,103; 112,125; 115,126; 120,132; 129,151; 133,134; 136,133; 141,152; 154,155; 157,165; 167,154; 169,180; 172,156; 175,188; 181,161; 183,186; 185,167; 187,158; 197,192; 201,184; 203,165; 209,190; 214,211; 217,192; 219,208; 221,180; 226,209; 229,205; 231,200; 235,191; 237,209; 241,197; 243,218; 245,187; 247,225; 252,215; 254,225; 256,226; 258,207; 260,232; 262,217; 266,223; 268,236; 270,227; 272,254; 276,224; 284,233; 286,234; 288,234; 298,248; 301,230; 315,265; 326,248; 332,233; 336,234; 343,263; 353,271; 367,246; 380,272; 413,265; 427,281; 444,294; 455,288; 472,294; 508,300; 526,323; 543,327; 554,337; 652,436; 673,361; 690,361; 806,437; 885,278; 902,303; 920,563; 1032,442; 1146,360; 1212,987; 1219,288; 1261,531; 1279,235; 1300,315; 1303,471; 1306,618; 1310,870; 1318,260; 1342,511; 1355,150; 1357,312; 1359,456; 1361,703; 1364,934; 1368,258; 1374,764
T. atroviride	**Elongation factor 3 (EF-3) K.RGEEVFSDEDDL.- (NOT significant)**
$[MH]^+$ 1490.677 Da	
Fragment masses	70,038; 84,048; 86,073; 102,052; 110,052; 112,082; 115,075; 120,077; 129,102; 136,084; 141,086; 154,083; 157,111; 167,096; 169,108; 172,100; 175,123; 181,102; 183,107; 185,107; 187,087; 197,116; 201,128; 214,128; 217,111; 227,115; 229,114; 232,133; 235,112; 237,119; 240,129; 242,139; 244,116; 246,135; 254,144; 257,135; 259,112; 261,122; 268,152; 270,136; 272,143; 274,145; 276,134; 285,149; 288,154; 290,110; 294,136; 296,122; 298,129; 301,120; 310,117; 315,142; 326,127; 330,141; 332,111; 343,140; 361,153; 365,152; 413,141; 427,148; 444,168; 455,151; 472,165; 508,203; 526,155; 543,206; 554,176; 571,203; 690,238; 718,260; 787,285; 805,289; 822,244; 885,263; 902,325; 913,427; 920,307; 968,621; 1000,310; 1031,404; 1048,320; 1129,456; 1146,510; 1155,937; 1164,602; 1170,517; 1244,536; 1261,623; 1270,335; 1273,215; 1279,677; 1287,063; 1289,523; 1359,711; 1375,907;

	1380,341; 1383,352; 1392,878; 1410,908; 1441,468; 1444,754; 1467,100
T. atroviride	**Elongation factor 3 (EF-3) K.RGEEVFSDEDDL.- + Phospho (significant)**
$[MH]^+$ 1538.327 Da	
Fragment masses	70,057; 84,080; 101,109; 110,075; 112,099; 115,101; 120,098; 129,122; 136,096; 141,122; 152,119; 157,139; 159,107; 167,117; 169,137; 172,119; 175,145; 185,140; 187,110; 195,125; 197,135; 201,140; 203,134; 209,146; 212,150; 214,144; 217,126; 226,155; 229,151; 231,135; 235,135; 237,150; 243,184; 246,181; 250,155; 252,149; 255,143; 259,129; 262,142; 268,199; 272,173; 276,181; 278,143; 280,189; 282,169; 285,216; 288,181; 292,156; 294,145; 296,141; 298,156; 301,163; 303,188; 316,148; 326,176; 332,148; 334,185; 340,171; 342,160; 345,205; 354,164; 360,182; 362,176; 367,183; 369,184; 383,174; 385,194; 387,194; 400,190; 413,197; 415,178; 426,235; 431,212; 443,243; 455,207; 461,184; 471,242; 508,260; 555,265; 572,268; 583,255; 600,284; 648,254; 654,305; 671,309; 682,280; 699,285; 713,350; 818,345; 1015,255; 1030,243; 1032,333; 1048,469; 1089,344; 1177,262; 1203,392; 1274,122; 1389,255; 1407,102; 1415,549; 1426,021; 1432,352; 1434,551; 1450,347; 1467,487; 1470,683; 1487,456; 1489,549; 1491,787; 1496,196; 1512,038; 1519,653
T. atroviride	**Elongation factor 3 (EF-3) R.KRGEEVFSDEDDL.- (significant)**
$[MH]^+$ 1618.786 Da	
Fragment masses	70,061; 72,043; 84,068; 110,056; 112,077; 115,068; 120,084; 129,090; 141,111; 155,093; 157,094; 159,075; 167,083; 175,117; 185,095; 195,093; 197,110; 201,105; 209,100; 212,101; 217,098; 226,121; 229,108; 231,100; 246,157; 250,129; 252,137; 259,104; 268,145; 272,136; 285,157; 303,144; 314,161; 316,110; 342,153; 360,161; 443,216; 471,198; 555,235; 572,254; 583,231; 600,251; 654,308; 671,308; 675,222; 682,284; 699,314; 767,294; 818,389; 846,384; 915,419; 933,393; 950,420; 1013,372; 1030,473; 1033,338; 1041,293; 1048,449; 1091,409; 1128,464; 1159,556; 1177,587; 1274,648; 1283,868; 1292,618; 1298,101; 1372,671; 1389,733; 1398,309; 1401,234; 1407,768; 1415,058; 1417,495; 1420,724; 1487,687; 1492,867; 1494,920; 1502,974; 1505,764; 1509,225; 1512,447; 1520,951; 1530,465; 1538,980; 1577,232; 1592,043
T. atroviride	**Elongation factor 3 (EF-3) R.KRGEEVFSDEDDL.- + Phospho (significant)**
$[MH]^+$ 1684.857 Da	
Fragment masses	70,055; 84,066; 101,083; 110,071; 112,091; 115,079; 120,088; 129,112; 136,081; 141,107; 154,102; 157,122; 171,114; 175,127; 181,109; 185,123; 195,116; 197,139; 199,117; 212,148; 226,150; 229,138; 268,190; 272,172; 285,207; 303,163; 316,164; 342,223; 399,273; 431,202; 471,261; 528,337; 600,333; 657,358; 756,395; 844,411; 887,423; 903,456; 972,432; 1030,442; 1087,447; 1136,568; 1308,753; 1331,421; 1423,973; 1446,445; 1457,909; 1464,445; 1474,224; 1520,433; 1545,424; 1560,552; 1563,574; 1577,451; 1587,126; 1595,451; 1616,570; 1630,325; 1634,587; 1659,071
T. atroviride	**Not significant**
$[MH]^+$ 1774.905 Da	
Fragment masses	70,066; 84,092; 86,102; 101,086; 110,079; 112,098; 115,100; 120,099; 129,117; 136,090; 141,109; 157,124; 159,108; 167,116; 175,141; 186,141; 195,118; 197,143; 209,127; 226,158; 244,159; 272,181; 399,223; 441,254; 498,235; 528,261; 627,306; 756,356; 827,444; 855,448; 1002,469; 1032,446; 1071,546; 1088,572; 1169,551; 1186,592; 1204,631; 1284,629; 1430,868; 1530,104; 1546,964; 1557,121; 1564,100; 1572,584; 1632,099; 1635,233; 1638,578; 1643,137; 1660,312; 1670,791; 1677,243; 1695,234; 1706,813; 1724,705; 1728,028; 1743,952; 1752,492; 1755,816
T. atroviride	**Not significant**

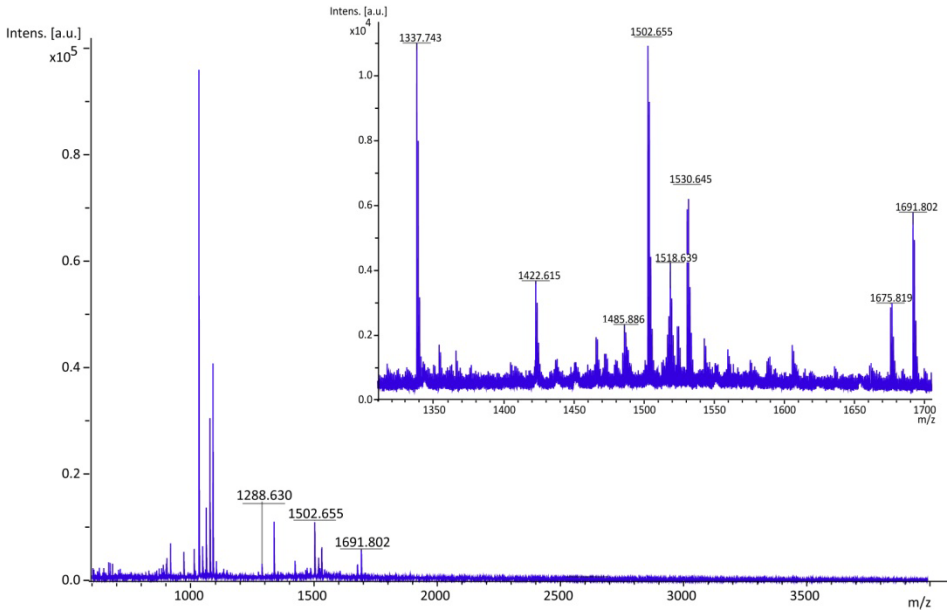


Figure 6.55 Positive ion reflector TOF - MALDI mass spectrum of 2_2_4

$[MH]^+$ 1288.630 Da	
Fragment masses	69,959; 83,978; 85,998; 100,004; 101,960; 109,976; 111,998; 114,998; 129,008; 135,977; 153,986; 157,996; 166,983; 175,015; 180,988; 194,979; 197,013; 214,997; 216,983; 226,005; 227,994; 232,007; 243,992; 248,985; 250,976; 252,968; 254,977; 256,966; 258,970; 261,991; 269,984; 272,001; 274,970; 276,983; 281,972; 285,995; 288,019; 295,979; 304,000; 309,960; 313,991; 315,976; 345,030; 365,962; 385,005; 387,027; 417,039; 508,085; 524,970; 665,958; 709,014; 781,029; 899,116; 908,657; 916,107; 943,988; 1014,908; 1030,793; 1097,779; 1114,282; 1132,461; 1187,384; 1233,682; 1235,815; 1237,804; 1240,128; 1242,401; 1244,587; 1260,587; 1262,625; 1264,375; 1266,516
T. atroviride	**Not related**
$[MH]^+$ 1337.743 Da	
Fragment masses	70,051; 84,076; 86,089; 101,096; 110,085; 112,105; 115,109; 129,128; 135,118; 138,107; 141,119; 154,119; 158,132; 167,130; 172,146; 175,162; 185,133; 188,159; 197,166; 205,139; 207,128; 213,152; 215,164; 217,138; 223,194; 229,158; 232,169; 235,159; 240,175; 245,140; 251,192; 257,198; 262,167; 269,163; 272,180; 275,150; 277,166; 286,176; 288,219; 293,149; 296,180; 304,196; 311,149; 314,183; 329,187; 331,189; 345,207; 361,229; 364,254; 373,197; 379,237; 396,237; 471,244; 484,235; 488,272; 501,234; 508,270; 525,186; 587,344; 685,328; 702,363; 751,410; 822,449; 831,382; 850,521; 946,623; 1032,265; 1087,862; 1129,386; 1135,573; 1139,764; 1142,860; 1145,057; 1234,370; 1284,112; 1286,318; 1288,289; 1290,630; 1301,877; 1307,829; 1312,033; 1314,128; 1316,745
T. atroviride	**Not related**
$[MH]^+$ 1422.615 Da	
Fragment masses	70,060; 84,069; 86,108; 110,097; 112,118; 115,115; 120,115; 129,143; 136,119; 141,150; 147,131; 154,133; 159,142; 167,146; 172,155; 175,173; 179,152; 181,147; 195,158; 197,178; 215,182; 219,149; 232,197; 242,193; 244,177; 249,201; 253,161; 255,204; 257,182; 262,176; 275,173; 286,203; 288,228; 293,157; 296,207; 298,194; 311,172; 314,217; 328,228; 345,274; 373,158; 382,229; 387,175; 391,160; 401,233; 410,225; 508,334; 518,304; 525,254; 588,316; 606,308; 623,347; 688,300; 801,386; 918,433; 988,548; 1015,524; 1032,655; 1221,752; 1229,096; 1302,531; 1307,025; 1325,032; 1343,087; 1372,486; 1375,720; 1398,913
T. atroviride	**Not related**
$[MH]^+$ 1485.886 Da	
Fragment masses	70,055; 84,079; 86,097; 110,081; 112,094; 129,122; 136,099; 154,102; 158,117; 167,121; 172,128; 175,148; 185,128; 195,118; 197,145; 213,164; 215,136; 217,130; 219,126; 232,159; 240,168; 242,183; 244,154; 249,166; 253,133;

	255,149; 257,151; 259,122; 268,150; 270,163; 272,161; 277,154; 279,136; 284,170; 286,164; 296,141; 304,176; 310,139; 314,181; 328,182; 332,186; 345,224; 355,189; 361,199; 373,130; 385,173; 387,181; 405,227; 410,173; 473,187; 508,265; 525,177; 588,225; 606,238; 623,277; 688,188; 707,298; 774,233; 836,365; 908,756; 918,372; 988,239; 1014,429; 1032,386; 1089,363; 1097,688; 1103,912; 1286,607; 1289,725; 1292,953; 1302,673; 1361,156; 1377,110; 1381,414; 1384,682; 1388,062; 1393,390; 1399,419; 1404,927; 1419,801; 1422,528; 1426,771; 1431,037; 1433,135; 1435,344; 1438,578; 1441,950; 1459,115; 1462,014; 1465,847
T. atroviride	**FAD/FMN containing dehydrogenase R.IVLKNTGHDYLGR.S (NOT significant)**
$[MH]^+$ 1502.655 Da	
Fragment masses	70,066; 84,074; 86,097; 102,076; 110,087; 112,106; 115,097; 129,128; 136,107; 141,127; 154,112; 158,121; 167,119; 172,132; 175,155; 181,132; 195,124; 197,156; 213,172; 215,156; 232,170; 242,194; 244,158; 253,141; 268,163; 275,149; 277,172; 286,173; 289,182; 296,164; 304,185; 310,154; 314,186; 329,183; 345,235; 355,209; 373,158; 508,282; 518,247; 525,213; 588,255; 606,256; 623,284; 688,224; 918,343; 1014,447; 1017,279; 1032,473; 1089,232; 1285,658; 1288,713; 1302,741; 1308,914; 1318,756; 1361,925; 1387,964; 1392,038; 1395,188; 1404,928; 1422,975; 1450,226; 1457,762; 1459,983; 1467,797; 1484,231
T. atroviride	**Not related**
$[MH]^+$ 1518.639 Da	
Fragment masses	70,036; 84,061; 86,075; 110,059; 112,079; 129,098; 136,072; 158,096; 167,090; 175,123; 183,117; 190,098; 195,092; 197,121; 201,101; 215,114; 232,146; 253,097; 257,131; 259,111; 268,132; 286,134; 301,124; 310,117; 345,210; 355,184; 361,143; 367,135; 385,152; 403,122; 410,145; 508,246; 518,211; 525,155; 588,217; 606,198; 623,228; 688,186; 812,335; 1015,257; 1032,317; 1089,217; 1135,747; 1286,526; 1302,597; 1318,719; 1324,852; 1376,849; 1403,772; 1420,911; 1423,759; 1432,419; 1436,704; 1438,877; 1467,227; 1483,918; 1495,492
T. atroviride	**Not related**
$[MH]^+$ 1530.645 Da	
Fragment masses	70,082; 84,085; 86,101; 110,089; 112,107; 115,104; 129,129; 136,091; 154,103; 158,122; 167,123; 172,133; 175,150; 195,121; 197,150; 199,136; 215,149; 232,172; 244,144; 253,132; 277,164; 286,171; 288,203; 304,171; 310,150; 314,174; 316,162; 330,140; 345,239; 355,210; 387,173; 392,159; 402,105; 405,186; 410,186; 416,192; 431,217; 482,091; 508,291; 518,251; 525,212; 588,277; 606,271; 623,286; 688,254; 801,299; 988,372; 1015,379; 1032,423; 1089,378; 1302,084; 1305,234; 1316,820; 1319,068; 1330,676; 1416,016; 1419,998; 1422,212; 1425,385; 1428,581; 1432,957; 1438,019; 1443,394; 1450,991; 1483,880; 1488,127; 1498,594; 1500,803; 1505,119; 1512,617;
T. atroviride	**Not related**
$[MH]^+$ 1675.819 Da	
Fragment masses	70,054; 84,071; 86,091; 101,068; 110,066; 112,083; 115,086; 129,101; 133,070; 136,082; 141,085; 154,084; 158,099; 167,112; 175,119; 185,102; 195,096; 197,132; 199,131; 212,099; 216,099; 229,109; 232,129; 245,105; 255,101; 262,134; 272,120; 276,080; 289,137; 301,111; 346,140; 366,149; 389,142; 401,155; 415,155; 474,196; 508,273; 572,196; 589,227; 641,223; 659,202; 676,217; 686,276; 704,266; 772,287; 774,323; 887,391; 990,418; 1000,506; 1015,338; 1032,399; 1089,425; 1098,484; 1104,474; 1115,478; 1202,557; 1275,698; 1330,659; 1389,729; 1431,840; 1483,832; 1501,914; 1519,922; 1562,259; 1567,203; 1570,482; 1574,794; 1578,050; 1585,082; 1616,104; 1625,243; 1634,071; 1640,984; 1648,868
T. atroviride	**Heat shock 70 kDa protein R.EDRCDIIANDQGNR.T (significant)**
$[MH]^+$ 1691.802 Da	
Fragment masses	70,051; 84,043; 86,085; 110,064; 112,081; 115,081; 120,084; 129,099; 133,057; 136,079; 158,095; 167,091; 172,101; 175,122; 186,115; 189,082; 197,127; 211,101; 213,104; 223,130; 229,111; 232,121; 239,093; 242,110; 244,109; 251,122; 253,094; 255,121; 272,136; 276,118; 289,115; 345,143; 352,154; 359,135; 404,138; 431,218; 474,290; 508,243; 533,184; 551,192; 589,287; 624,240; 642,241; 659,269; 666,223; 670,239; 676,263; 704,283; 755,305; 764,312; 783,301; 840,304; 844,388; 852,272; 879,366; 909,316; 1000,434; 1015,303; 1022,417; 1032,361; 1067,341; 1089,339;

	1141,428; 1159,539; 1202,225; 1260,615; 1308,516; 1403,778; 1518,968; 1567,989; 1584,986; 1588,644; 1590,824; 1595,182; 1615,010; 1631,830; 1634,943; 1641,442; 1648,014; 1657,670; 1661,881; 1673,359
T. atroviride	**Heat shock 70 kDa protein K.STAGDTHLGGEDFDNR.L (significant)**

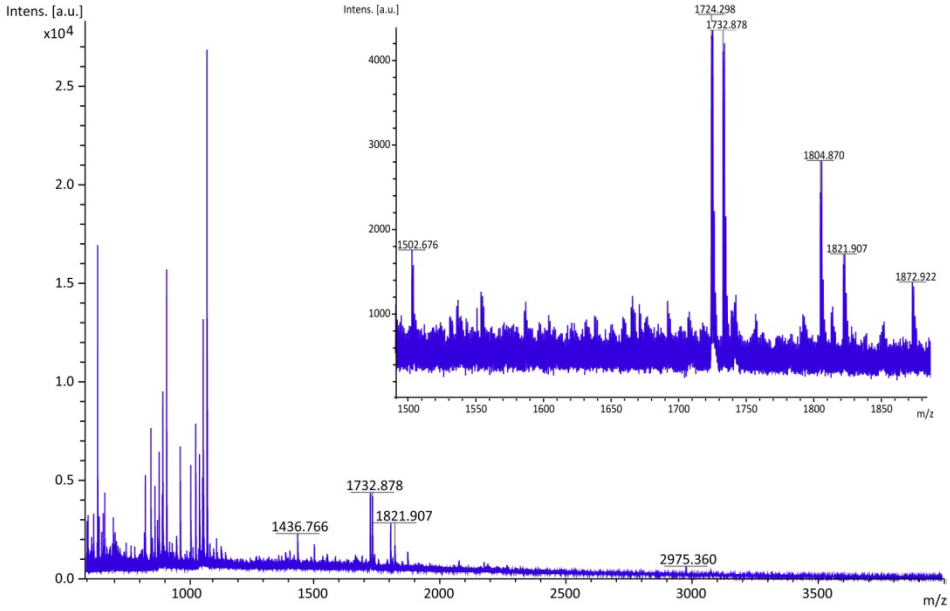


Figure 6.56 Positive ion reflector TOF - MALDI mass spectrum of 2_2_5

$[MH]^+$ 1436.766 Da	
Fragment masses	70,071; 84,092; 86,109; 101,108; 110,115; 112,135; 115,136; 120,124; 129,161; 136,138; 147,129; 154,162; 157,170; 159,171; 169,188; 171,187; 175,205; 181,184; 185,203; 187,182; 193,204; 195,191; 197,214; 199,212; 201,196; 209,202; 212,221; 214,221; 216,214; 223,223; 227,235; 229,235; 232,236; 235,229; 237,231; 240,239; 243,224; 246,249; 249,236; 252,247; 255,242; 258,228; 262,243; 266,226; 268,243; 270,254; 272,254; 278,241; 288,281; 294,252; 298,247; 303,283; 311,274; 313,285; 323,254; 326,264; 328,265; 361,299; 365,278; 508,399; 672,390; 760,996; 766,399; 804,985; 826,259; 865,036; 871,134; 887,370; 909,008; 930,502; 1000,758; 1032,460; 1044,748; 1054,081; 1097,969; 1119,513; 1135,568; 1233,691; 1237,901; 1240,022; 1243,186; 1324,338; 1327,382; 1342,196; 1382,369; 1385,623; 1388,787; 1393,206; 1404,941; 1407,284; 1410,130; 1414,580
T. atroviride	**Not related**
$[MH]^+$ 1502.676 Da	
Fragment masses	70,051; 84,076; 86,092; 101,083; 110,085; 112,107; 115,103; 129,128; 136,102; 159,129; 167,116; 175,156; 181,115; 185,136; 187,129; 195,126; 197,150; 201,141; 207,117; 209,137; 215,146; 217,136; 226,168; 230,150; 232,166; 258,163; 272,192; 276,167; 286,182; 288,184; 296,187; 304,192; 310,173; 314,174; 316,181; 345,209; 357,186; 508,278; 588,253; 623,259; 633,257; 685,280; 908,551; 930,849; 1015,526; 1032,481; 1059,856; 1097,380; 1103,480; 1113,676; 1119,889; 1132,624; 1135,255; 1138,737; 1151,465; 1157,518; 1286,948; 1292,398; 1302,663; 1305,754; 1308,962; 1323,781; 1392,004; 1399,631; 1404,960; 1423,003; 1475,892; 1483,461
T. atroviride	**Not related**
$[MH]^+$ 1724.298 Da	
Fragment masses	70,044; 86,076; 101,070; 110,059; 112,081; 115,079; 120,074; 129,101; 136,076; 147,101; 155,083; 157,087; 159,103; 167,087; 171,097; 175,114; 195,100; 197,118; 200,107; 209,120; 211,134; 213,091; 217,093; 221,114; 225,131; 227,106; 230,106; 240,116; 242,133; 244,127; 249,106; 255,113; 258,118;

	305,173; 311,135; 318,140; 329,147; 370,153; 419,232; 434,193; 447,171; 482,094; 527,176; 562,227; 568,215; 584,287; 611,184; 633,271; 715,269; 744,263; 761,307; 798,220; 816,252; 833,244; 834,262; 886,304; 902,300; 925,276; 1017,297; 1030,388; 1088,328; 1135,474; 1145,338; 1173,341; 1214,363; 1220,433; 1324,474; 1330,589; 1334,673; 1340,809; 1342,875; 1513,435; 1521,714; 1529,830; 1578,178; 1615,351; 1619,676; 1662,258; 1673,716; 1689,076; 1698,449; 1705,875
T. atroviride	**Ribosome associated chaperon zuotin R.TFSEDDRIQAQESAK.K (NOT significant)**
$[MH]^+$ 1732.878 Da	
Fragment masses	70,050; 84,051; 86,071; 101,070; 110,065; 113,067; 115,072; 120,072; 129,101; 136,080; 147,105; 157,104; 167,105; 175,121; 185,099; 195,102; 200,114; 217,102; 221,116; 244,107; 249,130; 255,111; 258,118; 267,089; 271,107; 276,131; 305,191; 315,125; 329,154; 370,162; 454,155; 482,155; 529,223; 546,221; 562,261; 611,180; 645,280; 668,220; 769,250; 797,242; 808,347; 814,276; 897,286; 925,320; 936,402; 1030,425; 1060,382; 1088,382; 1099,388; 1122,504; 1145,389; 1187,498; 1244,512; 1251,630; 1324,414; 1330,468; 1340,628; 1343,684; 1346,792; 1358,669; 1364,936; 1388,747; 1457,778; 1529,618; 1534,938; 1537,952; 1586,986; 1596,548; 1618,078; 1662,446; 1680,570; 1689,016; 1706,060
T. atroviride	**Rossmann-fold NAD(P)$^+$ binding protein (FAD-binding containing protein, FAD-Monooxygenase) R.DTQHEGEQYVGNVEK.H (significant)**
$[MH]^+$ 1804.870 Da	
Fragment masses	70,063; 84,085; 86,104; 101,093; 110,091; 112,118; 115,113; 120,113; 129,139; 136,109; 167,142; 175,168; 200,148; 227,166; 229,166; 242,177; 329,287; 562,285; 633,364; 761,441; 816,391; 833,415; 874,485; 1030,630; 1074,527; 1110,636; 1128,652; 1145,684; 1216,651; 1260,759; 1389,883; 1579,119; 1589,840; 1596,734; 1605,931; 1663,302; 1666,806; 1677,130; 1689,352; 1693,415; 1695,620; 1699,948; 1707,352; 1725,386; 1742,182; 1752,591
T. atroviride	**Ribosome associated chaperon zuotin R.TFSEDDRIQAQESAK.K + Phospho (significant)**
$[MH]^+$ 1821.907 Da	
Fragment masses	70,070; 86,092; 101,101; 110,096; 112,108; 115,099; 120,102; 129,134; 136,103; 175,152; 259,177; 373,204; 488,239; 687,344; 705,339; 785,300; 833,481; 1013,549; 1030,612; 1037,542; 1145,581; 1389,518; 1433,790; 1551,289; 1578,306; 1589,431; 1596,217; 1689,344; 1696,507; 1706,315; 1709,377; 1724,357; 1742,398; 1770,785; 1794,706
T. atroviride	**Not related**
$[MH]^+$ 1872.922Da	
Fragment masses	70,057; 74,173; 86,103; 110,097; 112,113; 115,111; 129,140; 158,141; 175,163; 185,172; 245,152; 262,163; 364,185; 448,216; 473,184; 527,183; 563,266; 661,283; 758,355; 775,381; 874,446; 989,524; 1012,564; 1032,591; 1118,576; 1145,694; 1324,693; 1347,100; 1482,868; 1551,364; 1760,493; 1763,655; 1768,975; 1773,206
T. atroviride	**Ribosome associated chaperon zuotin R.SFEYLDEDVPDDGESR.D(significant)**
$[MH]^+$ 2975.360 Da	
Fragment masses	73,972; 175,131; 226,137; 355,187; 628,341; 697,357; 825,385; 1051,500; 1069,613; 1122,593; 1209,621; 1296,787; 1383,729; 1608,912; 1680,093; 1766,974; 1935,100; 2516,763; 2733,105; 2874,698; 2905,333; 2950,285
T. atroviride	**Not related**

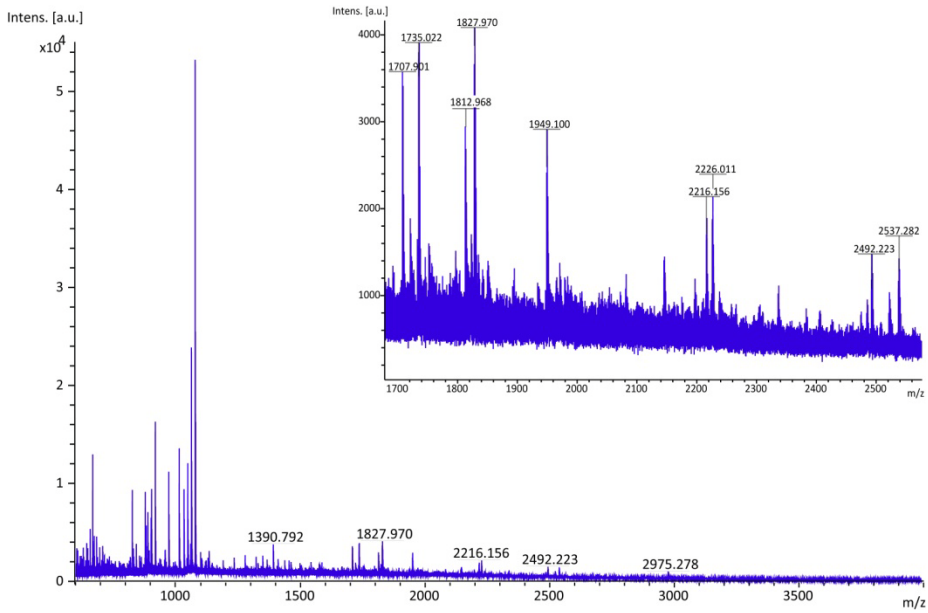


Figure 6.57 Positive ion reflector TOF - MALDI mass spectrum of 2_2_6

$[MH]^+$ 1390.792 Da	
Fragment masses	70,052; 84,073; 86,094; 100,082; 104,140; 110,090; 112,113; 115,114; 120,131; 129,137; 136,126; 138,116; 143,143; 147,135; 154,130; 157,159; 159,149; 169,157; 172,149; 175,178; 186,171; 197,172; 201,167; 209,191; 215,204; 217,174; 225,179; 227,206; 229,183; 232,200; 235,175; 243,203; 246,219; 252,192; 254,210; 257,194; 259,188; 262,215; 264,189; 266,202; 268,209; 270,219; 272,210; 274,219; 282,203; 286,211; 288,233; 290,191; 292,213; 295,196; 299,221; 301,210; 311,211; 313,235; 327,198; 341,229; 449,272; 466,281; 537,326; 645,343; 1008,121; 1180,439; 1197,106; 1319,555; 1323,587; 1340,499; 1343,718; 1347,049; 1364,220; 1365,987; 1368,220; 1372,018
T. atroviride	**Not related**
$[MH]^+$ 1707.091 Da	
Fragment masses	70,046; 84,066; 86,089; 101,068; 110,058; 112,080; 115,072; 129,093; 136,077; 154,080; 157,108; 172,106; 175,115; 186,110; 197,118; 209,093; 212,103; 215,122; 217,095; 226,103; 240,133; 244,086; 272,125; 345,126; 473,161; 544,179; 640,186; 663,283; 673,195; 753,287; 829,264; 899,327; 1032,315; 1494,273; 1506,665; 1559,107; 1577,134; 1635,511; 1639,690; 1644,172; 1655,392; 1658,756; 1660,895; 1664,092; 1682,276; 1685,873; 1689,162
T. atroviride	**Not related**
$[MH]^+$ 1735.022 Da	
Fragment masse s	70,063; 84,083; 86,094; 98,102; 101,086; 110,084; 112,102; 115,105; 129,122; 136,085; 143,134; 147,108; 154,113; 159,113; 169,115; 171,126; 175,144; 181,123; 195,115; 197,150; 215,153; 229,155; 240,162; 243,147; 254,168; 258,164; 272,173; 344,182; 543,270; 611,265; 619,347; 748,377; 797,342; 925,386; 973,480; 987,508; 1088,454; 1122,535; 1147,634; 1187,589; 1218,774; 1289,832; 1341,565; 1358,532; 1418,867; 1458,652; 1531,924; 1659,445; 1662,585; 1678,245; 1683,623; 1686,827; 1705,322; 1707,552; 1711,123
T. atroviride	**Not related**
$[MH]^+$ 1812.968 Da	
Fragment masses	70,045; 84,067; 86,089; 101,062; 110,075; 112,096; 115,092; 129,107; 136,099; 154,101; 172,128; 175,133; 195,100; 197,152; 227,138; 342,145; 488,207; 640,302; 773,450; 959,449; 1032,453; 1113,421; 1188,453; 1227,561; 1350,553; 1559,558; 1611,696; 1650,314; 1706,734; 1742,628; 1745,957; 1758,588; 1762,713; 1767,048; 1771,398; 1783,071; 1789,463
T. atroviride	**Not related**
$[MH]^+$ 1827.970 Da	

Fragment masses	70,052; 74,189; 84,085; 86,102; 101,080; 110,085; 112,104; 115,097; 129,122; 136,100; 147,119; 154,113; 172,135; 175,153; 195,127; 197,165; 202,136; 229,152; 342,209; 488,289; 505,249; 559,326; 583,351; 640,420; 660,365; 717,407; 785,381; 832,452; 947,461; 959,494; 1011,545; 1032,499; 1038,512; 1062,521; 1095,503; 1112,494; 1176,576; 1188,576; 1227,572; 1269,681; 1323,751; 1484,839; 1706,900; 1712,244; 1723,893; 1741,947; 1753,640; 1761,103; 1765,473; 1770,407; 1774,682; 1777,773; 1782,097; 1795,039; 1804,327
T. atroviride	**Rossmann-fold NAD(P)$^+$ -binding protein (NADP binding domain containing protein, 6-phosphogluconate dehydrogenase) R.DILYFNDDDGTALVEK.I (NOT significant)**
[MH]$^+$ 1949.100 Da	
Fragment masses	70,058; 84,078; 86,099; 110,074; 112,094; 115,101; 129,118; 136,088; 143,154; 159,091; 167,102; 175,130; 185,111; 189,137; 195,103; 197,131; 242,149; 255,159; 272,174; 286,157; 300,130; 345,191; 443,201; 557,226; 585,235; 698,266; 765,350; 799,285; 1032,366; 1587,149; 1753,266; 1793,332; 1845,890; 1890,330; 1897,671; 1905,295; 1907,413; 1930,469
T. atroviride	**Not related**
[MH]$^+$ 2216.156 Da	
Fragment masses	70,031; 84,069; 110,064; 112,085; 115,092; 129,109; 136,076; 175,125; 195,111; 197,122; 226,140; 319,146; 355,149; 603,309; 720,302; 731,282; 787,271; 860,414; 888,480; 906,398; 975,460; 1003,419; 1021,474; 1032,485; 1131,500; 1149,478; 1317,602; 1507,748; 1862,266; 2110,088; 2137,462; 2150,999; 2152,842; 2155,055; 2163,756; 2168,150; 2172,650; 2178,883; 2192,662; 2195,263; 2198,146
T. atroviride	**Malic enzyme -.MASSSRSADSSDVYTPR.S + Phospho (NOT significant)**
[MH]$^+$ 2226.011 Da	
Fragment masses	70,059; 84,064; 110,081; 112,097; 115,089; 129,116; 175,137; 195,121; 319,224; 355,297; 546,277; 603,312; 624,313; 674,307; 720,407; 731,403; 842,415; 860,405; 886,422; 888,451; 906,483; 975,498; 1003,484; 1021,508; 1032,504; 1131,573; 1149,546; 1221,643; 1310,640; 1317,631; 1507,725; 1861,773; 2050,405; 2155,435; 2167,321; 2172,854; 2181,439; 2195,389; 2198,506
T. atroviride	**Rossmann-fold NAD(P)$^+$ -binding protein (NADP binding domain containing protein, 6-phosphogluconate dehydrogenaseK.SDGEACCEWVGDEGAGHYVK.M (NOT significant)**
[MH]$^+$ 2492.223 Da	
Fragment masses	74,016; 110,067; 129,102; 175,118; 232,136; 579,240; 673,312; 762,311; 802,407; 921,474; 930,424; 1036,517; 1046,501; 1114,496; 1152,532; 1268,572; 1715,752; 2127,457; 2384,789; 2400,497; 2433,046; 2448,544; 2469,722
T. atroviride	**Rossmann-fold NAD(P)$^+$ binding protein (GDP dissociated inhibitor) K.SYDATSHFETTTDDVKDIYQR.A (NOT significant)**
[MH]$^+$ 2537.282 Da	
Fragment masses	74,018; 110,082; 129,118; 175,143; 232,172; 258,173; 267,151; 508,343; 536,237; 564,335; 673,314; 721,476; 737,258; 776,453; 802,379; 866,344; 892,454; 930,450; 958,507; 978,496; 994,444; 1029,494; 1043,529; 1046,581; 1091,562; 1158,610; 1202,677; 1206,578; 1271,705; 1331,633; 1392,677; 1427,689; 1476,690; 1491,775; 1543,938; 1564,523; 1671,560; 1761,916; 1938,179; 2439,847; 2457,255; 2474,041; 2503,390; 2512,816
T. atroviride	**Elongation factor 1 alpha (EF1B) K.SVEMHHEQLVEGVPGDNVGFNVK.N (NOT significant)**
[MH]$^+$ 2975.278 Da	
Fragment masses	73,995; 109,999; 226,111; 313,122; 355,132; 640,168; 753,283; 825,332; 1041,554; 1051,473; 1122,519; 1209,539; 1296,568; 1437,949; 1609,776; 1832,311; 1936,216; 2124,333; 2202,707; 2516,700; 2672,506; 2731,667; 2875,786
T. atroviride	**Dihydrolipoamide acetyltransferase component K.KDSEPAPQSTPASAPQSSSAPEQYSSQGR.I (NOT significant)**

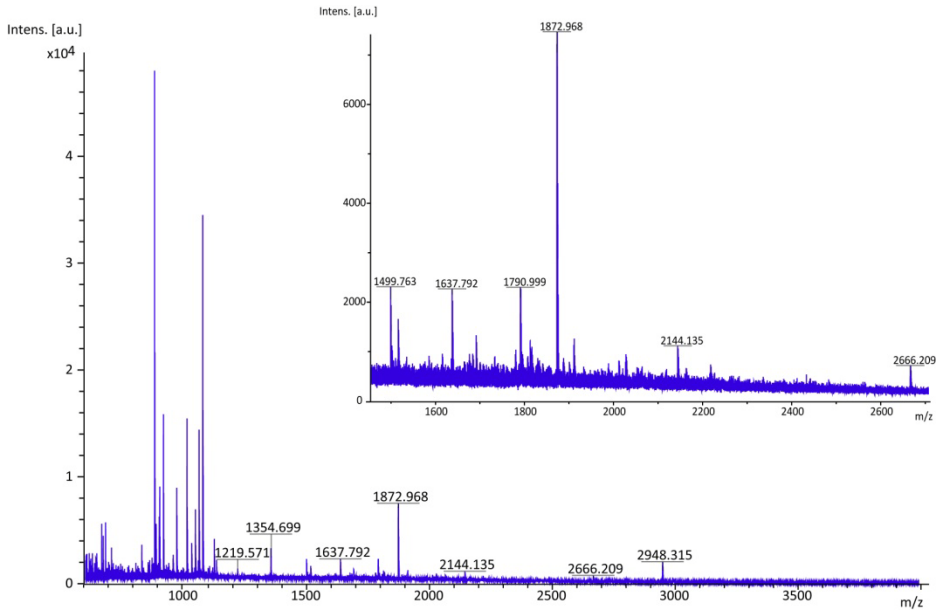


Figure 6.58 Positive ion reflector TOF - MALDI mass spectrum of 2_2_7

$[MH]^+$ 1219.571 Da	
Fragment masses	70,033; 84,050; 86,071; 104,098; 110,054; 112,066; 115,074; 120,074; 123,071; 129,084; 136,058; 154,069; 158,054; 167,069; 169,077; 172,067; 175,096; 181,058; 186,072; 191,059; 193,077; 195,065; 197,092; 199,080; 201,080; 205,078; 209,053; 213,070; 217,075; 219,087; 227,076; 229,079; 231,058; 235,074; 243,063; 246,094; 254,083; 258,084; 260,078; 262,065; 268,077; 272,084; 274,067; 277,053; 279,072; 286,075; 288,110; 294,049; 299,078; 301,064; 311,054; 314,092; 327,056; 338,125; 1022,774; 1025,931; 1028,001; 1029,211; 1145,975; 1148,175; 1152,055; 1156,623; 1165,933; 1168,102; 1170,288; 1173,638; 1175,848; 1189,729; 1192,845; 1195,006; 1197,122; 1201,321
T. atroviride	**Not related**
$[MH]^+$ 1354.699 Da	
Fragment masses	70,024; 72,050; 84,061; 86,074; 101,073; 110,063; 112,092; 115,085; 120,086; 129,118; 136,096; 154,114; 159,116; 167,113; 169,139; 171,128; 175,146; 183,140; 185,136; 187,125; 195,127; 197,152; 200,142; 203,113; 212,148; 216,156; 223,142; 226,148; 229,139; 231,142; 233,153; 235,157; 244,149; 246,153; 251,143; 254,159; 257,174; 259,136; 262,168; 264,149; 269,163; 272,165; 274,160; 286,189; 289,190; 292,173; 294,144; 298,161; 303,211; 311,167; 314,177; 316,152; 327,164; 329,181; 331,166; 341,180; 343,159; 345,175; 348,145; 351,201; 355,164; 360,182; 366,148; 373,193; 390,228; 465,179; 589,305; 718,369; 1151,499; 1154,574; 1157,753; 1160,998; 1164,200; 1240,015; 1248,309; 1258,140; 1293,910; 1305,495; 1308,784; 1311,981; 1324,765; 1326,784; 1328,762; 1332,062
T. atroviride	**Not related**
$[MH]^+$ 1499.763 Da	
Fragment masses	70,068; 84,069; 86,072; 110,093; 112,096; 115,094; 129,122; 136,110; 157,128; 167,104; 171,133; 175,150; 186,129; 195,138; 197,151; 201,141; 212,130; 214,150; 217,123; 232,164; 235,143; 237,154; 240,163; 242,151; 244,150; 246,152; 252,167; 255,142; 258,149; 268,174; 270,180; 272,173; 279,135; 286,144; 295,170; 298,172; 301,156; 312,190; 314,167; 327,172; 329,183; 343,177; 345,188; 355,184; 365,201; 369,197; 371,179; 394,212; 508,272; 519,197; 852,579; 981,561; 1032,443; 1302,697; 1392,248; 1405,166; 1410,283; 1447,397; 1477,509; 1480,239
T. atroviride	**Not related**
$[MH]^+$ 1637.792Da	

Fragment masses	70,063; 84,081; 86,100; 110,068; 112,087; 115,090; 129,116; 136,090; 147,122; 155,100; 158,110; 175,141; 185,141; 187,113; 195,126; 197,153; 199,154; 201,142; 209,118; 221,120; 229,123; 231,108; 244,133; 272,169; 286,155; 310,180; 343,170; 451,168; 629,279; 757,393; 872,403; 959,476; 1032,507; 1066,463; 1074,465; 1189,527; 1213,532; 1250,780; 1328,702; 1409,647; 1522,043; 1561,182; 1570,805; 1589,822; 1615,254; 1617,135
T. atroviride	**S-adenosylmethionine synthase K.DIGYDDSDKGFDYK.T (significant)**
$[MH]^+$ 1790.999 Da	
Fragment masses	70,049; 74,208; 86,087; 110,066; 112,083; 115,071; 129,108; 136,073; 175,122; 202,139; 212,109; 227,160; 229,114; 262,137; 274,174; 304,139; 331,182; 380,132; 398,170; 504,296; 783,371; 844,392; 1086,546; 1226,380; 1626,069; 1663,646; 1679,294; 1685,809; 1689,015; 1701,801; 1712,460; 1719,745; 1741,781; 1759,795
T. atroviride	**Not related**
$[MH]^+$ 1872.968 Da	
Fragment masses	70,070; 72,082; 86,106; 102,081; 112,115; 115,123; 129,140; 133,095; 136,106; 158,140; 175,158; 199,217; 212,155; 216,151; 227,210; 244,151; 262,190; 283,215; 311,216; 326,264; 331,140; 343,206; 373,206; 380,252; 398,249; 405,180; 422,205; 444,155; 455,290; 472,228; 509,235; 518,229; 535,300; 545,255; 569,332; 585,298; 623,300; 641,304; 683,333; 698,400; 754,399; 778,378; 865,384; 964,493; 1061,542; 1078,597; 1095,615; 1158,588; 1175,614; 1304,679; 1418,842; 1690,403; 1758,414; 1763,923; 1775,541; 1793,592; 1826,163; 1854,511
T. atroviride	**Glycogen synthase kinase 3 K.ILVENEPNVSYICSR.Y + Phospho (significant)**
$[MH]^+$ 2144.135Da	
Fragment masses	110,075; 112,093; 115,087; 129,107; 136,075; 175,125; 197,119; 296,142; 343,190; 382,159; 424,172; 638,355; 766,454; 895,505; 1081,573; 1736,629; 2029,549; 2033,597; 2046,604; 2064,705; 2082,549; 2125,716
T. atroviride	**Elicitor Protein R.FAYLGNDSDGEEKPVVPVK.T + Phospho (NOT significant)**
$[MH]^+$ 2666.209 Da	
Fragment masses	74,001; 112,085; 175,130; 643,506; 659,314; 774,346; 887,565; 1059,590; 1071,639; 1186,649; 1191,603; 1196,567; 1389,822; 1665,953; 1714,572; 2302,863; 2555,469; 2639,049
T. atroviride	**Carboxypeptidase A R.SYDAFQSSDLYPTSGASDDYAYSR.H (NOT significant)**
$[MH]^+$ 2948.315 Da	
Fragment masses	112,074; 175,126; 215,119; 232,148; 287,094; 302,148; 312,172; 319,170; 400,174; 406,157; 445,164; 463,211; 482,258; 499,244; 561,216; 578,237; 757,383; 774,389; 857,418; 875,432; 946,478; 1093,614; 1190,665; 1207,731; 1278,725; 1375,763; 1392,752; 1489,815; 1507,766; 1791,935; 1809,060; 2123,200; 2662,033; 2886,169; 2903,650; 2911,646
T. atroviride	**Not related**

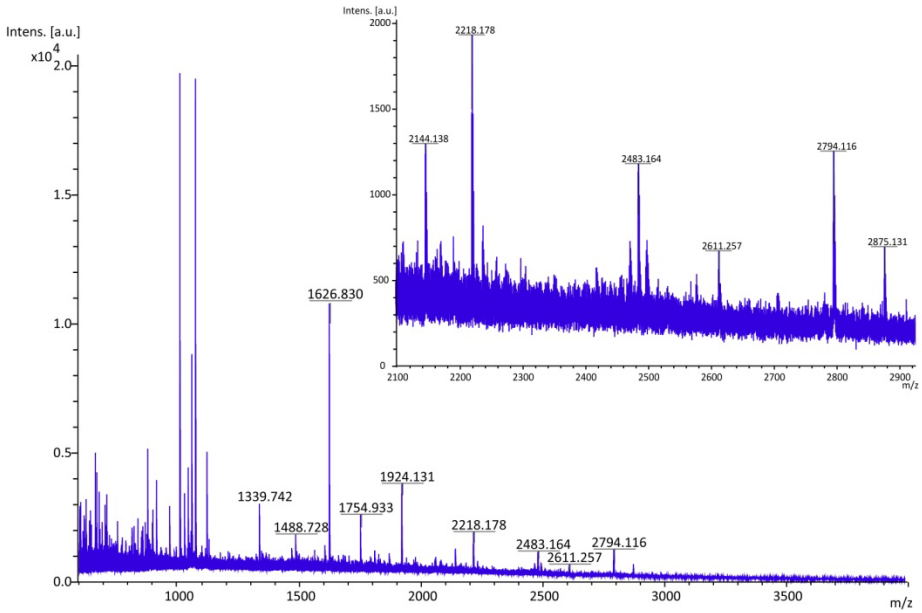


Figure 6.59 Positive ion reflector TOF - MALDI mass spectrum of 2_2_8

$[MH]^+$ 1339.742 Da	
Fragment masses	70,030; 76,677; 84,059; 86,077; 101,085; 104,123; 110,070; 112,088; 115,099; 120,106; 129,121; 136,094; 141,125; 143,123; 154,120; 158,128; 172,121; 175,155; 181,131; 184,130; 186,146; 193,125; 195,137; 197,154; 201,143; 203,136; 209,137; 212,148; 214,168; 217,129; 221,146; 223,160; 225,158; 227,162; 229,163; 232,157; 235,146; 241,160; 243,169; 245,153; 250,120; 252,156; 254,166; 257,186; 259,143; 261,162; 266,154; 268,176; 271,163; 273,149; 275,172; 278,160; 283,175; 286,180; 288,202; 292,167; 295,170; 298,183; 300,161; 303,193; 311,177; 313,180; 316,172; 322,166; 327,169; 329,180; 341,182; 343,176; 356,193; 368,194; 374,204; 382,181; 398,199; 542,291; 798,378; 946,551; 948,677; 1119,283; 1137,634; 1141,791; 1144,911; 1148,168; 1211,990; 1286,106; 1288,285; 1290,502; 1294,878; 1312,113; 1315,327; 1317,690; 1319,888
T. atroviride	**Not related**
$[MH]^+$ 1488.728 Da	
Fragment masses	70,031; 84,059; 86,080; 110,068; 112,089; 115,092; 120,093; 129,111; 136,095; 143,109; 147,111; 157,119; 167,110; 169,131; 172,115; 175,136; 184,109; 186,138; 197,139; 201,126; 203,093; 207,125; 212,150; 214,120; 216,135; 219,130; 224,131; 226,146; 228,149; 230,131; 232,129; 235,127; 244,133; 253,129; 258,151; 262,158; 266,157; 268,144; 270,146; 272,161; 274,154; 276,155; 282,147; 284,143; 286,154; 288,172; 290,156; 301,153; 303,164; 308,152; 310,152; 312,154; 314,144; 316,152; 320,179; 329,164; 331,154; 338,174; 341,167; 343,164; 355,165; 359,152; 373,156; 375,176; 446,222; 508,218; 529,250; 593,243; 653,205; 721,294; 836,323; 896,246; 1032,372; 1097,619; 1103,861; 1122,865; 1179,286; 1286,527; 1288,754; 1290,871; 1292,864; 1296,051; 1380,170; 1393,179; 1417,386; 1435,174; 1438,500; 1441,755; 1459,024; 1461,076; 1464,384; 1467,490; 1470,545
T. atroviride	**Not related**
$[MH]^+$ 1626.830 Da	
Fragment masses	70,048; 86,083; 101,069; 110,069; 113,079; 115,082; 129,103; 136,075; 138,091; 159,091; 167,103; 175,119; 181,114; 185,111; 195,098; 197,120; 199,110; 201,117; 209,103; 213,123; 216,108; 225,101; 229,126; 244,098; 253,086; 273,120; 282,131; 290,117; 298,128; 304,165; 313,136; 315,147; 324,116; 331,121; 334,155; 341,124; 343,170; 352,146; 359,101; 403,188; 423,177; 426,182; 437,191; 444,177; 454,198; 474,223; 552,214; 567,240; 569,230; 587,207; 594,275; 611,300; 638,265; 674,286; 682,261; 691,284; 709,308; 726,321; 785,273; 802,340; 825,415; 866,320; 953,439; 1040,543; 1153,497; 1239,849; 1268,745; 1410,373; 1428,774; 1452,889; 1497,996; 1520,423; 1558,549; 1575,441; 1578,745; 1582,751; 1599,296; 1608,231
T. atroviride	**Transaldolase like protein K.EGGDIDSQVDHALDR.L (significant)**
$[MH]^+$ 1754.933 Da	

Fragment masses	70,076; 84,072; 101,080; 110,081; 112,097; 115,096; 129,116; 136,100; 155,112; 158,111; 175,136; 181,115; 195,117; 209,099; 324,146; 474,256; 487,193; 611,294; 726,324; 1040,521; 1155,541; 1235,632; 1268,718; 1350,600; 1368,964; 1386,862; 1411,485; 1539,618; 1557,993; 1581,230; 1728,505
T. atroviride	**Transaldolase like protein K.KEGGDIDSQVDHALDR.L (NOT significant)**
$[MH]^+$ 1924.131 Da	
Fragment masses	70,058; 72,082; 84,083; 86,100; 110,093; 112,111; 115,112; 129,135; 136,112; 158,145; 175,165; 183,196; 186,152; 195,185; 201,200; 211,188; 228,177; 243,201; 258,277; 271,258; 286,208; 300,171; 301,194; 325,176; 327,213; 368,288; 385,298; 400,244; 415,235; 513,356; 553,384; 570,400; 639,452; 667,418; 685,448; 883,549; 928,543; 996,689; 1295,962; 1351,098; 1540,186; 1729,364; 1752,560; 1859,308; 1874,939; 1881,531; 1899,244
T. atroviride	**Not related**
$[MH]^+$ 2144.138 Da	
Fragment masses	110,075; 112,090; 115,093; 129,109; 136,087; 175,115; 197,128; 296,159; 343,199; 382,137; 424,189; 638,357; 739,346; 766,454; 895,487; 914,349; 1081,615; 1196,604; 1265,582; 1363,570; 1704,063; 1753,800; 1803,057; 2028,398; 2046,640; 2064,613; 2100,368; 2123,795
T. atroviride	**Elicitor Protein R.FAYLGNDSDGEEKPVVPVK.T + Phospho (NOT significant)**
$[MH]^+$ 2218.178 Da	
Fragment masses	110,070; 112,080; 115,087; 129,107; 175,121; 197,125; 244,111; 516,176; 583,186; 629,292; 670,238; 766,382; 853,449; 906,408; 968,492; 1066,538; 1083,480; 1118,488; 1197,594; 1497,622; 1636,057; 1837,057; 2107,551
T. atroviride	**F-actin capping protein R.QVEQDLPVENDDSHIANVGR.L (significant)**
$[MH]^+$ 2483.164 Da	
Fragment masses	110,064; 129,101; 175,111; 213,109; 276,175; 456,235; 527,270; 697,365; 779,269; 795,349; 812,392; 909,323; 913,421; 916,376; 1014,504; 1017,390; 1074,435; 1211,526; 1256,598; 1268,538; 1383,563; 1440,617; 1555,779; 1684,854; 1704,869; 2269,205; 2425,117; 2437,404; 2464,512
T. atroviride	**Not related**
$[MH]^+$ 2611.257 Da	
Fragment masses	74,072; 110,051; 129,087; 175,121; 456,208; 545,229; 697,408; 724,438; 812,439; 907,435; 981,618; 1044,517; 1070,549; 1202,626; 1268,559; 1340,749; 1396,685; 1451,759; 1568,764; 2057,081; 2302,035; 2511,817; 2586,179; 2590,451
T. atroviride	**Not related**
$[MH]^+$ 2794.116 Da	
Fragment masses	175,096; 201,069; 240,112; 257,143; 272,124; 274,127; 300,087; 311,123; 316,051; 328,123; 345,182; 445,127; 474,182; 484,162; 545,260; 555,210; 615,213; 617,163; 625,194; 643,189; 657,179; 660,280; 714,240; 771,199; 789,330; 829,218; 900,292; 918,386; 928,324; 982,402; 1043,287; 1047,408; 1114,326; 1145,309; 1162,451; 1242,430; 1260,395; 1277,486; 1346,492; 1403,541; 1663,568; 1681,918; 1877,613; 2688,292; 2738,764; 2758,681; 2775,497
T. atroviride	**Not related**
$[MH]^+$ 2875.131 Da	
Fragment masses	175,113; 272,123; 274,164; 345,182; 474,226; 484,179; 545,249; 555,203; 625,264; 643,256; 660,265; 670,205; 771,285; 789,328; 900,325; 918,387; 928,336; 981,527; 987,461; 1029,430; 1047,464; 1114,374; 1127,434; 1144,441; 1162,502; 1242,491; 1259,454; 1277,498; 1346,597; 1403,529; 1663,762; 1681,638; 1761,691; 1877,776; 1975,940; 1992,886; 2090,899; 2108,171; 2207,032; 2223,888; 2609,658; 2707,137; 2750,097; 2757,487; 2760,474; 2766,693; 2777,876; 2795,871; 2833,034; 2855,045
T. atroviride	**Elongation factor 1 beta (EF1B) K.APAAEDDDDVDLFGSDDEEEDAEARR.I + Phospho (significant)**

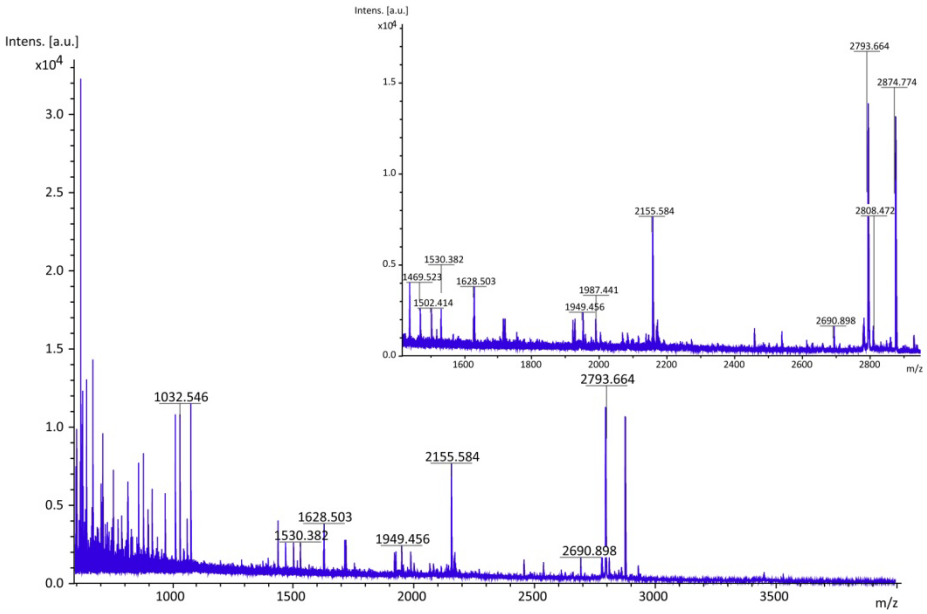


Figure 6.60 Positive ion reflector TOF - MALDI mass spectrum of 2_2_9

$[MH]^+$ 1032.546 Da	
Fragment masses	58,011; 70,065; 72,064; 84,076; 86,091; 95,070; 100,089; 102,073; 107,071; 110,086; 112,096; 115,096; 121,091; 123,101; 125,094; 129,111; 132,105; 136,087; 139,099; 141,102; 143,124; 149,099; 151,077; 154,095; 158,100; 161,096; 167,099; 169,105; 172,086; 175,123; 179,091; 181,099; 185,101; 187,097; 190,091; 192,098; 197,119; 202,107; 207,096; 209,107; 212,108; 215,118; 218,118; 223,094; 225,103; 227,105; 232,125; 235,098; 240,116; 242,120; 245,104; 253,099; 260,113; 268,113; 270,139; 288,147; 294,085; 310,110; 345,175; 382,144; 410,143; 473,136; 508,253; 525,174; 660,240; 688,267; 837,840; 840,973; 845,258; 917,889; 924,189; 966,141; 971,647; 981,983; 984,056; 986,371; 988,682; 991,896; 997,483; 1005,951; 1008,029
T. atroviride	**FAD/FMN containing dehydrogenase R.NTGHDYLGR.S (NOT significant)**
$[MH]^+$ 1469.523 Da	
Fragment masses	86,100; 110,088; 112,100; 115,115; 127,116; 129,131; 136,104; 139,132; 141,134; 143,136; 147,130; 154,129; 159,137; 169,153; 172,129; 175,158; 179,145; 181,146; 185,162; 187,148; 197,179; 207,145; 212,185; 214,187; 218,196; 226,186; 229,175; 232,182; 240,217; 244,170; 249,167; 255,182; 257,191; 268,189; 270,205; 272,186; 282,213; 288,215; 345,232; 508,288; 545,289; 577,270; 1032,422; 1271,640; 1403,577; 1406,727; 1410,845; 1415,174; 1416,944; 1420,567; 1423,901; 1447,988
T. atroviride	**Not related**
$[MH]^+$ 1502.414 Da	
Fragment masses	70,038; 84,047; 86,064; 102,068; 110,060; 112,082; 115,082; 120,079; 123,072; 125,084; 127,097; 129,099; 136,086; 139,104; 141,093; 143,111; 145,082; 147,082; 154,097; 158,094; 165,097; 167,101; 169,114; 171,119; 175,122; 179,106; 181,113; 183,120; 185,110; 190,107; 192,121; 197,131; 201,112; 203,111; 207,109; 209,125; 212,122; 214,146; 216,117; 218,141; 221,113; 223,128; 227,121; 229,122; 232,134; 235,125; 237,128; 240,140; 242,136; 244,126; 246,136; 250,120; 253,123; 255,137; 257,138; 259,121; 262,139; 268,151; 270,149; 272,133; 274,139; 277,120; 288,171; 299,150; 301,131; 303,154; 310,129; 312,120; 314,146; 324,135; 326,139; 345,172; 355,137; 484,195; 508,207; 545,177; 588,176; 789,194; 1032,264; 1302,568; 1391,886; 1403,613; 1422,783; 1445,935; 1448,011; 1450,134; 1452,242; 1475,912; 1478,521; 1481,561
T. atroviride	**Not related**
$[MH]^+$ 1530.382 Da	
Fragment masses	70,063; 84,079; 86,090; 100,084; 110,076; 112,101; 115,094; 129,120; 136,094; 141,104; 143,128; 147,095; 154,112; 157,128; 159,122; 167,122; 172,121; 175,141; 183,118; 185,130; 190,123; 197,150; 201,129; 205,116; 209,127;

	212,141; 214,153; 216,137; 218,157; 221,137; 226,160; 229,142; 232,156; 238,148; 240,165; 242,153; 244,137; 246,154; 252,155; 254,159; 257,167; 259,148; 264,155; 266,174; 268,159; 270,173; 272,152; 288,188; 304,172; 343,186; 345,194; 508,248; 1015,253; 1301,919; 1420,966; 1425,276; 1432,780; 1437,964; 1443,159; 1450,805; 1479,201; 1500,488; 1506,334
T. atroviride	**Not related**
$[MH]^+$ 1628.503 Da	
Fragment masses	70,045; 84,069; 86,080; 100,055; 110,050; 112,063; 115,059; 129,082; 136,066; 141,076; 143,087; 147,044; 154,074; 157,088; 163,076; 167,071; 169,082; 172,080; 175,095; 181,077; 183,091; 185,097; 187,074; 192,082; 197,102; 201,082; 203,065; 207,081; 209,086; 212,095; 214,098; 216,091; 218,107; 226,103; 228,100; 230,075; 240,094; 244,089; 246,094; 253,087; 257,110; 259,094; 262,077; 270,116; 272,109; 288,133; 298,091; 314,121; 383,109; 435,148; 564,175; 611,202; 778,290; 1032,184; 1040,323; 1513,781; 1520,079; 1568,756; 1576,193; 1579,418; 1582,580; 1597,824; 1603,178
T. atroviride	**Not related**
$[MH]^+$ 1949.456 Da	
Fragment masses	70,045; 84,054; 86,076; 110,049; 112,063; 115,071; 129,073; 136,055; 154,058; 172,074; 175,081; 197,077; 259,067; 451,062; 468,130; 484,114; 504,076; 545,126; 580,101; 799,212; 882,124; 1032,233; 1068,208; 1137,190; 1183,226; 1320,269; 1506,409; 1587,036; 1837,081; 1843,304; 1854,178; 1861,392; 1872,250; 1924,068
T. atroviride	**Acetolactate synthase R.EISNGEHNGESTNEFER.T (NOT significant)**
$[MH]^+$ 1987.441 Da	
Fragment masses	70,038; 84,053; 86,059; 110,058; 112,070; 115,074; 129,089; 154,076; 167,070; 172,079; 175,098; 181,091; 183,091; 197,099; 201,077; 213,090; 229,085; 288,144; 345,138; 545,180; 586,187; 1018,148; 1267,342; 1276,194; 1877,136; 1882,522; 1888,819; 1895,279; 1900,543; 1908,979; 1921,792; 1939,667; 1965,346
T. atroviride	**Not related**
$[MH]^+$ 2155.584 Da	
Fragment masses	70,027; 74,094; 86,064; 110,047; 112,057; 115,062; 129,077; 136,056; 143,080; 154,061; 172,074; 175,086; 181,077; 197,081; 214,084; 244,089; 301,091; 345,068; 384,068; 409,076; 416,009; 516,122; 539,139; 545,173; 587,169; 605,173; 638,328; 644,084; 701,142; 799,236; 912,239; 997,303; 1012,303; 1081,410; 1108,367; 1125,380; 1225,358; 1337,408; 1438,423; 1569,548; 1811,937; 2028,163; 2041,190; 2045,364; 2048,543; 2064,527; 2079,369; 2112,359; 2132,503; 2135,653; 2139,706
T. atroviride	**Heme binding peroxidase R.DNDAAACTPDGRLPDASSQGPK.H (significant)**
$[MH]^+$ 2690.898 Da	
Fragment masses	75,048; 110,072; 112,071; 129,107; 169,110; 175,127; 197,141; 226,159; 245,134; 257,171; 259,116; 272,164; 274,171; 298,149; 345,231; 361,181; 369,205; 427,182; 474,253; 545,292; 556,228; 642,260; 687,257; 715,245; 781,296; 789,364; 829,347; 843,324; 900,326; 918,310; 1047,436; 1068,438; 1162,470; 1269,501; 1293,564; 1398,585; 1623,711; 1848,874; 1921,226; 2050,085; 2576,554; 2590,308; 2594,556; 2609,528; 2664,301
T. atroviride	**14-3-3-like protein K.KEEGEAAKPAEEEEPKPAEEPAPEAAS.- (NOT significant)**
$[MH]^+$ 2793.664 Da	
Fragment masses	70,004; 73,986; 102,034; 112,049; 129,060; 141,066; 143,084; 158,066; 169,066; 171,079; 175,090; 187,057; 195,069; 201,056; 215,081; 222,078; 229,083; 231,037; 240,094; 245,040; 257,115; 261,102; 272,078; 274,131; 300,061; 311,110; 316,064; 328,128; 330,083; 345,160; 357,055; 360,076; 369,105; 374,045; 387,094; 399,108; 427,061; 429,067; 440,136; 445,099; 457,133; 461,024; 474,174; 484,138; 486,102; 504,112; 545,226; 555,161; 560,115; 572,090; 574,113; 590,101; 599,156; 615,122; 625,172; 633,109; 643,186; 660,235; 670,184; 675,142; 689,144; 714,155; 732,154; 744,132; 771,216; 785,153; 789,256; 804,157; 829,168; 859,168; 875,189; 882,204; 900,237; 918,279; 928,235; 972,268; 1029,268; 1043,243; 1047,303; 1114,259; 1127,280; 1145,286; 1162,310; 1242,298; 1260,270; 1277,290; 1346,264; 1403,253; 1421,313; 1550,234; 1568,291; 1663,276; 1681,457; 1761,171; 1779,137; 1877,203; 1895,368; 1992,685; 2010,391; 2079,981; 2107,394; 2124,965; 2177,166; 2222,071; 2240,882; 2276,028; 2337,244; 2608,457; 2704,111; 2706,996; 2758,600; 2776,230; 2784,527

T. atroviride	**Not related**
$[MH]^+$ 2808.472 Da	
Fragment masses	70,035; 73,951; 102,038; 112,069; 120,067; 129,100; 141,085; 158,077; 169,081; 171,096; 175,106; 187,064; 201,071; 215,093; 222,112; 229,092; 231,049; 240,108; 245,051; 257,127; 274,142; 284,110; 298,090; 300,093; 303,134; 311,119; 316,062; 328,136; 345,158; 355,128; 357,064; 360,060; 369,115; 374,077; 387,096; 399,128; 407,111; 412,147; 427,109; 440,128; 445,092; 456,167; 461,040; 468,100; 474,177; 484,146; 504,092; 516,132; 527,191; 545,206; 555,178; 558,126; 560,107; 572,109; 574,148; 590,100; 599,145; 607,189; 615,137; 618,155; 625,187; 633,123; 643,185; 660,219; 670,202; 675,144; 689,155; 714,175; 732,189; 744,165; 762,172; 771,264; 785,196; 789,256; 799,235; 802,163; 804,181; 811,203; 829,209; 841,195; 859,182; 875,234; 882,229; 900,263; 918,303; 928,283; 972,305; 988,239; 999,280; 1006,258; 1025,278; 1029,352; 1043,308; 1047,354; 1057,341; 1096,291; 1114,315; 1127,343; 1144,376; 1162,381; 1172,382; 1227,401; 1242,367; 1260,385; 1277,388; 1287,389; 1328,411; 1346,437; 1364,439; 1385,432; 1403,449; 1416,263; 1421,456; 1426,400; 1444,363; 1501,362; 1550,499; 1562,518; 1568,500; 1578,491; 1645,589; 1648,446; 1663,597; 1675,167; 1681,615; 1691,176; 1743,545; 1761,549; 1778,659; 1838,824; 1859,607; 1877,694; 1888,373; 1895,707; 1975,605; 1992,681; 2003,035; 2010,798; 2081,514; 2090,646; 2107,838; 2117,673; 2125,860; 2178,033; 2205,761; 2222,900; 2232,437; 2240,881; 2277,716; 2320,839; 2338,019; 2379,210; 2538,060; 2558,221; 2591,289; 2609,255; 2616,551; 2623,412; 2627,525; 2707,109; 2733,295; 2740,203; 2743,103; 2746,576; 2749,632; 2755,850; 2759,583; 2765,388; 2767,888; 2771,855; 2777,520; 2795,565
T. atroviride	**WD40 domain containing proetein R.SLSMRIFTLKWSSEGDSIEASLVR.T + Phospho (NOT significant)**
$[MH]^+$ 2874.774 Da	
Fragment masses	73,957; 110,033; 175,103; 272,124; 284,126; 289,149; 296,121; 324,114; 342,126; 358,102; 381,118; 397,130; 418,127; 443,125; 515,121; 532,118; 629,123; 646,107; 717,175; 814,195; 831,201; 928,238; 938,260; 946,234; 985,266; 1002,284; 1005,233; 1012,405; 1071,321; 1100,316; 1117,301; 1144,466; 1174,382; 1259,496; 1273,468; 1360,434; 1550,534; 1568,530; 1665,529; 1683,553; 1893,527; 1911,632; 2048,580; 2448,014; 2511,887; 2590,743; 3222,072; 3333,031; 3349,568; 3368,869
T. atroviride	**Elongation factor 1 beta (EF1B) K.APAAEDDDDVDLFGSDDEEEDAEAVR.I + Phospho (significant)**

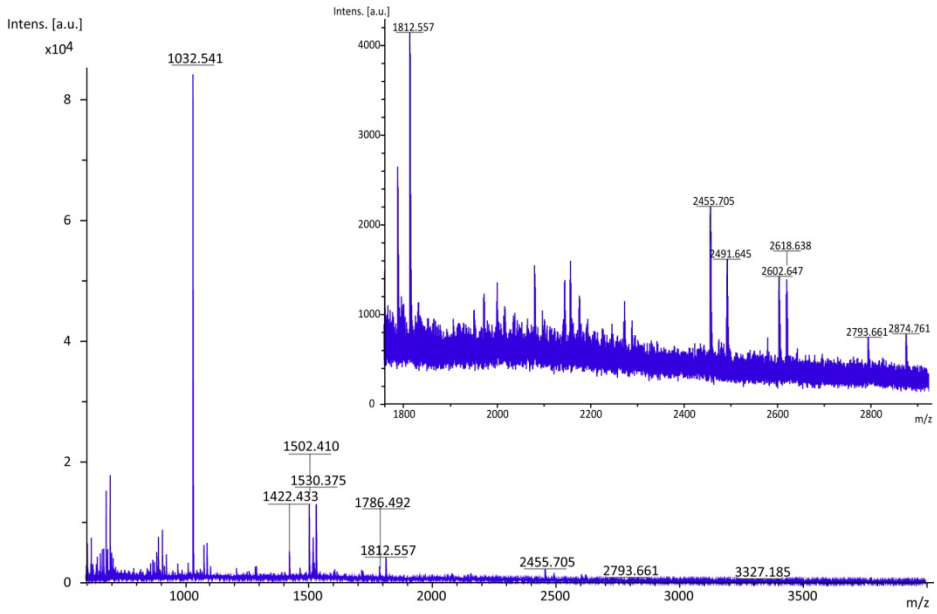


Figure 6.61 Positive ion reflector TOF - MALDI mass spectrum of 2_2_10

$[MH]^+$ 1032.541 Da

Fragment masses	70,065; 86,109; 110,089; 113,093; 115,098; 129,124; 136,088; 154,097; 158,106; 167,105; 172,114; 175,131; 181,109; 188,120; 190,127; 195,098; 198,107; 207,105; 212,121; 215,117; 232,142; 238,121; 249,155; 253,100; 265,977; 268,131; 270,128; 273,117; 279,105; 284,118; 286,133; 296,135; 306,113; 310,116; 328,185; 345,215; 355,177; 365,140; 377,114; 382,174; 386,395; 388,130; 393,142; 403,117; 410,165; 416,148; 421,134; 445,156; 449,130; 453,183; 466,162; 473,170; 481,154; 491,170; 501,164; 508,272; 518,225; 525,199; 529,201; 546,174; 574,214; 586,234; 606,284; 623,312; 643,242; 660,277; 663,394; 671,243; 688,292; 700,654; 743,373; 760,433; 773,367; 801,437; 817,492; 840,948; 858,488; 876,546; 918,680; 924,063; 953,665; 964,191; 972,618; 980,962; 983,108; 985,304; 988,676; 997,652
T. atroviride	**FAD/FMN containing dehydrogenase R.NTGHDYLGR.S (significant)**
$[MH]^+$ 1422.433 Da	
Fragment masses	70,056; 84,074; 86,085; 98,072; 110,091; 112,108; 115,112; 120,111; 127,124; 129,138; 136,109; 141,137; 143,135; 154,135; 158,141; 167,145; 169,151; 175,169; 181,150; 186,164; 190,158; 195,158; 197,180; 212,183; 215,171; 218,181; 221,167; 227,181; 232,192; 235,170; 243,194; 249,188; 253,172; 255,186; 262,180; 266,134; 270,210; 275,173; 288,218; 293,157; 296,205; 304,222; 311,168; 314,218; 328,218; 345,256; 373,141; 387,164; 391,174; 508,301; 525,224; 588,263; 606,277; 623,285; 660,265; 688,235; 801,280; 817,283; 918,344; 942,247; 1015,401; 1032,501; 1301,897; 1306,217; 1307,959; 1317,392; 1324,853; 1342,899; 1370,240; 1373,464; 1377,861; 1387,680; 1397,107; 1399,336
T. atroviride	**Not related**
$[MH]^+$ 1502.410 Da	
Fragment masses	70,045; 84,058; 86,078; 110,063; 112,085; 115,081; 120,073; 129,103; 136,076; 141,100; 143,104; 154,100; 157,103; 159,110; 167,109; 169,111; 172,112; 175,129; 186,119; 195,107; 197,131; 201,123; 207,117; 209,132; 212,131; 215,126; 218,134; 221,120; 227,129; 232,141; 240,126; 242,144; 244,127; 246,132; 249,138; 253,113; 255,142; 257,125; 262,135; 268,145; 270,141; 286,138; 288,168; 301,139; 310,123; 314,157; 319,139; 328,154; 345,192; 355,166; 367,154; 508,217; 518,179; 525,132; 588,170; 606,162; 623,188; 918,126; 1015,162; 1032,269; 1285,434; 1288,591; 1302,556; 1361,805; 1387,821; 1391,868; 1395,040; 1404,780; 1422,833; 1432,211; 1450,151; 1453,430; 1458,739; 1467,540; 1478,340
T. atroviride	**Not related**
$[MH]^+$ 1530.375 Da	
Fragment masses	70,073; 72,066; 84,082; 86,100; 110,085; 112,103; 115,107; 129,121; 136,096; 141,120; 143,108; 154,113; 158,122; 169,132; 172,129; 175,149; 195,130; 197,149; 209,144; 213,154; 215,146; 226,148; 232,167; 249,144; 253,133; 273,173; 286,159; 288,178; 296,163; 310,155; 312,156; 314,176; 345,235; 355,203; 402,104; 508,267; 525,197; 588,234; 606,237; 623,248; 688,204; 801,214; 1015,283; 1032,341; 1276,587; 1290,645; 1301,963; 1305,066; 1316,723; 1372,718; 1415,852; 1419,890; 1425,206; 1432,770; 1437,908; 1443,227; 1450,799; 1483,675; 1485,733; 1495,639; 1499,659; 1505,395
T. atroviride	**Not related**
$[MH]^+$ 1786.492 Da	
Fragment masses	70,072; 84,082; 86,101; 110,082; 112,097; 115,102; 129,115; 136,084; 141,110; 143,133; 154,108; 157,126; 169,127; 172,125; 175,140; 181,137; 197,146; 250,128; 508,363; 536,173; 608,315; 649,308; 706,299; 764,308; 776,346; 863,350; 913,381; 1015,406; 1032,364; 1081,416; 1143,492; 1291,615; 1371,671; 1432,404; 1689,066; 1707,041; 1735,454
T. atroviride	**Not related**
$[MH]^+$ 1812.557 Da	
Fragment masses	70,057; 84,068; 86,082; 98,066; 101,070; 110,067; 112,082; 115,082; 120,076; 125,092; 129,105; 136,077; 141,099; 154,098; 157,100; 159,097; 167,101; 172,105; 175,116; 181,107; 183,126; 186,110; 195,097; 197,124; 226,123; 250,095; 508,211; 640,262; 918,316; 1015,309; 1089,372; 1448,163; 1458,302;

	1461,424; 1466,549; 1512,873; 1633,107; 1649,946; 1706,513; 1710,758; 1743,463; 1754,161; 1759,358; 1762,645; 1765,849; 1771,087; 1784,057; 1787,793; 1794,724
T. atroviride	**Not related**
$[MH]^+$ 2455.705 Da	
Fragment masses	70,017; 75,043; 84,050; 110,041; 115,062; 129,077; 136,055; 155,068; 167,059; 175,084; 195,067; 197,093; 209,079; 212,087; 226,098; 229,088; 232,082; 237,091; 246,133; 255,090; 257,118; 266,095; 272,114; 285,095; 386,120; 414,105; 430,139; 442,174; 513,155; 558,087; 610,093; 614,137; 657,137; 709,125; 718,247; 745,161; 759,128; 766,199; 794,166; 810,243; 855,276; 874,186; 945,195; 954,332; 1032,298; 1070,301; 1156,299; 1285,397; 1502,335; 1511,540; 1582,581; 1711,512; 1738,585; 1858,865; 1886,809; 1970,862; 2014,749; 2341,372; 2357,226; 2431,437; 2432,837; 2434,969; 2437,380
T. atroviride	**Ran-binding domain containing protein R.DAKGDEEEAPESEDVHFEPVVK.L (significant)**
$[MH]^+$ 2491.645 Da	
Fragment masses	74,044; 84,045; 110,048; 112,060; 115,051; 129,078; 154,061; 167,071; 175,089; 181,079; 195,068; 197,096; 212,090; 255,093; 272,108; 386,129; 430,129; 499,150; 527,130; 545,144; 766,236; 792,253; 810,224; 879,246; 907,237; 925,243; 992,271; 1138,306; 1156,321; 1225,248; 1253,308; 1271,303; 1484,285; 1502,404; 2461,044; 2467,274; 2470,628
T. atroviride	**Not related**
$[MH]^+$ 2602.647 Da	
Fragment masses	110,046; 112,066; 129,099; 155,091; 172,097; 175,112; 195,099; 197,111; 212,119; 217,111; 226,120; 244,115; 430,196; 479,250; 607,216; 643,348; 710,204; 781,232; 793,297; 810,321; 844,462; 892,340; 1032,380; 1095,358; 1251,551; 1352,465; 1467,488; 1596,632; 1711,603; 1996,699; 2114,140; 2126,313; 2230,305; 2500,025; 2504,355; 2525,307; 2579,845
T. atroviride	**p23 hB-ind1 like protein K.TDFDKWVDEDEQNEAADDDMSK.F (significant)**
$[MH]^+$ 2618.638 Da	
Fragment masses	74,020; 110,069; 112,081; 129,102; 155,094; 175,121; 181,100; 186,105; 195,106; 197,119; 217,095; 226,125; 244,133; 272,141; 430,189; 479,184; 643,313; 758,336; 765,352; 775,373; 781,369; 793,347; 804,316; 810,316; 860,267; 868,318; 892,387; 1007,420; 1032,433; 1047,373; 1095,426; 1111,381; 1175,468; 1223,471; 1251,365; 1304,465; 1352,425; 1368,468; 1467,375; 1596,431; 1612,568; 1727,605; 1949,869; 2009,890; 2124,949; 2238,993; 2503,097; 2555,392
T. atroviride	**p23 hB-ind1 like protein K.TDFDKWVDEDEQNEAADDDMSK.F (NOT significant)**
$[MH]^+$ 2793.761 Da	
Fragment masses	175,102; 226,101; 246,117; 257,129; 272,112; 345,170; 361,140; 545,240; 643,188; 660,245; 789,305; 844,287; 900,242; 918,313; 1012,381; 1047,364; 1162,349; 1178,462; 1196,452; 1663,374; 1877,461; 2019,337; 2066,354; 2396,141; 2463,610; 2669,310; 2685,641; 2701,879; 2766,878
T. atroviride	**Not related**
$[MH]^+$ 2874.761 Da	
Fragment masses	175,069; 197,063; 226,068; 240,052; 257,085; 274,089; 345,117; 545,157; 625,084; 643,080; 660,162; 789,197; 900,159; 918,237; 1029,230; 1047,280; 1127,203; 1162,316; 1242,265; 1260,234; 1277,322; 1404,360; 1488,611; 1663,504; 1681,571; 1761,400; 1878,692; 1975,902; 1992,627; 2056,480; 2107,700; 2758,910; 2763,866; 2777,363; 2796,553; 2849,664; 2854,710
T. atroviride	**Elongation factor 1 beta (EF1B) K.APAAEDDDDVDLFGSDDEEEDAEAVR.I + Phoshpo (significant)**

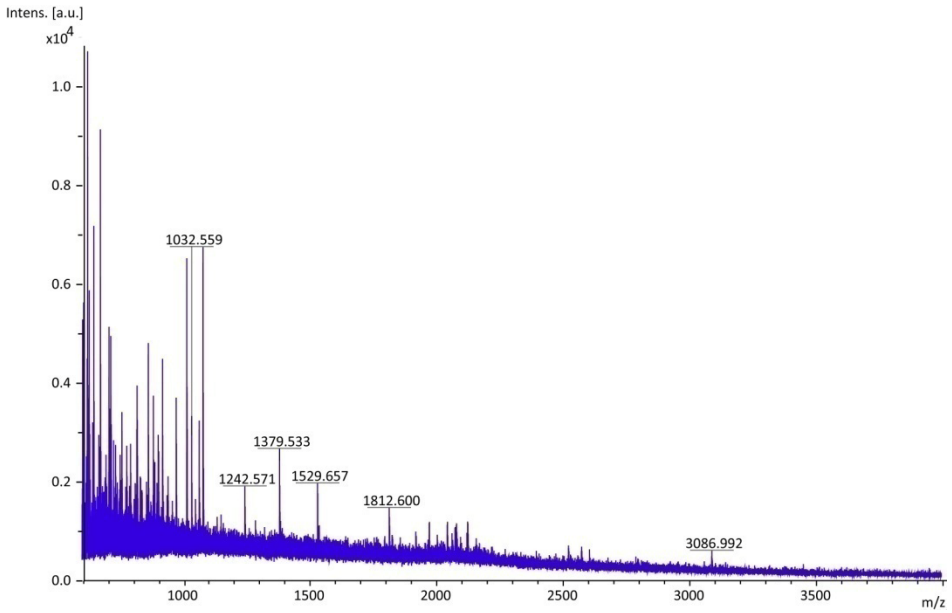


Figure 6.62 Positive ion reflector TOF - MALDI mass spectrum of 2_2_11

$[MH]^+$ 1032.559 Da	
Fragment masses	70,057; 72,051; 84,079; 86,087; 100,086; 102,076; 107,063; 110,079; 112,099; 115,094; 120,085; 123,095; 129,111; 132,105; 137,077; 139,097; 141,092; 143,102; 146,084; 149,087; 151,067; 154,091; 158,101; 161,104; 167,091; 175,118; 179,091; 181,101; 183,110; 186,103; 190,098; 192,089; 197,121; 201,107; 204,109; 207,105; 209,101; 212,109; 215,119; 218,119; 221,102; 225,120; 227,111; 229,118; 232,124; 235,102; 237,116; 240,122; 243,123; 245,180; 247,131; 249,111; 251,114; 253,110; 255,117; 257,121; 259,119; 262,126; 268,121; 271,132; 279,104; 284,115; 286,124; 288,137; 292,128; 294,084; 297,108; 310,112; 382,143; 398,093; 410,132; 508,234; 525,156; 688,248; 697,892; 831,540; 833,613; 835,751; 837,838; 840,995; 917,893; 924,157; 966,173; 977,774; 979,825; 981,923; 984,247; 986,463; 988,703; 1005,758; 1009,034
T. atroviride	**FAD/FMN containing dehydrogenase R.NTGHDYLGR.S (NOT significant)**
$[MH]^+$ 1242.571 Da	
Fragment masses	70,033; 72,042; 84,050; 86,068; 98,076; 101,075; 110,070; 112,083; 115,083; 120,073; 123,085; 125,091; 127,088; 129,094; 136,077; 138,072; 141,087; 143,082; 154,083; 158,096; 161,084; 163,072; 165,087; 167,088; 169,100; 175,115; 181,093; 184,097; 186,103; 197,105; 201,090; 203,100; 205,072; 207,082; 209,091; 212,092; 215,105; 218,110; 221,090; 223,090; 225,099; 228,110; 230,109; 232,097; 235,083; 237,099; 240,115; 243,114; 245,100; 250,095; 252,114; 254,106; 257,109; 259,097; 262,102; 264,103; 266,103; 269,104; 272,119; 274,095; 277,097; 280,112; 282,108; 285,113; 288,130; 292,095; 295,113; 301,094; 306,098; 311,105; 313,122; 315,105; 323,116; 328,102; 342,112; 344,112; 397,116; 459,166; 529,140; 673,124; 1044,654; 1047,910; 1189,957; 1193,275; 1195,434; 1197,606; 1214,867; 1216,787; 1219,015; 1221,564
T. atroviride	**WD40 domain containing protein R.QSGSFSSMLR.R (Not significant)**
$[MH]^+$ 1379.533 Da	
Fragment masses	70,023; 84,053; 86,063; 110,066; 112,085; 115,082; 120,084; 129,104; 136,079; 141,103; 143,098; 146,089; 154,099; 157,112; 159,118; 167,106; 172,120; 175,138; 181,117; 185,126; 187,130; 190,123; 192,123; 197,145; 201,133; 207,129; 209,150; 212,138; 214,145; 217,135; 219,139; 221,128; 223,137; 227,146; 229,136; 231,154; 235,148; 237,148; 240,155; 243,156; 245,156; 247,121; 249,138; 252,152; 254,165; 256,150; 258,145; 260,149; 262,158; 266,165; 268,168; 270,180; 272,171; 275,158; 278,151; 280,157; 282,170; 284,153; 286,169; 288,177; 291,159; 294,137; 297,159;

	299,151; 301,155; 306,165; 311,163; 314,173; 316,165; 319,163; 325,164; 331,181; 341,171; 343,185; 480,195; 513,250; 713,188; 823,332; 1139,617; 1179,670; 1181,554; 1183,581; 1292,911; 1314,452; 1328,081; 1331,438; 1333,649; 1350,889; 1353,124; 1356,264; 1359,363
T. atroviride	**Not related**
$[MH]^+$ 1529.657 Da	
Fragment masses	70,058; 84,092; 86,093; 101,075; 110,063; 112,080; 115,083; 120,080; 125,089; 129,102; 136,081; 139,070; 141,095; 143,080; 154,087; 157,100; 159,096; 169,103; 171,107; 175,118; 181,101; 186,104; 190,089; 197,122; 201,099; 207,085; 209,092; 211,110; 213,106; 215,122; 217,104; 219,110; 221,108; 226,117; 229,108; 232,117; 235,105; 240,113; 242,129; 244,102; 247,111; 249,113; 254,119; 258,111; 260,130; 262,117; 264,110; 266,120; 268,138; 270,132; 273,119; 278,128; 283,124; 286,124; 288,141; 292,096; 294,113; 299,116; 301,129; 308,129; 312,117; 314,144; 316,120; 327,132; 333,120; 345,123; 355,133; 371,133; 385,141; 399,136; 461,153; 508,191; 513,204; 574,168; 590,152; 699,176; 718,186; 831,334; 1032,254; 1145,512; 1229,574; 1328,499; 1335,640; 1414,864; 1461,324; 1475,008; 1479,274; 1482,530; 1485,822; 1500,686; 1502,669; 1505,973; 1509,569; 1511,976
T. atroviride	**Cyclophilin K.DGKPTAEIKEQTGR.I (significant)**
$[MH]^+$ 1812.600 Da	
Fragment masses	70,044; 84,059; 86,079; 110,060; 112,080; 115,078; 120,078; 129,097; 136,073; 141,088; 154,084; 167,102; 172,093; 175,106; 181,105; 195,086; 197,119; 227,081; 288,148; 513,206; 597,184; 809,327; 924,337; 1168,370; 1271,468; 1405,356; 1706,493; 1758,378; 1761,393; 1765,892; 1771,046; 1783,000; 1789,702
T. atroviride	**Not related**
$[MH]^+$ 3089.992 Da	
Fragment masses	74,027; 805,278; 949,414; 1432,777; 1735,624; 1913,765; 2076,876; 2259,443; 2589,963; 2747,693; 2826,856; 2883,487; 2924,775; 2952,856; 2982,051
T. atroviride	**Not related**

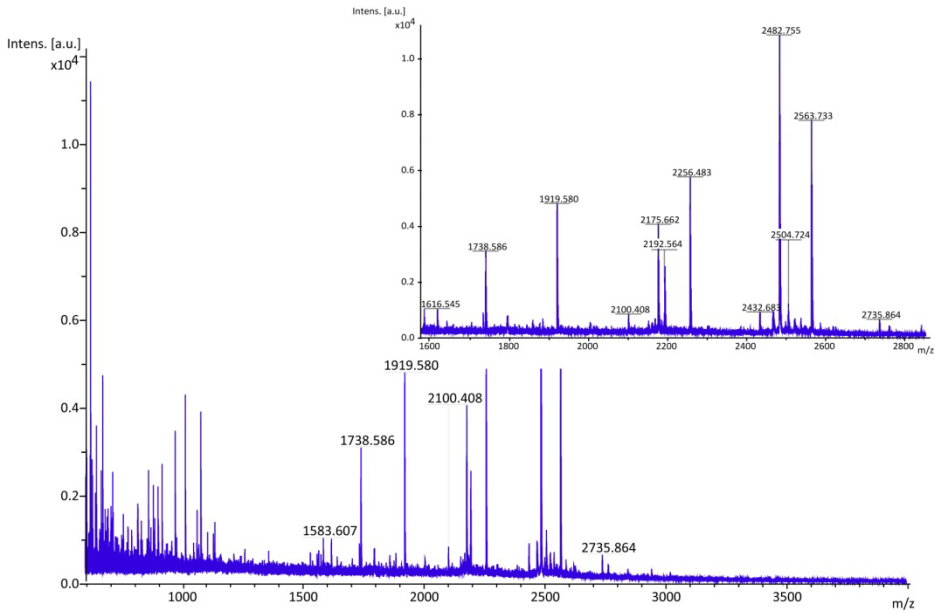


Figure 6.63 Positive ion reflector TOF - MALDI mass spectrum of 2_2_12

$[MH]^+$ 1583.607 Da	
Fragment masses	70,054; 84,038; 110,060; 112,067; 115,075; 129,091; 136,077; 143,086; 147,071; 154,087; 157,095; 167,088; 169,097; 171,104; 175,118; 181,106; 183,106; 185,099; 187,082; 197,114; 201,110; 212,102; 216,113; 227,088; 230,097; 232,085; 235,112; 237,102; 244,138; 250,102; 252,118; 257,104; 259,086; 262,109; 268,145; 270,125; 282,119; 288,148; 298,113; 308,123; 310,120; 312,060; 315,144; 326,127; 331,110;

	358,106; 397,163; 425,164; 430,134; 455,143; 457,143; 487,146; 526,169; 554,186; 574,187; 584,161; 586,172; 655,208; 668,222; 673,238; 683,220; 754,250; 782,286; 802,269; 884,157; 901,355; 906,181; 911,305; 1010,388; 1030,338; 1159,550; 1386,423; 1509,128; 1555,075; 1557,205; 1560,349; 1563,051
T. atroviride	**Not related**
$[MH]^+$ 1616.545 Da	
Fragment masses	70,053; 84,075; 86,077; 100,076; 110,062; 112,081; 115,076; 129,099; 136,067; 141,087; 143,103; 147,102; 154,092; 157,104; 167,100; 169,097; 172,091; 175,116; 179,094; 181,100; 186,115; 192,098; 197,126; 209,114; 211,112; 217,100; 227,107; 230,099; 232,118; 237,120; 240,156; 244,123; 250,083; 252,134; 257,133; 259,088; 268,126; 270,152; 272,122; 288,152; 298,140; 312,085; 315,146; 326,155; 358,145; 425,164; 487,148; 502,161; 554,148; 574,162; 586,139; 655,170; 673,163; 683,114; 687,182; 745,250; 782,066; 802,113; 816,216; 872,250; 910,995; 1155,387; 1410,249; 1521,008; 1544,238; 1549,602; 1565,233; 1582,324; 1594,595
T. atroviride	**Ankyrin repeat protein R.YGKTPVSKAVENSR.L + Phospho (not significant)**
$[MH]^+$ 1738.586 Da	
Fragment masses	70,063; 84,087; 86,083; 101,073; 110,077; 113,095; 115,093; 129,114; 136,082; 141,107; 147,114; 154,102; 157,134; 159,093; 169,117; 172,114; 175,133; 181,122; 183,118; 185,138; 197,142; 200,135; 209,142; 212,144; 214,163; 216,121; 218,144; 226,136; 228,146; 232,126; 237,129; 240,165; 244,158; 252,141; 254,163; 258,146; 272,154; 276,165; 285,151; 288,195; 294,147; 298,169; 312,124; 315,163; 326,177; 389,183; 409,163; 517,219; 522,226; 588,245; 611,232; 693,276; 703,270; 778,346; 797,272; 804,322; 806,339; 925,303; 933,363; 935,389; 1036,438; 1046,389; 1088,337; 1151,484; 1160,506; 1187,391; 1217,526; 1222,543; 1330,717; 1350,642; 1388,513; 1407,671; 1502,883; 1522,863; 1685,177; 1712,961
T. atroviride	**Copper/Zinc superoxid dismutase R.HVGDLGNIETDAQGNAK.G (significant)**
$[MH]^+$ 1919.580 Da	
Fragment masses	70,057; 74,241; 84,089; 101,101; 110,105; 112,116; 115,114; 120,097; 129,135; 136,121; 141,148; 154,136; 158,141; 167,141; 169,156; 172,164; 175,158; 186,157; 197,200; 226,170; 244,201; 272,269; 284,164; 373,224; 431,241; 502,282; 513,256; 530,290; 547,312; 601,281; 618,360; 687,341; 765,430; 801,434; 844,427; 872,439; 1048,605; 1119,585; 1176,648; 1233,698; 1401,670; 1490,909; 1548,049; 1805,327; 1890,016
T. atroviride	**Plectin/S10 domain containing protein R.DAGEGKEGGAPGEFAPQFR.G (significant)**
$[MH]^+$ 2100.408 Da	
Fragment masses	70,035; 74,121; 84,045; 101,052; 110,047; 112,064; 115,068; 129,077; 136,054; 154,064; 157,076; 172,069; 175,086; 181,075; 197,094; 226,097; 240,098; 244,101; 275,090; 425,117; 564,136; 775,183; 793,199; 864,208; 1027,253; 1141,283; 1212,421; 1327,371; 1986,618; 2003,017; 2021,194; 2074,511
T. atroviride	**HMG box protein R.YEDEKQAYNADQEDESS.- + Phospho (NOT significant)**
$[MH]^+$ 2175.662 Da	
Fragment masses	70,035; 84,063; 101,054; 110,056; 112,070; 115,075; 129,086; 136,063; 140,061; 154,075; 157,086; 175,091; 186,063; 197,113; 200,093; 212,097; 229,071; 233,112; 240,119; 244,100; 258,102; 260,086; 275,122; 303,115; 421,174; 449,162; 466,171; 492,201; 547,176; 564,188; 648,180; 665,226; 676,207; 693,225; 710,285; 727,330; 804,326; 821,309; 904,323; 921,320; 932,338; 949,372; 975,364; 992,378; 1003,338; 1010,340; 1027,425; 1084,499; 1138,385; 1155,388; 1166,389; 1183,374; 1200,425; 1280,434; 1298,453; 1386,459; 1466,517; 1483,505; 1663,673; 1855,398; 1935,768; 2065,177; 2069,591; 2071,657; 2090,274; 2114,138; 2131,213; 2141,311; 2149,574
T. atroviride	**Not related**
$[MH]^+$ 2192.564 Da	
Fragment masses	70,030; 74,075; 84,066; 87,061; 101,067; 110,066; 112,081; 115,080; 129,099; 136,070; 141,089; 154,086; 157,103; 167,097; 169,103; 172,096; 175,120; 181,108; 186,101; 195,094; 197,123; 201,104; 209,107; 212,114; 227,105; 229,097; 233,136; 240,139; 244,127; 255,098; 258,135; 260,139; 275,159; 278,121; 293,156; 300,163; 303,153; 320,170; 421,208; 449,248; 466,257; 483,146; 492,259; 500,155; 547,252; 564,288; 596,210; 665,267; 676,275; 693,316; 710,324; 727,428; 804,366; 821,368; 904,371; 921,402; 932,390; 975,391; 992,425; 995,405; 1003,374; 1027,426; 1076,448; 1084,525; 1138,435; 1155,426; 1166,441; 1183,413; 1189,471; 1200,466; 1298,401; 1386,412;

	1419,423; 1466,387; 1483,382; 1567,792; 1577,483; 1578,556; 1648,605; 1850,174; 1855,302; 1917,078; 2064,325; 2079,145; 2141,500; 2149,362; 2158,488; 2166,431; 2176,135
T. atroviride	**Not related**
$[MH]^+$ 2256.483 Da	
Fragment masses	70,061; 74,050; 84,085; 101,099; 112,106; 115,107; 129,124; 136,103; 141,121; 154,114; 157,131; 175,151; 186,136; 197,153; 240,180; 244,177; 258,182; 275,170; 292,181; 303,166; 320,185; 421,247; 449,212; 459,232; 466,241; 492,257; 547,258; 564,223; 665,298; 676,281; 693,273; 710,296; 804,372; 821,374; 914,401; 921,437; 932,421; 949,439; 975,457; 992,482; 1003,443; 1020,462; 1138,550; 1155,540; 1166,510; 1183,532; 1200,582; 1269,611; 1280,591; 1297,610; 1340,625; 1351,603; 1368,632; 1385,696; 1411,649; 1466,628; 1483,740; 1565,578; 1740,997; 1758,056; 1838,283; 1856,084; 1867,931; 1884,052; 1985,181; 2054,345; 2072,452; 2079,739; 2097,470; 2114,510; 2124,632; 2131,512; 2141,660; 2144,652; 2147,999; 2156,094; 2159,474; 2177,521; 2230,585; 2239,053
T. atroviride	**HMG box protein K.RYEDEKQAYNADQEDESS.- + Phospho (significant)**
$[MH]^+$ 2432.683 Da	
Fragment masses	70,001; 110,045; 112,066; 129,078; 154,059; 175,077; 195,072; 197,090; 227,049; 244,103; 298,099; 315,116; 326,085; 358,088; 416,106; 425,122; 455,050; 487,090; 513,127; 554,156; 574,130; 584,071; 673,155; 683,147; 802,156; 812,131; 861,247; 866,104; 883,130; 932,293; 1020,245; 1047,287; 1145,348; 1275,365; 1583,306; 2004,934; 2314,459; 2320,428; 2329,853; 2405,504; 2407,987; 2413,509
T. atroviride	**Not related**
$[MH]^+$ 2482.755 Da	
Fragment masses	70,030; 72,054; 110,062; 112,077; 129,085; 169,099; 175,116; 195,105; 197,116; 199,122; 227,102; 244,163; 259,099; 280,151; 298,160; 301,129; 308,152; 310,169; 315,201; 326,172; 331,134; 344,159; 358,162; 369,172; 373,170; 397,219; 407,198; 412,186; 425,241; 430,207; 455,191; 457,242; 469,215; 473,180; 487,234; 496,262; 509,188; 511,242; 526,246; 541,198; 554,274; 558,214; 566,203; 568,227; 574,269; 584,209; 587,245; 610,266; 625,257; 655,285; 665,270; 673,326; 683,282; 698,230; 754,331; 764,299; 767,255; 782,340; 784,314; 795,236; 802,351; 812,256; 830,236; 838,254; 848,263; 853,320; 866,268; 883,288; 893,337; 901,348; 911,359; 982,335; 992,366; 1010,400; 1012,378; 1030,402; 1092,306; 1097,421; 1109,328; 1141,383; 1159,411; 1191,360; 1240,451; 1251,394; 1258,439; 1269,391; 1340,446; 1357,490; 1565,481; 1583,491; 1654,480; 1768,466; 1882,580; 2374,882; 2449,107
T. atroviride	**Not related**
$[MH]^+$ 2504.724 Da	
Fragment masses	110,052; 129,082; 169,072; 175,103; 199,085; 201,105; 227,085; 229,095; 244,144; 259,083; 298,146; 300,117; 315,193; 326,145; 344,151; 358,123; 397,169; 412,133; 425,225; 430,172; 455,153; 473,167; 487,210; 541,163; 554,255; 558,185; 574,245; 584,184; 586,224; 625,217; 655,249; 665,212; 673,291; 683,274; 698,192; 754,264; 767,209; 782,301; 784,277; 795,186; 802,303; 812,219; 830,244; 866,201; 883,219; 901,312; 911,328; 982,311; 1010,316; 1030,367; 1092,258; 1141,311; 1159,353; 1258,385; 1357,413; 1379,341; 1583,420; 1654,460; 1768,658; 1905,375; 2075,198; 2173,424; 2359,563; 2448,140
T. atroviride	**Not related**
$[MH]^+$ 2563.733 Da	
Fragment masses	70,062; 72,064; 129,102; 147,115; 169,102; 187,114; 199,120; 201,131; 227,110; 244,174; 259,114; 280,154; 298,160; 300,134; 308,179; 310,174; 315,196; 326,166; 331,149; 340,157; 344,149; 358,149; 369,176; 373,147; 397,213; 407,225; 412,176; 425,214; 430,182; 439,196; 455,171; 457,205; 469,205; 487,210; 496,232; 511,211; 526,232; 536,246; 541,195; 554,243; 558,197; 568,253; 574,239; 584,206; 586,242; 610,265; 625,272; 638,236; 655,279; 665,274; 673,298; 683,282; 698,227; 724,309; 736,320; 739,291; 754,316; 764,346; 767,264; 772,286; 782,337; 784,326; 787,282; 795,251; 802,343; 812,273; 830,288; 838,300; 848,289; 853,364; 866,290; 883,303; 893,380; 901,399; 911,386; 964,333; 967,416; 981,288; 984,351; 992,439; 1010,448; 1013,436; 1030,459; 1064,413; 1074,359; 1079,452; 1081,452; 1092,383; 1097,474; 1109,394; 1123,442; 1141,493; 1159,501; 1169,470; 1191,421; 1208,398; 1210,446; 1222,486; 1240,543; 1251,530; 1258,567; 1269,531; 1290,486; 1307,515; 1322,556;

	1340,570; 1357,621; 1468,629; 1486,693; 1547,678; 1565,722; 1583,769; 1636,829; 1654,807; 1704,481; 1751,756; 1756,673; 1768,900; 1847,785; 1865,933; 1882,989; 1943,607; 2012,103; 2141,187; 2240,383; 2260,061; 2355,482; 2431,909; 2435,185; 2438,761; 2446,907; 2449,563; 2454,471; 2457,009; 2466,603; 2474,153; 2484,635; 2503,986
T. atroviride	**Not related**
$[MH]^+$ 2735.864 Da	
Fragment masses	73,976; 110,052; 129,088; 175,102; 216,091; 226,102; 240,112; 244,101; 257,122; 315,126; 326,120; 425,157; 554,178; 687,204; 740,241; 802,248; 918,286; 1014,281; 1032,260; 1038,305; 1117,316; 1145,339; 1148,395; 1167,383; 1266,334; 1357,404; 1379,516; 1470,449; 1591,621; 1704,630; 1819,704; 1934,849; 2466,238; 2590,437; 2609,604; 2616,765; 2619,845; 2622,716; 2627,258; 2633,788; 2638,252
T. atroviride	**NAC domain containing protein K.AGEKGEDDDDIPDLVEGENFESKVE.- (significant)**

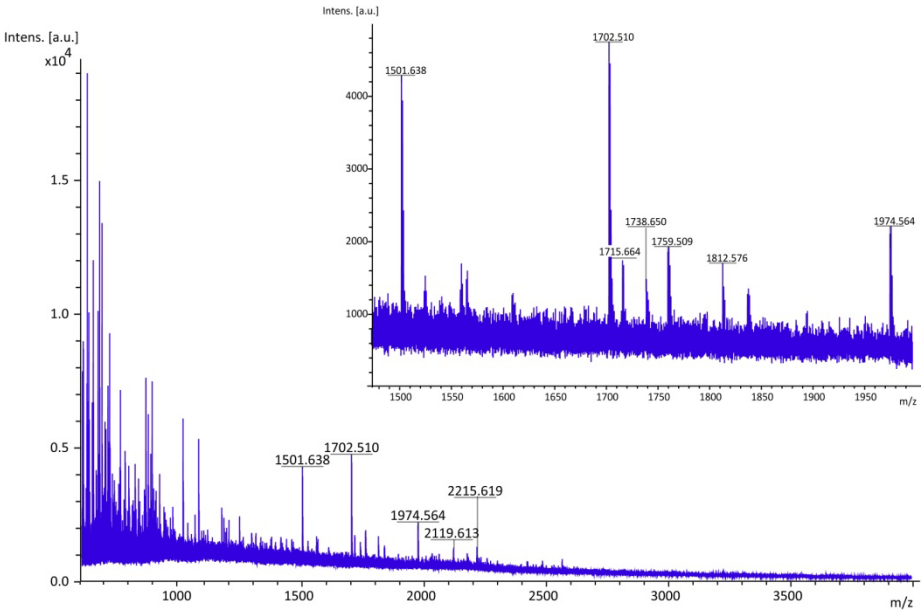


Figure 6.64 Positive ion reflector TOF - MALDI mass spectrum of 2_2_13

$[MH]^+$ 1501.638 Da	
Fragment masses	70,032; 84,062; 86,057; 100,050; 110,054; 112,070; 115,070; 129,089; 133,062; 136,059; 139,081; 141,086; 143,079; 154,080; 157,086; 169,099; 171,093; 175,106; 181,092; 183,108; 185,108; 187,087; 190,104; 197,111; 200,114; 202,095; 204,106; 207,086; 209,106; 212,102; 214,103; 217,096; 221,086; 223,103; 226,115; 229,114; 232,102; 235,095; 237,103; 240,121; 243,108; 245,108; 248,113; 250,093; 252,104; 255,114; 257,125; 259,123; 262,104; 264,116; 266,097; 268,116; 271,118; 273,104; 276,101; 278,112; 280,103; 282,111; 284,111; 286,107; 288,133; 292,111; 294,105; 297,115; 300,104; 303,115; 308,119; 310,118; 313,130; 315,119; 320,096; 327,121; 329,118; 331,114; 338,107; 343,129; 355,111; 368,127; 529,166; 625,200; 781,213; 1033,158; 1129,756; 1301,251; 1373,907; 1391,919; 1428,120; 1447,107; 1450,319; 1452,346; 1454,362; 1474,437; 1476,447; 1479,404; 1482,866; 1485,973
T. atroviride	**Not related**
$[MH]^+$ 1702.510 Da	
Fragment masses	70,042; 84,064; 86,077; 101,071; 110,070; 112,082; 115,084; 120,080; 129,104; 136,086; 141,110; 143,111; 146,096; 154,100; 156,105; 158,098; 167,105; 169,111; 171,110; 175,122; 186,117; 195,095; 197,129; 216,120; 226,137; 228,148; 231,119; 240,146; 252,150; 254,157; 257,150; 312,135; 358,134; 427,154; 471,157; 641,236; 657,198; 1647,117; 1651,490; 1655,687; 1674,137;

	1677,418; 1680,113
T. atroviride	**40S ribosomal protein S15 K.HGYIGEFEEVDDHR.S (NOT significant)**
$[MH]^+$ 1715.664 Da	
Fragment masses	70,057; 84,069; 86,081; 101,073; 110,071; 112,086; 115,088; 120,085; 129,105; 136,086; 138,086; 141,102; 143,091; 154,097; 156,103; 158,106; 167,099; 169,106; 171,108; 175,128; 183,113; 185,115; 187,104; 195,101; 197,132; 200,135; 202,104; 205,113; 212,132; 214,136; 216,126; 223,145; 226,143; 228,137; 235,128; 244,135; 268,163; 277,147; 312,199; 358,175; 427,223; 525,184; 542,228; 641,257; 657,233; 770,268; 933,226; 1046,276; 1391,125; 1516,741; 1614,810; 1646,648; 1655,058; 1664,493; 1683,074; 1684,899; 1689,896
T. atroviride	**Not related**
$[MH]^+$ 1738.650 Da	
Fragment masses	70,060; 74,447; 84,078; 86,077; 110,078; 112,092; 115,096; 129,110; 136,087; 138,099; 141,107; 143,104; 154,102; 157,122; 159,105; 168,122; 175,135; 181,118; 183,136; 185,122; 195,115; 197,141; 201,132; 209,141; 211,153; 216,136; 218,158; 221,141; 223,160; 225,147; 227,148; 229,125; 240,157; 244,148; 312,207; 431,173; 626,270; 657,247; 686,287; 723,279; 740,296; 1129,420; 1167,524; 1325,218; 1446,356; 1669,379; 1681,182; 1684,416; 1686,561; 1689,664; 1706,930; 1712,578; 1715,435
T. atroviride	**Not related**
$[MH]^+$ 1759.509 Da	
Fragment masses	70,037; 84,048; 86,072; 110,052; 112,063; 115,075; 129,087; 136,068; 141,082; 143,090; 154,083; 167,080; 172,084; 175,097; 181,092; 185,097; 195,065; 197,105; 212,102; 216,111; 312,118; 369,128; 427,099; 484,161; 1464,251; 1557,201; 1645,051; 1703,230; 1707,470; 1710,587; 1732,175; 1735,758
T. atroviride	**Not related**
$[MH]^+$ 1812.576 Da	
Fragment masses	70,048; 84,064; 86,085; 101,071; 110,062; 112,078; 115,084; 129,092; 136,071; 138,071; 154,088; 157,103; 167,097; 175,112; 181,103; 186,108; 195,099; 197,128; 226,125; 369,093; 484,192; 599,214; 919,299; 1145,401; 1307,256; 1396,496; 1424,549; 1566,225; 1604,289; 1706,578; 1758,330; 1764,833; 1789,521
T. atroviride	**Not related**
$[MH]^+$ 1974.564 Da	
Fragment masses	70,024; 74,106; 84,049; 110,038; 112,056; 115,063; 129,073; 136,044; 141,072; 155,069; 157,077; 167,070; 169,064; 171,073; 175,075; 181,071; 186,069; 195,041; 197,078; 272,105; 358,054; 456,102; 513,145; 584,151; 699,147; 1718,346; 1907,804; 1947,302; 1950,213; 1954,604; 1958,321; 1960,206
T. atroviride	**Not related**
$[MH]^+$ 2119.613 Da	
Fragment masses	70,034; 74,146; 84,058; 110,058; 112,081; 115,080; 129,090; 136,079; 141,084; 155,089; 175,099; 181,094; 197,105; 226,146; 385,210; 513,153; 727,203; 756,220; 895,310; 918,366; 1058,333; 1089,396; 1666,446; 1831,089; 1975,266; 2039,942; 2093,561; 2097,883; 2101,918
T. atroviride	**Not related**
$[MH]^+$ 2215.619 Da	
Fragment masses	70,035; 101,087; 110,087; 112,090; 115,091; 129,116; 136,084; 155,112; 175,139; 197,152; 551,224; 564,212; 664,308; 752,298; 779,377; 824,370; 878,468; 938,425; 991,548; 1091,557; 1121,514; 1275,575; 1934,324; 2141,121
T. atroviride	**Not related**

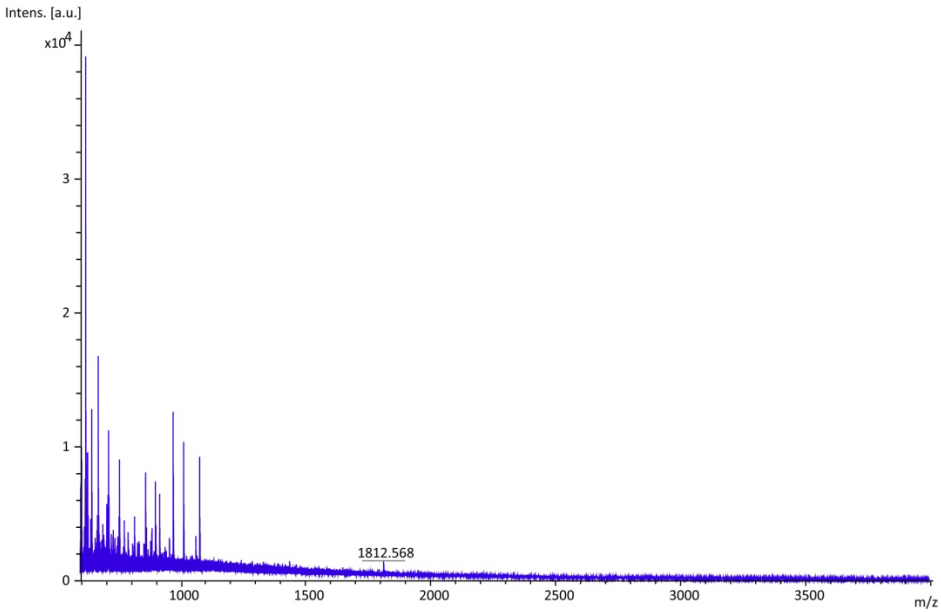


Figure 6.65 Positive ion reflector TOF - MALDI mass spectrum of 2_2_14

$[MH]^+$ 1812.568 Da	
Fragment masses	70,042; 84,060; 86,071; 98,072; 100,073; 110,063; 112,079; 115,083; 129,097; 136,071; 139,092; 141,090; 143,089; 146,081; 154,094; 157,094; 167,092; 172,100; 175,115; 181,094; 185,117; 197,127; 218,127; 288,175; 1751,162; 1753,149; 1757,432; 1760,457; 1763,786; 1767,289; 1771,174; 1779,003; 1783,370; 1786,397; 1788,537; 1792,993
T. atroviride	**Not related**

6.2.4 *Trichoderma atroviride* $_{tmk1}$ vs. *Rhizoctonia solani* (reduced mycoparasitism)

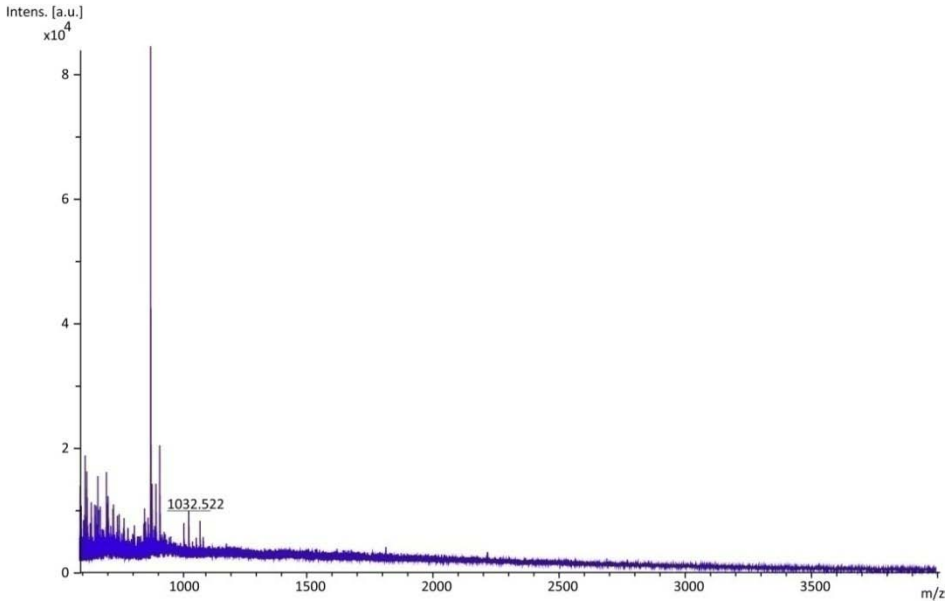


Figure 6.66 Positive ion reflector TOF - MALDI mass spectrum of 3_1_1

$[MH]^+$ 1032.522 Da	
Fragement masses	70,069; 86,094; 100,093; 102,068; 107,063; 110,077; 112,097; 115,089; 127,1; 129,106; 141,106; 143,108; 154,097; 158,099; 167,105; 169,112; 172,08; 175,127; 181,097; 184,099; 188,11; 190,091; 195,091; 197,118; 200,104; 202,107; 211,118; 213,116; 215,124; 218,142; 227,102; 229,138; 235,1; 246,132; 248,101; 253,109; 260,124; 279,096; 286,129; 294,076; 304,088; 310,091; 345,15; 382,14; 410,14; 508,23; 525,144; 544,055; 688,208; 696,875; 797,951; 836,825; 838,889; 840,962; 843,029; 924,168; 968,16; 980,813; 983,074; 986,279; 988,462; 990,828; 1006,879; 1009,687
T. atroviride	**FAD/FMN containing dehydrogenase R.NTGHDYLGR.S (NOT significant)**

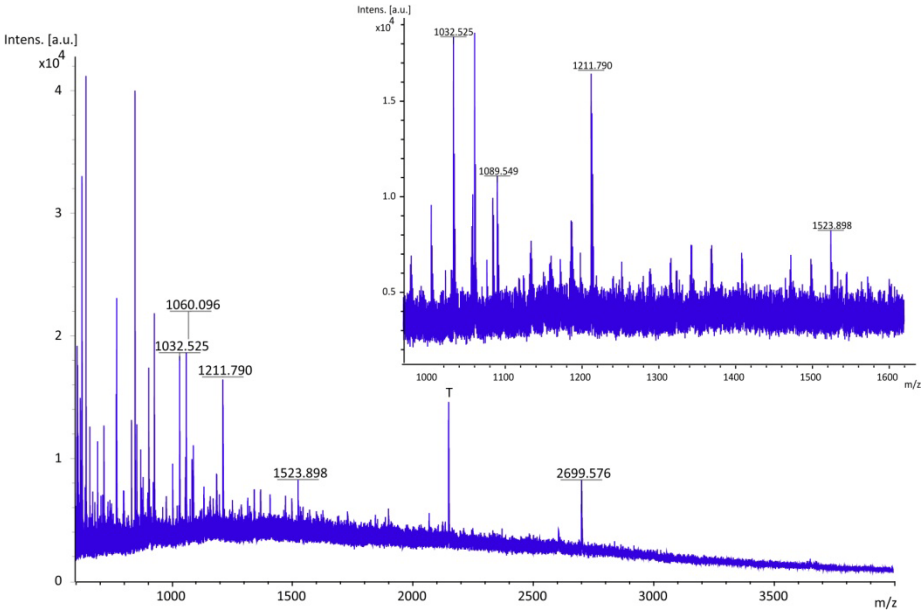


Figure 6.67 Positive ion reflector TOF - MALDI mass spectrum of 3_1_2

$[MH]^+$ 1032.522 Da	
Fragment masses	60,027; 70,052; 84,067; 86,088; 98,081; 101,08; 104,112; 112,093; 115,092; 120,083; 126,097; 129,103; 136,081; 140,092; 143,108; 147,078; 151,086; 154,091; 157,109; 167,101; 169,111; 172,091; 175,119; 181,100; 184,084; 187,100; 191,088; 195,100; 197,108; 199,118; 201,119; 203,101; 205,087; 207,093; 209,095; 211,113; 213,103; 215,105; 217,099; 219,099; 226,113; 229,130; 231,107; 236,129; 240,129; 244,115; 251,111; 254,138; 258,114; 268,122; 271,159; 279,125; 286,123; 289,127; 294,092; 296,142; 310,105; 313,175; 329,138; 331,158; 373,125; 382,143; 400,166; 407,115; 410,132; 434,148; 442,170; 460,152; 508,245; 525,174; 529,144; 538,165; 555,218; 563,129; 589,198; 597,228; 643,763; 652,044; 681,604; 697,883; 718,233; 727,290; 820,178; 824,291; 826,412; 832,586; 836,782; 838,902; 840,847; 843,087; 874,417; 907,969; 959,775; 970,513; 979,814; 987,460; 989,671; 1006,989; 1009,256
T. atroviride	**Not related**
$[MH]^+$ 1060.096 Da	
Fragement masses	60,02; 70,047; 84,07; 86,085; 95,058; 101,077; 104,116; 112,089; 115,092; 120,090; 129,109; 136,078; 140,087; 143,122; 152,084; 157,114; 164,103; 169,116; 172,103; 175,123; 181,105; 184,087; 187,107; 191,088; 193,112; 195,104; 197,123; 199,120; 201,108; 209,101; 211,116; 213,112; 216,101; 226,119; 229,132; 231,118; 236,143; 240,139; 243,126; 245,110; 251,127; 254,146; 258,138; 261,124; 268,135; 271,171; 279,145; 286,134; 289,145; 296,155; 303,150; 313,189; 329,152; 331,183; 373,138; 400,188; 407,128; 434,169; 442,189; 464,139; 529,169; 538,199; 555,239; 563,166; 597,247;

	637,944; 698,390; 703,797; 711,348; 753,414; 820,773; 824,659; 827,069; 831,276; 841,374; 845,510; 858,431; 864,814; 871,095; 883,413; 901,459; 908,551; 959,598; 972,457; 975,881; 980,520; 997,527; 1000,765; 1003,502; 1006,814; 1013,363; 1015,447; 1018,763; 1022,417; 1031,362; 1038,467
T. atroviride	**Not related**
$[MH]^+$ 1089.549 Da	
Fragment masses	60,025; 70,054; 84,073; 86,095; 95,068; 98,089; 101,08; 104,113; 112,094; 115,095; 120,095; 125,096; 129,110; 136,086; 140,096; 143,123; 147,093; 149,085; 154,095; 157,119; 160,117; 167,109; 171,111; 175,126; 181,109; 184,092; 187,097; 189,112; 191,095; 193,111; 195,115; 197,116; 199,124; 201,112; 203,118; 209,115; 211,128; 213,115; 216,111; 219,115; 221,114; 226,125; 229,140; 231,120; 236,144; 240,139; 244,136; 251,124; 254,151; 258,136; 261,117; 268,140; 271,174; 279,148; 286,142; 289,150; 296,155; 299,138; 313,195; 329,159; 331,192; 373,141; 400,193; 407,145; 434,173; 508,279; 529,190; 538,214; 555,218; 563,186; 582,228; 597,247; 681,464; 703,784; 771,466; 820,353; 867,363; 870,372; 880,440; 886,500; 892,758; 896,960; 900,209; 909,328; 927,368; 999,380; 1002,935; 1007,503; 1024,408; 1027,545; 1041,369; 1044,561; 1049,173; 1059,290; 1066,197
T. atroviride	**Not related**
$[MH]^+$ 1211.790 Da	
Fragment masses	70,042; 84,056; 86,079; 98,076; 101,062; 104,107; 112,078; 115,079; 120,073; 126,085; 129,096; 136,066; 139,076; 141,095; 143,106; 149,055; 154,076; 157,098; 165,082; 167,086; 169,086; 172,076; 175,106; 181,083; 184,071; 187,079; 191,074; 193,100; 195,084; 197,091; 199,095; 201,085; 209,082; 211,096; 213,090; 216,079; 219,086; 226,094; 229,099; 231,089; 236,115; 240,104; 244,090; 251,091; 254,115; 258,084; 268,094; 271,136; 279,101; 282,100; 286,093; 289,115; 296,110; 302,114; 304,095; 313,149; 323,082; 325,084; 329,106; 331,139; 373,086; 407,082; 442,140; 529,150; 538,172; 555,216; 563,136; 597,215; 620,130; 754,253; 771,344; 870,587; 908,144; 926,984; 995,742; 999,463; 1013,640; 1015,738; 1037,742; 1055,752; 1096,859; 1113,253; 1127,883; 1131,241; 1135,944; 1152,942; 1162,115; 1169,921; 1177,902; 1183,758; 1185,845; 1187,985; 1191,761; 1194,018
T. atroviride	**Not related**
$[MH]^+$ 1523.898 Da	
Fragment masses	70,074; 84,075; 86,102; 98,088; 101,083; 104,109; 112,099; 115,102; 120,095; 126,106; 129,115; 136,090; 141,111; 143,127; 147,093; 157,123; 167,107; 169,114; 172,117; 175,137; 181,121; 184,106; 186,125; 189,123; 191,109; 193,130; 195,119; 197,131; 199,124; 201,134; 203,116; 207,125; 209,125; 211,133; 213,122; 216,131; 223,134; 226,141; 229,140; 231,127; 233,132; 235,132; 237,141; 240,150; 243,155; 245,130; 251,140; 254,153; 257,151; 259,124; 261,129; 268,152; 271,184; 278,141; 280,145; 286,152; 292,143; 294,146; 296,167; 298,158; 301,143; 303,167; 313,200; 316,155; 325,154; 329,164; 331,188; 339,160; 341,173; 356,180; 373,164; 400,203; 407,151; 434,189; 442,204; 529,212; 538,236; 555,262; 563,212; 597,287; 620,222; 813,299; 847,267; 870,337; 879,249; 904,303; 936,285; 1032,327; 1119,278; 1135,566; 1154,443; 1308,297; 1324,554; 1330,843; 1420,319; 1458,603; 1463,989; 1472,199; 1474,270; 1480,857; 1483,085; 1495,773; 1497,630; 1500,918
T. atroviride	**Not related**
$[MH]^+$ 2699.576 Da	
Fragment masses	70,005; 74,019; 84,021; 110,037; 112,046; 129,07; 169,062; 175,074; 183,076; 186,058; 189,102; 197,069; 200,066; 209,051; 212,044; 215,056; 226,059; 229,075; 240,069; 242,110; 244,054; 252,068; 258,078; 269,057; 271,073; 273,077; 287,076; 298,067; 313,093; 315,071; 341,058; 344,091; 355,073; 357,072; 398,091; 440,078; 458,074; 502,166; 780,201; 847,203; 895,200; 1010,217; 1200,305; 1310,328; 1315,54; 1617,525; 1686,707; 1785,7110; 2000,862; 2209,917; 2485,554; 2553,675; 2571,578; 2583,398; 2587,341; 2594,745; 2610,443; 2613,99; 2641,323; 2664,633; 2670,92; 2678,058; 2681,138
T. atroviride	**Not related**

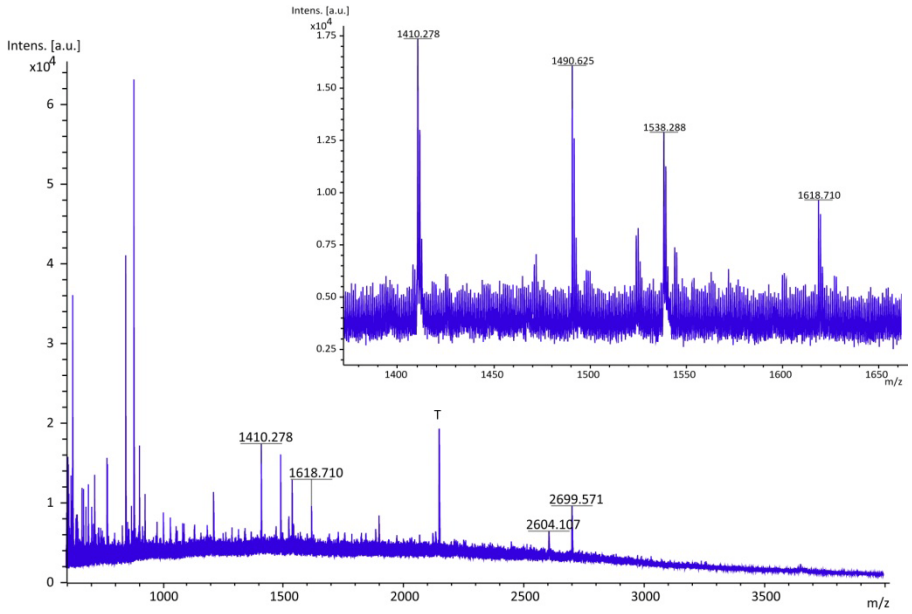


Figure 6.68 Positive ion reflector TOF - MALDI mass spectrum of 3_1_3

$[MH]^+$ 1410.278 Da	
Fragment masses	70,056; 84,075; 86,095; 98,102; 101,093; 112,115; 115,120; 120,118; 129,139; 136,111; 140,134; 143,147; 147,128; 157,159; 167,150; 169,167; 171,166; 175,178; 181,161; 183,182; 185,159; 187,154; 191,144; 197,182; 199,192; 201,181; 209,176; 211,191; 214,203; 217,166; 226,190; 229,193; 231,185; 235,195; 237,202; 240,208; 243,205; 245,178; 251,201; 254,221; 257,218; 259,192; 268,216; 271,243; 279,211; 286,220; 296,231; 298,215; 304,222; 313,266; 316,197; 329,243; 373,226; 400,263; 407,231; 425,263; 427,249; 442,282; 455,235; 485,283; 513,316; 529,296; 538,314; 555,345; 561,411; 563,279; 580,340; 597,368; 682,280; 684,350; 726,383; 737,408; 753,387; 769,405; 771,389; 796,375; 813,423; 821,270; 837,342; 847,366; 862,311; 879,388; 966,419; 969,501; 1035,488; 1095,488; 1278,757; 1338,321; 1343,472; 1348,852; 1352,936; 1356,134; 1359,332; 1362,549; 1365,781; 1381,975; 1386,162
T. atroviride	**Not related**
$[MH]^+$ 1490.625 Da	
Fragment masses	70,035; 84,053; 86,061; 98,047; 101,061; 112,072; 115,073; 120,070; 124,073; 129,089; 136,068; 140,081; 143,097; 147,076; 157,099; 167,079; 169,095; 171,101; 175,112; 181,094; 185,094; 187,084; 189,085; 191,088; 195,095; 197,108; 200,125; 207,102; 209,096; 212,112; 214,120; 217,099; 219,114; 226,113; 229,115; 232,105; 236,130; 240,124; 243,116; 245,105; 251,107; 254,131; 257,124; 259,103; 268,124; 271,155; 279,124; 286,125; 289,127; 296,136; 298,117; 300,110; 302,134; 304,122; 313,168; 316,104; 331,150; 339,131; 341,123; 343,121; 373,119; 400,154; 407,108; 425,144; 442,153; 444,124; 472,120; 513,167; 529,146; 538,169; 555,195; 563,130; 571,146; 580,168; 597,203; 718,165; 787,187; 813,185; 847,152; 902,236; 1097,325; 1146,378; 1170,274; 1244,410; 1261,501; 1273,082; 1279,524; 1286,219; 1289,414; 1375,712; 1392,697; 1410,726; 1424,426; 1435,879; 1439,124; 1442,359; 1445,642; 1461,670; 1463,704; 1468,760
T. atroviride	**Elongation factor 3 (EF-3) K.RGEEVFSDEDDL.- + Phospho (NOT significant)**
$[MH]^+$ 1538.288 Da	
Fragment masses	70,073; 84,078; 86,107; 98,080; 101,111; 112,095; 115,097; 120,099; 129,114; 136,088; 141,121; 143,115; 147,102; 157,121; 167,113; 169,122; 172,112; 175,136; 181,120; 183,139; 185,117; 191,108; 195,115; 197,137; 199,126; 201,122; 207,126; 209,121; 212,134; 214,137; 216,137; 219,134; 226,141; 229,134; 231,126; 235,131; 237,137; 240,148; 243,145; 245,110; 251,139; 254,157; 258,137; 261,143; 268,168; 271,177; 279,144; 286,153; 294,141; 296,164; 298,147; 304,151; 306,120; 313,194; 316,131; 325,165; 327,165; 329,172; 356,176; 373,161; 383,184; 407,156; 434,175; 442,204; 513,238; 529,214; 538,238; 555,269; 563,201; 580,244; 597,295; 658,243; 684,260; 724,199; 726,288; 769,334; 796,306; 813,341; 847,297; 862,260; 879,289; 904,262; 966,286; 1008,313; 1095,357; 1097,452; 1164,472; 1211,425; 1432,152;

	1465,042; 1468,284; 1473,588; 1477,794; 1482,109; 1484,141; 1488,328; 1491,531 1493,725; 1496,992; 1506,732; 1508,779; 1511,949; 1514,850; 1519,453
T. atroviride	**Not related**
$[MH]^+$ 1618.710 Da	
Fragment masses	70,048; 84,069; 86,089; 98,059; 101,064; 112,078; 115,084; 120,077; 129,093; 136,083; 141,091; 143,090; 153,092; 155,088; 157,103; 167,081; 169,102; 175,113; 181,094; 183,106; 185,098; 191,102; 195,089; 197,113; 200,127; 209,101; 212,116; 214,125; 226,115; 229,106; 231,112; 235,109; 237,116; 240,119; 244,113; 252,118; 254,143; 257,137; 259,112; 268,133; 271,162; 277,111; 285,154; 296,145; 298,128; 304,135; 313,177; 316,105; 329,156; 342,148; 373,147; 407,139; 442,211; 471,184; 529,217; 538,237; 555,261; 563,192; 572,217; 580,224; 597,287; 600,236; 684,281; 699,272; 718,264; 813,316; 847,296; 870,334; 904,295; 915,328; 936,319; 1030,382; 1092,437; 1274,498; 1389,611; 1401,081; 1407,632; 1417,352; 1502,769; 1512,258; 1520,770; 1530,225; 1538,799; 1554,626; 1564,048; 1567,194; 1569,337; 1571,590; 1574,765; 1598,146
T. atroviride	**Elongation factor 3 (EF-3) R.KRGEEVFSDEDDL.- + Phospho (NOT significant)**
$[MH]^+$ 2604.107 Da	
Fragment masses	70,018; 74,037; 84,048; 110,046; 112,069; 115,075; 129,089; 143,116; 155,095; 175,108; 181,091; 186,109; 189,143; 195,090; 197,096; 199,100; 201,096; 209,101; 211,107; 216,126; 226,121; 228,116; 230,117; 240,122; 242,149; 244,128; 246,147; 254,132; 258,129; 597,279; 685,269; 727,253; 771,357; 813,386; 847,317; 904,322; 936,292; 1160,375; 1505,383; 2132,914; 2155,659; 2274,750; 2401,199; 2418,283; 2514,113; 2527,099; 2531,343; 2546,066; 2566,462; 2569,347; 2573,531; 2575,759; 2579,392; 2583,036
T. atroviride	**Not related**
$[MH]^+$ 2699.571 Da	
Fragment masses	129,070; 175,075; 226,056; 286,059; 304,063; 357,082; 425,092; 440,066; 458,068; 511,129; 597,162; 701,143; 786,203; 988,194; 1013,315; 1200,294; 1315,447; 1617,761; 1686,614; 1785,734; 1913,814; 2000,890; 2210,227; 2485,647; 2554,491; 2571,528; 2587,192; 2593,659; 2615,163; 2625,435; 2629,424; 2633,273; 2641,741; 2644,211; 2655,830; 2664,610; 2669,165; 2672,654; 2675,505; 2679,374; 2684,205
T. atroviride	**Not related**

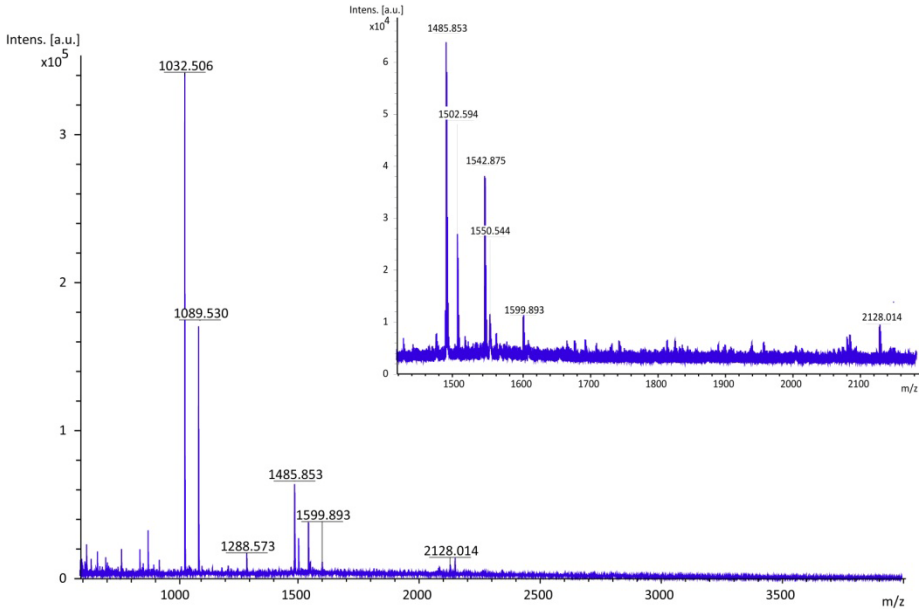


Figure 6.69 Positive ion reflector TOF - MALDI mass spectrum of 3_1_4

$[MH]^+$ 1032.506 Da	
Fragment masses	58,010; 60,006; 70,035; 86,080; 101,042; 110,058; 113,060; 115,063; 129,090;

	136,050; 140,058; 143,088; 158,069; 167,061; 172,061; 175,088; 181,063; 184,051; 188,072; 190,073; 195,052; 198,057; 212,054; 215,073; 226,065; 229,067; 232,094; 236,072; 238,064; 240,075; 242,073; 249,101; 253,043; 268,073; 271,093; 273,063; 279,048; 286,079; 296,077; 306,046; 310,052; 313,107; 328,118; 345,153; 365,068; 377,026; 382,100; 386,309; 393,068; 398,058; 400,099; 407,046; 410,097; 416,073; 421,056; 445,063; 449,041; 453,084; 473,080; 491,085; 508,205; 525,121; 529,107; 574,120; 586,144; 597,159; 606,212; 623,244; 643,146; 660,197; 663,322; 671,162; 688,214; 743,332; 760,382; 773,314; 801,365; 817,406; 841,053; 858,446; 875,443; 918,614; 953,625; 970,489; 972,696; 980,886; 986,348; 988,579; 997,569; 1007,945; 1010,201
T. atroviride	**FAD/FMN containing dehydrogenase R.NTGHDYLGR.S (significant)**
$[MH]^+$ 1089.530 Da	
Fragment masses	57,994; 70,059; 84,072; 86,101; 98,081; 101,077; 104,121; 112,101; 115,100; 120,081; 126,094; 129,119; 133,102; 136,095; 141,117; 143,134; 157,123; 167,108; 172,101; 175,131; 181,108; 184,095; 188,115; 190,114; 195,102; 197,123; 199,118; 201,110; 205,109; 207,110; 209,114; 212,127; 215,118; 224,123; 227,119; 229,109; 232,142; 236,136; 238,126; 240,143; 243,122; 245,117; 249,149; 252,119; 255,142; 258,137; 260,128; 262,129; 268,140; 271,175; 277,138; 279,127; 286,145; 294,113; 296,150; 299,147; 310,124; 313,187; 328,176; 331,155; 345,216; 353,147; 367,143; 407,147; 434,166; 439,198; 443,222; 450,152; 467,197; 473,195; 478,159; 508,301; 530,202; 538,203; 565,206; 582,246; 597,258; 606,294; 623,328; 703,820; 717,331; 720,348; 745,362; 754,394; 771,513; 817,493; 858,519; 874,529; 892,749; 896,968; 901,126; 909,305; 927,358; 933,636; 975,804; 1010,796; 1024,418; 1026,541; 1031,045; 1041,349; 1045,730; 1048,971; 1054,662; 1059,384; 1066,305
T. atroviride	**Not related**
$[MH]^+$ 1288.573 Da	
Fragment masses	70,013; 84,034; 86,062; 101,047; 104,078; 110,043; 112,062; 115,059; 120,048; 129,080; 136,057; 141,076; 143,080; 147,053; 157,080; 167,065; 172,076; 175,095; 181,072; 184,060; 186,078; 189,069; 191,054; 195,063; 197,080; 199,067; 201,081; 203,074; 209,074; 212,084; 215,080; 217,086; 226,084; 229,082; 232,096; 236,092; 240,084; 244,077; 249,086; 251,079; 254,095; 257,056; 259,058; 262,076; 268,084; 271,115; 277,079; 279,080; 286,086; 296,096; 298,071; 303,093; 310,063; 313,127; 331,112; 345,127; 407,088; 442,118; 508,191; 529,138; 555,169; 563,125; 597,187; 684,172; 709,173; 781,179; 813,161; 879,082; 916,281; 1031,889; 1091,392; 1097,869; 1224,394; 1226,684; 1228,751; 1234,843; 1238,089; 1240,252; 1243,587; 1245,834; 1247,983; 1261,814; 1263,771; 1266,394; 1269,440
T. atroviride	**Not related**
$[MH]^+$ 1485.853 Da	
Fragment masses	70,050; 84,075; 86,097; 98,072; 101,076; 110,071; 112,088; 115,082; 129,107; 136,085; 143,103; 158,102; 167,097; 172,108; 175,128; 181,104; 185,146; 190,113; 195,095; 197,126; 199,112; 213,158; 216,110; 226,128; 229,132; 232,139; 237,135; 242,175; 245,100; 249,143; 253,106; 258,112; 268,133; 271,145; 275,119; 277,135; 279,105; 286,139; 296,142; 299,140; 304,132; 310,112; 313,178; 326,170; 328,159; 345,197; 355,161; 382,155; 400,168; 411,128; 416,126; 473,139; 508,223; 518,183; 525,139; 529,172; 538,197; 555,221; 563,169; 588,192; 597,231; 606,197; 623,227; 817,264; 918,327; 1015,317; 1032,347; 1089,222; 1112,342; 1286,437; 1288,477; 1302,548; 1381,103; 1386,612; 1404,594; 1422,614; 1433,991; 1440,615; 1443,912; 1449,507; 1466,460
T. atroviride	**FAD/FMN containing dehydrogenase R.IVLKNTGHDYLGR.S (significant)**
$[MH]^+$ 1502.594 Da	
Fragment masses	70,049; 84,070; 86,081; 110,071; 112,086; 115,086; 120,081; 129,107; 136,084; 141,100; 143,111; 157,109; 159,094; 167,102; 172,108; 175,130; 181,101; 185,143; 195,093; 197,124; 201,112; 213,163; 215,126; 219,117; 226,124; 232,142; 237,115; 242,168; 244,111; 249,148; 251,126; 253,111; 259,119; 268,130; 271,153; 275,112; 279,114; 286,134; 296,143; 310,118; 313,174; 331,143; 339,140; 345,196; 355,155; 367,141; 382,153; 411,137; 473,153; 508,217; 518,165; 525,144; 529,174; 555,215; 588,175; 597,220; 606,182;

	623,199; 847,235; 918,136; 1015,210; 1032,347; 1302,531; 1361,760; 1387,728; 1391,884; 1404,734; 1422,772; 1438,662; 1441,651; 1450,099; 1453,387; 1456,606; 1459,901; 1466,665; 1484,410
T. atroviride	**60S ribosomal protein L16 R.SNGAAALLNAFQGLR.I (NOT significant)**
$[MH]^+$ 1542.875 Da	
Fragment masses	70,055; 84,077; 86,100; 110,082; 112,100; 115,099; 120,098; 129,116; 136,101; 143,137; 155,114; 157,124; 167,113; 171,126; 175,145; 181,122; 186,134; 195,113; 197,137; 200,157; 202,133; 213,170; 215,127; 217,125; 226,144; 229,142; 232,160; 235,149; 237,146; 240,152; 242,173; 244,143; 247,124; 249,146; 252,141; 254,156; 258,142; 268,169; 271,170; 274,167; 280,141; 283,154; 286,161; 296,166; 298,152; 301,167; 310,142; 313,195; 328,176; 345,209; 367,154; 370,156; 442,224; 473,179; 508,255; 525,189; 529,228; 555,280; 563,222; 582,201; 597,310; 606,227; 623,256; 813,343; 847,298; 879,288; 1032,302; 1089,444; 1211,321; 1431,818; 1442,570; 1449,942; 1483,947; 1488,811; 1494,377; 1496,519; 1498,926; 1502,095; 1512,511; 1520,275
T. atroviride	**Not related**
$[MH]^+$ 1550.544 Da	
Fragment masses	70,060; 84,077; 86,091; 101,080; 110,075; 112,093; 115,093; 120,097; 129,110; 136,075; 141,112; 143,119; 155,089; 157,111; 159,114; 167,112; 172,113; 175,130; 181,113; 185,139; 187,110; 195,107; 197,123; 200,129; 202,111; 213,159; 215,134; 217,119; 226,130; 229,129; 232,151; 235,131; 237,132; 240,145; 242,166; 244,125; 252,126; 254,144; 258,128; 268,153; 271,165; 273,130; 279,143; 286,142; 296,146; 298,145; 303,162; 310,132; 313,185; 328,166; 345,207; 353,151; 367,158; 383,169; 400,186; 407,141; 468,177; 473,156; 508,260; 529,210; 555,261; 563,208; 582,198; 597,281; 606,245; 623,245; 727,293; 813,299; 847,303; 879,256; 975,264; 1015,273; 1032,311; 1089,280; 1386,180; 1448,486; 1451,662; 1483,645; 1486,652; 1496,149; 1499,271; 1501,397; 1505,663; 1507,943; 1510,029; 1512,316; 1524,790; 1529,136
T. atroviride	**Not related**
$[MH]^+$ 1599.893 Da	
Fragment masses	70,030; 84,050; 86,078; 101,067; 110,062; 112,072; 115,071; 120,068; 129,090; 136,061; 141,085; 143,079; 155,081; 157,086; 159,094; 167,082; 175,106; 181,081; 185,097; 187,080; 195,089; 197,104; 199,091; 201,082; 213,107; 215,099; 226,113; 232,114; 235,088; 237,102; 240,115; 243,090; 268,118; 271,133; 286,109; 294,113; 296,112; 313,146; 345,167; 400,159; 407,127; 508,218; 529,168; 555,258; 563,180; 597,280; 623,229; 727,278; 813,301; 847,288; 870,358; 936,285; 1015,266; 1032,288; 1089,265; 1483,810; 1494,169; 1501,677; 1512,194; 1534,355; 1540,787; 1547,975; 1551,342; 1553,578; 1556,783; 1560,140; 1573,062; 1576,841
T. atroviride	**Not related**
$[MH]^+$ 2128.014 Da	
Fragment masses	70,033; 84,064; 86,080; 98,080; 110,058; 112,070; 115,069; 120,067; 129,090; 136,065; 141,086; 143,098; 155,087; 167,085; 169,085; 175,099; 186,102; 195,080; 197,091; 212,104; 226,103; 240,109; 258,099; 360,141; 560,234; 597,298; 689,270; 804,298; 847,324; 933,359; 1033,367; 1191,433; 1481,545; 1542,525; 1681,881; 2022,518; 2025,835; 2031,266; 2061,763; 2065,306; 2068,122; 2078,895; 2081,844; 2089,588; 2101,043; 2105,687
T. atroviride	**Not related**

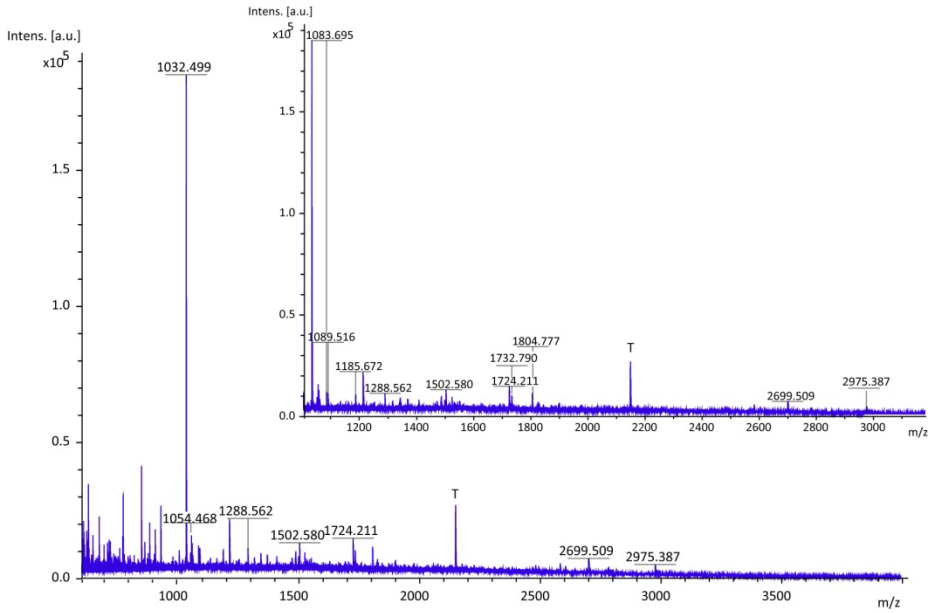


Figure 6.70 Positive ion reflector TOF - MALDI mass spectrum of 3_1_5

$[MH]^+$ 1032.499 Da	
Fragment masses	58,002; 60,027; 70,038; 86,083; 98,067; 101,059; 104,097; 110,063; 112,073; 115,070; 129,091; 136,057; 141,079; 143,101; 155,076; 158,075; 167,070; 172,074; 175,095; 181,068; 184,059; 188,081; 191,050; 195,061; 198,071; 200,098; 207,068; 209,069; 212,073; 215,078; 226,078; 232,097; 236,097; 238,084; 240,097; 242,088; 244,082; 249,099; 253,059; 258,079; 268,086; 271,121; 279,069; 286,091; 296,097; 304,087; 310,067; 313,131; 328,125; 331,106; 345,157; 373,079; 382,116; 386,289; 407,070; 410,111; 416,097; 421,077; 442,124; 445,096; 473,098; 508,219; 525,144; 529,116; 555,144; 563,104; 589,161; 597,189; 606,205; 623,268; 660,203; 671,167; 688,235; 718,192; 727,266; 743,352; 760,395; 801,352; 817,420; 874,397; 918,621; 953,655; 970,497; 972,706; 982,016; 985,240; 988,578; 997,596; 1010,223
T. atroviride	**FAD/FMN containing dehydrogenase T.NTGHDYLGR.S (significant)**
$[MH]^+$ 1054.468 Da	
Fragment masses	70,057; 84,075; 86,096; 101,080; 110,088; 112,099; 115,100; 129,120; 136,090; 157,127; 167,117; 175,136; 181,119; 184,110; 195,111; 197,131; 200,147; 204,140; 208,124; 225,125; 227,130; 231,138; 236,156; 240,158; 244,143; 251,138; 254,162; 268,151; 271,189; 279,151; 286,158; 289,172; 294,122; 296,174; 310,128; 313,213; 331,202; 382,181; 400,219; 407,168; 410,182; 434,200; 442,198; 508,135; 525,190; 538,203; 555,246; 563,209; 597,274; 652,219; 688,299; 851,480; 856,728; 858,814; 900,928; 990,463; 998,046; 1005,176; 1008,503; 1014,071; 1016,213; 1031,443
T. atroviride	**FAD/FMN containing dehydrogenase T.NTGHDYYGR.S (NOT significant)**
$[MH]^+$ 1083.695 Da	
Fragment masses	58,009; 70,066; 84,091; 86,106; 95,078; 98,105; 101,094; 104,135; 112,111; 115,111; 120,095; 126,108; 129,132; 136,103; 140,112; 143,152; 147,103; 154,123; 157,134; 164,117; 167,125; 171,140; 175,149; 181,123; 184,115; 193,142; 195,134; 197,144; 200,165; 209,133; 211,157; 214,150; 216,134; 223,160; 226,149; 229,158; 231,142; 236,169; 240,167; 244,150; 251,157; 254,182; 258,174; 268,162; 271,201; 279,178; 286,176; 289,169; 296,186; 303,192; 313,224; 325,164; 331,224; 373,180; 407,184; 434,215; 442,236; 529,240; 555,274; 563,238; 597,315; 643,891; 681,560; 697,814; 703,983; 725,587; 760,515; 820,429; 825,232; 836,601; 842,819; 847,068; 864,474; 870,343; 876,482; 880,583; 886,761; 893,112; 908,326; 924,496; 927,803; 959,555; 1003,491; 1015,192; 1018,449; 1023,912; 1026,023; 1031,184; 1034,192; 1036,356; 1039,757; 1042,004; 1049,921; 1055,940; 1059,106;

	1062,470
T. atroviride	**Ribosomal RNA-processing protein 7 K.QEQADLLKR.F (NOT significant)**
$[MH]^+$ 1089.516 Da	
Fragment masses	57,991; 60,028; 70,061; 84,082; 86,101; 95,067; 98,098; 101,089; 104,120; 112,103; 115,106; 120,100; 126,107; 129,126; 136,094; 140,108; 143,147; 154,118; 157,128; 167,120; 171,138; 175,140; 181,118; 184,110; 191,118; 193,123; 195,132; 197,131; 200,158; 203,125; 209,134; 211,147; 213,132; 216,130; 226,141; 229,151; 231,130; 236,165; 240,155; 244,142; 251,145; 254,172; 257,168; 261,129; 268,155; 271,199; 279,165; 282,166; 286,168; 289,175; 294,140; 296,183; 299,167; 306,149; 313,219; 331,210; 373,174; 400,227; 407,172; 434,222; 487,254; 508,265; 529,236; 538,251; 555,274; 563,233; 597,304; 703,843; 754,402; 771,511; 867,434; 871,383; 885,470; 892,797; 895,937; 898,084; 900,157; 902,249; 910,452; 927,423; 982,485; 999,471; 1002,870; 1008,657; 1024,475; 1027,616; 1031,103; 1033,768; 1041,424; 1044,633; 1046,872; 1049,241; 1061,797; 1066,140
T. atroviride	**Not related**
$[MH]^+$ 1185.672 Da	
Fragment masses	70,042; 84,060; 86,081; 95,033; 98,068; 101,066; 104,101; 112,076; 115,077; 120,070; 126,081; 129,093; 136,060; 140,073; 143,111; 154,080; 157,097; 167,072; 169,083; 171,095; 175,100; 181,083; 184,076; 191,060; 193,081; 195,080; 197,087; 200,091; 206,067; 209,073; 211,098; 214,089; 216,075; 223,092; 226,084; 229,094; 231,079; 237,088; 240,101; 244,082; 251,085; 254,111; 257,096; 268,095; 271,131; 279,089; 286,097; 289,108; 296,111; 313,146; 331,127; 373,090; 383,110; 400,125; 407,073; 434,109; 442,137; 460,147; 485,148; 529,153; 538,168; 555,206; 563,130; 586,163; 595,080; 597,222; 620,134; 652,099; 684,177; 739,102; 840,416; 868,106; 908,242; 936,168; 971,491; 995,546; 1029,870; 1119,324; 1125,893; 1128,148; 1137,178; 1141,706; 1143,925; 1151,881; 1160,975; 1163,101; 1167,411; 1169,241
T. atroviride	**Not related**
$[MH]^+$ 1288.562 Da	
Fragment masses	70,018; 84,041; 86,062; 95,042; 98,045; 112,068; 115,066; 120,067; 129,084; 136,064; 140,077; 143,099; 151,059; 157,092; 167,076; 172,059; 175,099; 181,079; 184,064; 186,071; 191,072; 193,077; 195,082; 197,090; 199,090; 201,081; 206,062; 209,076; 212,103; 214,078; 216,093; 219,083; 226,087; 229,090; 232,090; 236,103; 240,095; 243,093; 245,078; 251,096; 254,110; 257,095; 259,102; 268,105; 271,136; 279,112; 286,107; 289,113; 296,123; 313,153; 329,113; 331,124; 373,092; 382,128; 400,147; 407,101; 442,151; 508,213; 529,173; 538,173; 555,204; 563,157; 597,213; 620,149; 684,231; 813,199; 841,221; 879,133; 907,135; 1032,397; 1219,104; 1222,311; 1225,071; 1228,799; 1234,967; 1237,098; 1239,226; 1241,496; 1243,730; 1245,857; 1248,208; 1261,850; 1263,969; 1266,426; 1269,143
T. atroviride	**Not related**
$[MH]^+$ 1502.580 Da	
Fragment masses	70,050; 84,060; 86,079; 101,082; 112,094; 115,094; 129,110; 136,087; 140,102; 157,116; 167,102; 175,137; 181,115; 185,131; 195,111; 197,128; 200,149; 209,120; 212,144; 215,118; 217,121; 226,142; 232,150; 235,141; 237,161; 240,150; 243,146; 251,137; 254,148; 268,163; 271,175; 279,137; 286,157; 296,167; 304,154; 310,147; 313,204; 329,177; 331,190; 345,207; 355,165; 382,175; 407,151; 442,200; 508,233; 529,208; 538,221; 555,263; 563,203; 597,274; 813,269; 841,307; 847,275; 901,339; 1032,404; 1302,623; 1341,584; 1404,807; 1422,838; 1438,708; 1440,791; 1455,589; 1457,801; 1462,283; 1464,492; 1467,609; 1479,362; 1481,400; 1483,927
T. atroviride	**Not related**
$[MH]^+$ 1724.211 Da	
Fragment masses	70,065; 84,061; 86,079; 98,067; 101,064; 110,062; 112,075; 115,079; 120,075; 129,098; 136,068; 140,076; 143,105; 147,094; 157,102; 159,088; 167,092; 169,098; 172,097; 175,113; 181,101; 183,107; 185,110; 189,119; 195,098; 197,119; 200,116; 209,102; 212,113; 214,123; 217,095; 221,111; 226,127;

	228,132; 231,093; 235,105; 240,123; 242,131; 244,113; 249,107; 251,112; 255,115; 258,105; 268,136; 271,164; 286,132; 296,155; 305,155; 313,173; 329,143; 400,189; 434,178; 529,196; 555,254; 563,202; 597,283; 813,318; 841,349; 847,320; 879,291; 907,307; 1030,319; 1145,328; 1192,419; 1402,065; 1483,766; 1522,481; 1578,035; 1616,341; 1619,442; 1657,666; 1661,929; 1671,256; 1674,482; 1677,666; 1680,934; 1705,337
T. atroviride	**Not related**
$[MH]^+$ 1732.790 Da	
Fragment masses	70,050; 84,064; 86,084; 98,072; 101,069; 110,065; 112,081; 115,082; 120,078; 129,103; 136,077; 140,086; 143,110; 147,092; 155,086; 157,099; 159,100; 165,115; 167,093; 169,105; 171,100; 175,123; 181,097; 183,112; 186,107; 195,104; 197,119; 199,105; 201,117; 211,120; 213,117; 215,111; 217,092; 221,143; 223,120; 227,118; 230,126; 235,106; 240,130; 242,147; 244,130; 249,128; 254,140; 258,111; 268,127; 271,152; 286,149; 296,143; 313,182; 400,203; 407,165; 442,217; 482,172; 546,207; 555,245; 563,218; 597,298; 611,194; 668,200; 727,305; 769,297; 797,264; 813,329; 847,323; 879,274; 925,315; 936,338; 1032,288; 1088,367; 1187,431; 1358,625; 1388,721; 1401,610; 1457,745; 1631,750; 1657,071; 1662,466; 1667,846; 1679,262; 1681,303; 1684,618; 1687,882; 1706,076
T. atroviride	**Rossmann-fold $NAD(P)^+$ binding protein (FAD-binding containing protein, FAD-Monooxygenase) R.DTQHEGEQYVGNVEK.H (NOT significant)**
$[MH]^+$ 1804.777 Da	
Fragment masses	70,068; 84,090; 86,104; 98,114; 101,092; 110,091; 112,110; 115,110; 120,105; 129,132; 136,108; 143,149; 155,140; 157,145; 159,133; 167,130; 172,152; 175,161; 181,149; 185,159; 195,168; 209,174; 211,166; 226,179; 244,192; 313,258; 400,273; 563,337; 597,415; 813,444; 847,440; 870,464; 904,472; 1030,593; 1145,633; 1260,727; 1389,814; 1579,023; 1590,022; 1663,216; 1689,200; 1692,122; 1700,889; 1707,193; 1725,222; 1752,442; 1759,051
T. atroviride	**Not related**
$[MH]^+$ 2699.509 Da	
Fragment masses	69,991; 74,011; 84,040; 110,036; 112,043; 129,067; 169,073; 175,080; 181,071; 189,113; 197,067; 200,096; 211,083; 226,090; 228,081; 242,099; 244,078; 257,095; 268,095; 272,093; 310,093; 313,121; 328,095; 339,101; 341,083; 344,084; 346,123; 355,123; 358,079; 398,123; 459,151; 587,177; 684,187; 700,216; 771,235; 813,262; 847,250; 964,234; 993,422; 1041,452; 1057,356; 1127,344; 1200,341; 1418,477; 1643,284; 1686,829; 1885,578; 2000,818; 2485,811; 2552,145; 2572,495; 2575,725; 2590,435; 2593,717; 2610,557; 2626,768; 2631,051; 2633,481; 2641,517; 2644,934; 2656,516; 2664,407; 2671,972; 2678,383
T. atroviride	**Not related**
$[MH]^+$ 2975.287 Da	
Fragment masses	74,045; 129,063; 175,110; 226,090; 243,107; 313,131; 355,101; 396,124; 414,152; 673,267; 825,308; 972,473; 1051,416; 1069,516; 1122,462; 1209,454; 1296,416; 1454,568; 1608,681; 1819,140; 1934,784; 2168,614; 2517,057; 2731,753; 2802,126; 2874,384; 2904,460; 2930,989; 2949,623; 2953,225; 2957,430
T. atroviride	**Dihydrolipoamide acetyltransferase component K.KDSEPAPQSTPASAPQSSSAPEQYSSQGR.I (NOT significant)**

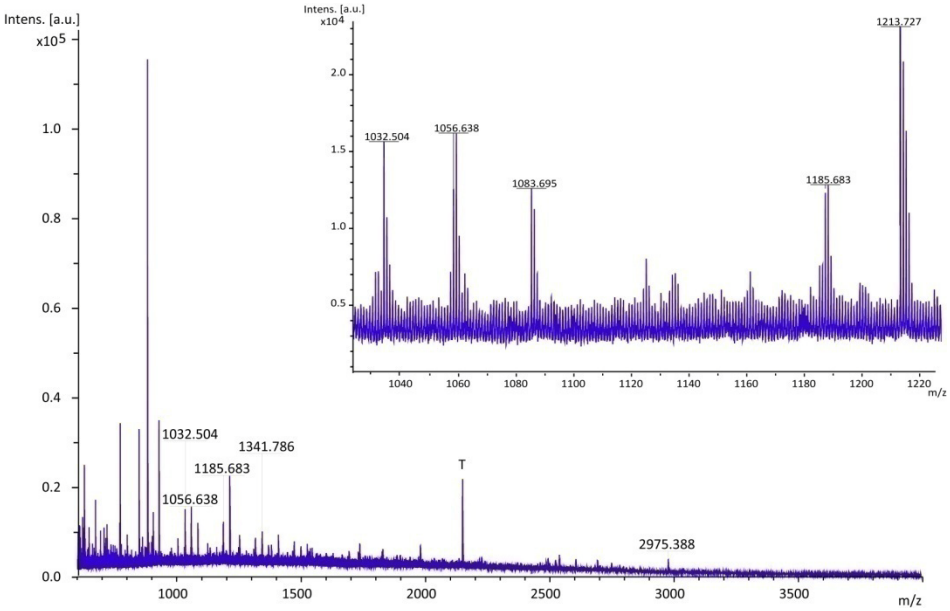


Figure 6.71 Positive ion reflector TOF - MALDI mass spectrum of 3_1_6

$[MH]^+$ 1032.504 Da	
Fragment masses	70,037; 84,052; 86,076; 88,067; 95,046; 101,053; 112,070; 115,067; 123,067; 125,052; 129,084; 132,083; 136,050; 139,074; 141,075; 147,053; 157,082; 167,081; 172,055; 175,095; 181,074; 184,070; 193,066; 195,059; 197,086; 199,073; 201,066; 209,069; 212,082; 215,078; 219,073; 226,082; 229,090; 232,083; 236,091; 240,089; 244,083; 251,076; 254,104; 258,094; 268,088; 271,124; 279,085; 286,091; 296,100; 304,102; 313,143; 331,120; 383,110; 400,124; 407,072; 442,144; 508,192; 529,105; 538,109; 555,164; 563,095; 589,197; 597,213; 652,039; 727,293; 874,424; 965,172; 968,400; 970,574; 978,764; 982,048; 985,345; 987,510; 989,742; 1006,906; 1010,448
T. atroviride	**Not related**
$[MH]^+$ 1056.638 Da	
Fragment masses	60,026; 70,038; 84,053; 86,078; 95,056; 101,061; 104,088; 107,061; 112,075; 115,076; 120,073; 125,081; 129,092; 132,080; 136,071; 140,074; 143,105; 157,096; 165,089; 167,078; 169,093; 172,069; 175,106; 181,085; 184,099; 187,082; 191,073; 193,097; 195,079; 197,091; 199,096; 201,091; 209,084; 211,100; 214,099; 217,087; 219,092; 226,099; 229,107; 231,098; 235,108; 237,104; 240,114; 243,109; 245,088; 251,102; 254,118; 258,104; 261,093; 268,107; 271,146; 279,124; 286,112; 289,127; 294,087; 296,125; 306,079; 313,164; 325,089; 329,124; 331,152; 400,162; 407,106; 434,142; 442,145; 538,152; 555,204; 563,127; 586,178; 597,220; 652,115; 858,652; 860,795; 862,897; 865,032; 883,761; 900,723 989,198; 997,934; 1008,265; 1014,890; 1031,422; 1034,421
T. atroviride	**Not related**
$[MH]^+$ 1083.695 Da	
Fragment masses	60,040; 70,064; 84,091; 86,112; 95,089; 98,101; 101,091; 104,141; 112,110; 115,114; 120,101; 126,109; 129,132; 136,111; 139,123; 141,132; 143,142; 147,104; 154,128; 157,135; 167,125; 169,134; 171,130; 175,154; 181,130; 184,123; 187,129; 191,122; 193,140; 195,143; 197,145; 200,169; 209,135; 211,145; 213,141; 216,156; 219,147; 221,134; 226,156; 229,169; 231,144; 237,163; 240,182; 242,161; 244,171; 251,153; 254,183; 257,185; 259,144; 268,168; 271,206; 279,184; 286,178; 289,194; 294,145; 296,194; 313,237; 329,210; 331,224; 407,198; 434,224; 442,231; 464,208; 487,291; 529,266; 555,277; 563,242; 597,319; 697,878; 771,541; 867,779; 886,834; 889,930; 893,137; 909,834; 927,831; 1000,019; 1003,423; 1008,089; 1020,601; 1025,046; 1032,152; 1034,290; 1037,574; 1039,789; 1042,041; 1049,965; 1056,396;

	1058,259; 1060,267; 1063,405
T. atroviride	**Not related**
$[MH]^+$ 1185.683 Da	
Fragment masses	70,038; 84,057; 86,077; 101,060; 104,086; 112,074; 115,073; 120,067; 129,090; 136,065; 140,072; 143,101; 154,073; 157,087; 167,070; 169,075; 171,084; 175,099; 181,073; 185,084; 191,068; 193,082; 195,076; 197,087; 199,086; 201,080; 203,074; 209,080; 212,087; 214,081; 216,085; 223,087; 226,084; 229,090; 231,068; 237,082; 240,097; 244,079; 251,083; 254,104; 258,075; 268,086; 271,129; 279,086; 286,088; 289,099; 296,100; 313,146; 331,119; 400,107; 407,063; 442,122; 485,144; 513,134; 529,159; 538,137; 555,191; 563,123; 586,153; 595,086; 597,225; 618,102; 652,109; 739,103; 868,117; 936,194; 996,668; 1012,791; 1029,760; 1119,323; 1126,002; 1128,246; 1137,256; 1141,784; 1143,971; 1151,714; 1162,107; 1166,230; 1168,754
T. atroviride	**Not related**
$[MH]^+$ 1213.727 Da	
Fragment masses	70,025; 84,045; 86,057; 98,040; 101,041; 104,092; 112,057; 115,056; 120,057; 126,055; 129,068; 136,041; 139,058; 141,069; 143,087; 147,036; 157,070; 165,062; 167,050; 172,042; 175,076; 181,049; 185,060; 189,064; 191,038; 193,062; 195,062; 197,064; 199,066; 201,052; 203,072; 205,042; 207,052; 209,048; 211,077; 213,061; 215,069; 217,056; 226,061; 229,058; 231,046; 233,039; 237,061; 240,072; 244,050; 251,058; 254,077; 258,060; 261,057; 268,064; 271,097; 279,058; 282,074; 286,062; 289,071; 296,073; 299,068; 302,070; 304,059; 313,110; 325,036; 327,056; 329,073; 331,100; 339,055; 341,063; 356,056; 373,054; 399,087; 407,035; 442,081; 513,103; 529,083; 538,100; 555,158; 563,073; 597,164; 620,084; 771,264; 901,478; 995,602; 999,297; 1013,534; 1022,794; 1037,602; 1039,818; 1055,615; 1127,770; 1131,092; 1136,958; 1152,797; 1154,997; 1162,000; 1169,764; 1171,967; 1177,791; 1191,212; 1194,390; 1197,395
T. atroviride	**Not related**
$[MH]^+$ 1341.786 Da	
Fragment masses	70,030; 84,051; 86,064; 98,062; 101,065; 112,086; 115,085; 120,085; 129,111; 136,083; 141,110; 143,118; 157,122; 169,128; 171,129; 175,136; 181,119; 184,135; 186,132; 191,108; 197,131; 200,149; 202,123; 209,129; 212,133; 214,141; 216,135; 219,134; 221,114; 226,141; 229,133; 231,138; 235,131; 237,155; 240,148; 244,141; 251,141; 254,166; 258,148; 261,136; 268,153; 271,188; 278,137; 280,135; 286,165; 289,165; 296,172; 304,158; 313,205; 325,140; 329,171; 331,198; 341,169; 356,184; 373,152; 385,190; 400,205; 407,157; 425,185; 434,181; 442,212; 513,222; 529,204; 538,242; 555,249; 563,201; 597,287; 620,196; 652,199; 684,286; 718,263; 745,305; 841,345; 870,294; 936,242; 1145,628; 1147,791; 1151,998; 1167,859; 1184,845; 1266,075; 1275,391; 1278,542; 1281,947; 1284,148; 1291,190; 1294,468; 1297,833; 1299,990; 1320,057; 1323,188
T. atroviride	**Not related**
$[MH]^+$ 2975.388 Da	
Fragment masses	73,939; 129,078; 175,106; 226,099; 313,106; 355,124; 640,136; 771,334; 825,288; 1051,406; 1209,470; 1296,516; 1608,851; 1679,587; 1880,498; 1934,751; 2517,016; 2732,900; 2864,549; 2905,333; 2910,940; 2931,762; 2945,366; 2951,469; 2956,760
T. atroviride	**Dihydrolipoamide acetyltransferase component K.KDSEPAPQSTPASAPQSSSAPEQYSSQGR.I (significant)**

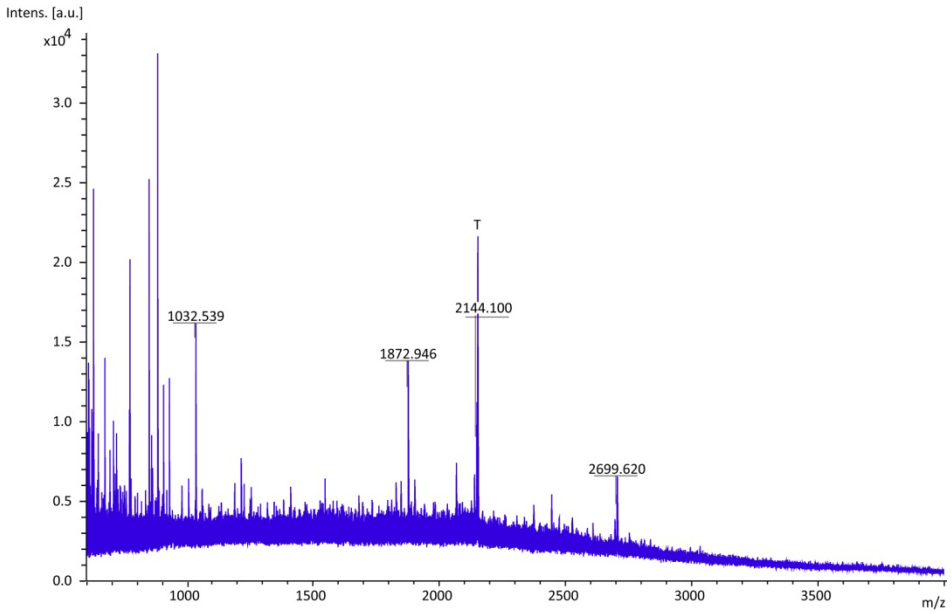


Figure 6.72 Positive ion reflector TOF - MALDI mass spectrum of 3_1_7

$[MH]^+$ 1032.539 Da	
Fragment masses	58,017; 70,056; 84,074; 86,099; 95,075; 98,093; 101,086; 104,129; 112,099; 115,100; 120,096; 124,107; 129,117; 133,097; 136,099; 139,102; 141,111; 143,121; 148,094; 154,103; 157,124; 164,097; 167,108; 169,114; 175,137; 181,112; 184,101; 187,111; 193,104; 195,111; 197,136; 199,131; 201,130; 209,119; 212,130; 214,122; 216,111; 219,116; 221,123; 226,122; 229,139; 231,129; 234,105; 236,146; 240,146; 243,140; 245,115; 251,125; 254,154; 258,132; 261,125; 268,138; 271,174; 279,146; 286,143; 289,161; 294,110; 296,161; 299,145; 310,129; 313,192; 329,159; 331,157; 373,149; 382,175; 407,145; 410,152; 442,195; 508,278; 525,190; 555,222; 563,159; 597,238; 652,055; 836,926; 838,994; 841,045; 874,499; 968,388; 970,557; 980,998; 983,171; 985,421; 987,586; 989,816; 995,501; 1009,298
T. atroviride	**Not related**
$[MH]^+$ 1872.945 Da	
Fragment masses	70,054; 84,084; 86,104; 98,112; 101,092; 110,094; 112,112; 115,110; 120,112; 129,137; 136,118; 143,158; 155,143; 157,153; 159,141; 167,147; 169,155; 175,162; 197,193; 199,197; 212,175; 227,209; 262,206; 311,205; 313,284; 422,194; 597,432; 813,483; 847,462; 879,431; 1095,551; 1175,556; 1418,805; 1775,393; 1793,408; 1800,722; 1803,901; 1808,220; 1813,287; 1819,728; 1823,994; 1828,357; 1841,967; 1847,165; 1851,736; 1854,810
T. atroviride	**Glycogen synthase kinase 3 K.ILVENEPNVSYICSR.Y + Phospho (NOT significant)**
$[MH]^+$ 2144.100 Da	
Fragment masses	70,042; 84,063; 98,088; 101,075; 110,071; 112,087; 115,092; 120,083; 129,105; 136,076; 143,113; 155,099; 157,105; 159,099; 169,125; 175,118; 181,109; 183,145; 197,129; 219,129; 226,138; 230,126; 240,159; 258,118; 270,130; 296,176; 341,161; 343,195; 359,144; 382,160; 424,240; 440,195; 610,251; 638,357; 766,459; 895,489; 914,341; 1081,549; 1196,582; 1265,565; 1363,593; 1703,903; 1801,948; 2024,061; 2028,429; 2031,449; 2041,173; 2046,455; 2064,456; 2076,092; 2080,362; 2086,496; 2089,748; 2093,896; 2102,951; 2116,482; 2120,646; 2123,307; 2125,622
T. atroviride	**Elicitor protein R.FAYLGNDSDGEEKPVVPVK.T + Phospho (NOT significant)**
$[MH]^+$ 2699.620 Da	
Fragment masses	70,004; 73,991; 84,047; 110,057; 112,060; 129,095; 155,070; 171,091; 175,111; 181,090; 189,143; 195,087; 197,106; 200,119; 213,123; 216,111; 226,106; 228,112; 230,108; 235,109; 238,116; 240,114; 242,140; 244,109; 252,113; 254,115; 257,120; 266,109; 268,118; 270,132; 272,100; 286,113; 298,120;

	301,119; 303,142; 311,143; 313,148; 316,118; 325,127; 327,120; 339,158; 341,114; 343,146; 345,145; 369,140; 398,146; 440,153; 458,156; 643,237; 724,278; 771,335; 844,336; 957,275; 1012,382; 1085,450; 1196,446; 1200,438; 1418,413; 1686,841; 1786,995; 2001,194; 2211,465; 2485,842; 2554,197; 2572,074; 2625,947; 2637,889; 2642,950; 2655,620; 2670,625; 2674,197; 2677,673
T. atroviride	**Not related**

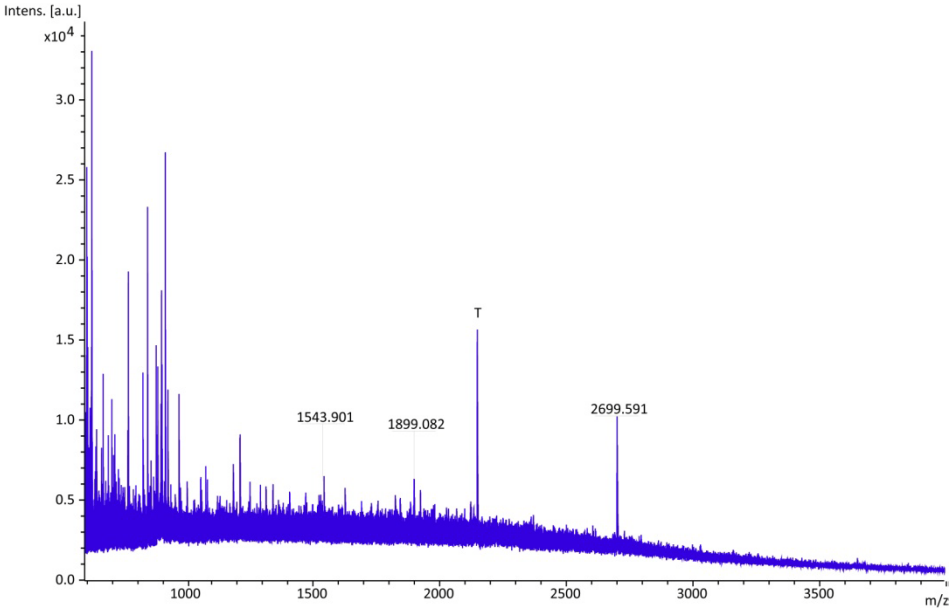


Figure 6.73 Positive ion reflector TOF - MALDI mass spectrum of 3_1_8

$[MH]^+$ 1543.901 Da	
Fragment masses	70,052; 84,056; 86,084; 98,062; 101,074; 104,106; 112,082; 115,084; 120,076; 126,087; 129,098; 136,077; 143,096; 147,078; 151,081; 157,106; 159,094; 169,101; 171,107; 175,116; 181,096; 184,086; 186,106; 189,097; 191,082; 193,103; 195,093; 197,113; 199,117; 201,114; 203,102; 205,094; 207,100; 209,110; 211,121; 214,120; 216,108; 218,122; 226,121; 228,137; 231,110; 233,120; 235,120; 237,127; 240,131; 243,125; 245,113; 251,118; 254,145; 257,129; 259,112; 261,112; 268,135; 271,156; 278,130; 280,133; 286,137; 289,139; 292,124; 294,124; 296,142; 298,122; 300,128; 302,136; 304,136; 313,177; 325,137; 327,143; 329,145; 331,160; 340,143; 356,161; 373,152; 383,156; 385,145; 407,132; 442,189; 529,193; 538,214; 555,258; 563,193; 597,284; 658,234; 769,305; 796,271; 813,311; 847,272; 879,258; 943,298; 966,237; 1009,264; 1164,305; 1211,274; 1472,296; 1475,500; 1478,726; 1480,829; 1483,053; 1485,030; 1488,089; 1490,133; 1493,340; 1495,484; 1497,651; 1502,064; 1511,731; 1513,818; 1517,231; 1519,445; 1523,215; 1526,818
T. atroviride	**Not related**
$[MH]^+$ 1899.082 Da	
Fragment masses	70,069; 84,092; 86,114; 98,120; 101,104; 104,130; 110,104; 112,121; 115,124; 120,120; 129,145; 136,123; 141,147; 143,167; 155,153; 157,160; 159,156; 167,163; 169,173; 175,179; 181,176; 184,156; 186,187; 195,178; 197,193; 211,206; 226,218; 313,291; 597,443; 847,514; 1692,350; 1812,273; 1823,635; 1827,112; 1830,151; 1833,171; 1836,443; 1840,518; 1842,611; 1845,689; 1848,978; 1852,115; 1854,403; 1857,613; 1860,778; 1865,543; 1869,091; 1872,331
T. atroviride	**Not related**
$[MH]^+$ 2699.591 Da	

Fragment masses	69,983; 74,058; 84,037; 110,045; 112,054; 115,047; 129,072; 143,081; 155,067; 169,068; 171,078; 175,067; 181,057; 183,091; 186,065; 189,115; 195,059; 197,074; 201,069; 209,074; 212,073; 214,087; 216,074; 226,082; 229,080; 235,067; 237,071; 240,082; 242,110; 244,076; 252,078; 254,090; 257,108; 266,078; 268,087; 270,082; 272,084; 278,066; 283,093; 286,077; 296,081; 298,088; 300,083; 313,103; 315,078; 328,078; 337,102; 339,096; 341,083; 344,106; 355,094; 357,097; 359,089; 361,064; 367,097; 398,110; 440,092; 454,112; 458,096; 1013,379; 1200,382; 1686,761; 1785,779; 2000,942; 2210,372; 2485,895; 2553,800; 2571,959; 2615,724; 2619,495; 2623,187; 2626,994;2629,539; 2632,521; 2637,934; 2642,989; 2646,095; 2648,887; 2652,599; 2655,846; 2660,078; 2663,267; 2668,187; 2672,257; 2676,738; 2680,637; 2683,392
T. atroviride	**Ca^{2+} dependent lipid-binding protein R.QGTSTFQGTFGGGSRIVTGVAGVPFK.G + Phoshpo (NOT significant)**

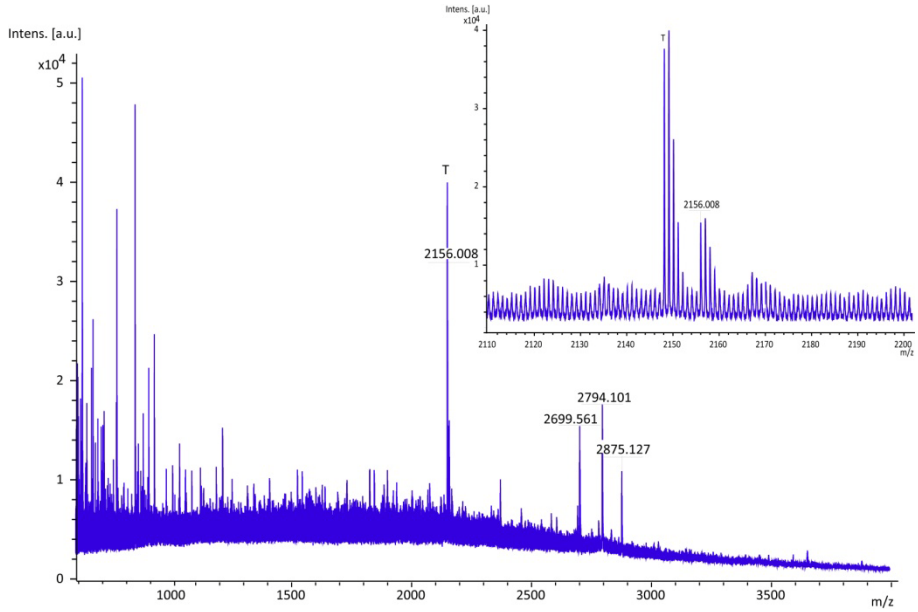


Figure 6.74 Positive ion reflector TOF - MALDI mass spectrum of 3_1_9

$[MH]^+$ 2156.008 Da	
Fragment masses	70,057; 74,136; 84,082; 86,094; 98,111; 101,086; 110,089; 112,104; 115,103; 120,100; 129,124; 136,097; 138,104; 141,119; 143,132; 155,119; 157,129; 159,114; 167,122; 169,130; 172,131; 175,141; 181,133; 183,151; 186,143; 195,131; 197,151; 212,159; 214,164; 219,143; 226,168; 230,165; 235,157; 240,154; 244,158; 252,160; 254,179; 258,152; 270,161; 301,174; 341,204; 359,210; 409,210; 440,259; 497,324; 593,368; 610,412; 708,381; 799,412; 845,476; 1125,631; 1329,598; 1337,624; 1438,649; 1502,748; 1569,801; 1812,211; 1880,078; 1950,825; 1968,807; 1988,177; 2015,921; 2028,471; 2034,037; 2040,269; 2042,599; 2045,710; 2048,609; 2059,226; 2065,359; 2079,685; 2083,913; 2086,067; 2090,383; 2094,376; 2097,682; 2100,795; 2103,930; 2107,127; 2112,418; 2115,868; 2119,037; 2130,975
T. atroviride	**Heme binding peroxidase R.DNDAAACTPDGRLPDASQPK.H (NOT significant)**
$[MH]^+$ 2699.561 Da	
Fragment masses	69,996; 74,018; 84,038; 98,063; 110,037; 112,050; 115,048; 129,068; 136,032; 143,090; 155,062; 157,063; 159,063; 167,065; 169,059; 171,058; 175,077; 181,066; 186,074; 189,107; 195,064; 197,080; 200,088; 209,057; 212,083; 216,076; 226,087; 229,084; 235,063; 237,079; 240,080; 242,100; 244,069; 252,083; 254,074; 257,094; 259,077; 266,075; 268,086; 270,089; 272,068; 275,077; 283,078; 286,082; 297,085; 299,092; 301,088; 311,086; 313,104;

	315,073; 325,101; 328,103; 339,107; 341,082; 344,116; 357,085; 440,096; 458,102; 545,136; 786,192; 847,249; 1013,422; 1200,366; 1617,708; 1686,776; 1784,961; 1913,948; 2000,992; 2211,142; 2485,735; 2553,651; 2572,745; 2609,310; 2614,222; 2617,775; 2621,037; 2626,405; 2630,228; 2633,486; 2637,796; 2641,911; 2645,605; 2656,093; 2660,718; 2668,694; 2672,046; 2678,393; 2682,556
T. atroviride	**Not related**
$[MH]^+$ 2794.101 Da	
Fragment masses	69,971; 74,000; 112,049; 129,071; 141,077; 155,056; 158,074; 169,075; 171,090; 175,097; 187,069; 197,085; 201,070; 212,100; 215,078; 226,097; 229,096; 231,050; 240,100; 243,094; 245,052; 252,089; 257,117; 272,090; 274,128; 284,101; 298,097; 300,085; 311,114; 316,069; 328,127; 330,083; 345,166; 357,080; 369,120; 374,091; 387,085; 440,134; 445,098; 474,183; 484,151; 486,114; 545,228; 555,162; 625,172; 643,209; 660,236; 789,276; 829,190; 900,260; 918,305; 1029,339; 1043,283; 1047,349; 1114,349; 1145,371; 1162,357; 1260,356; 1346,366; 1403,425; 1663,413; 1681,595; 1877,444; 1992,491; 2106,641; 2717,520; 2759,737
T. atroviride	**Not related**
$[MH]^+$ 2875.127 Da	
Fragment masses	110,038; 112,073; 129,084; 141,098; 169,105; 171,110; 175,116; 186,107; 201,091; 226,131; 229,125; 231,090; 240,129; 245,058; 257,147; 274,165; 286,122; 328,166; 345,191; 357,116; 369,152; 374,118; 440,183; 445,110; 474,216; 484,185; 527,244; 545,246; 555,247; 625,243; 643,240; 660,277; 771,320; 789,328; 829,288; 900,337; 918,382; 928,362; 1029,428; 1043,366; 1047,438; 1114,431; 1127,442; 1144,462; 1162,473; 1242,497; 1260,487; 1277,513; 1346,541; 1403,586; 1444,543; 1550,590; 1663,772; 1675,305; 1681,697; 1761,698; 1778,813; 1877,824; 1888,545; 1895,814; 1975,805; 1992,864; 2081,088; 2090,881; 2108,014; 2178,296; 2205,888; 2223,070; 2277,609; 2320,537; 2609,499; 2617,298; 2623,423; 2625,423; 2699,142; 2707,420; 2742,889; 2748,727; 2756,937; 2759,838; 2763,504; 2774,372; 2777,740; 2795,741; 2804,452; 2824,310; 2842,962; 2849,718
T. atroviride	**Elongation factor 1 beta (EF1B) K.APAAEDDDDVDLFGSDDEEEDAEAVR.I + Phospho (significant)**

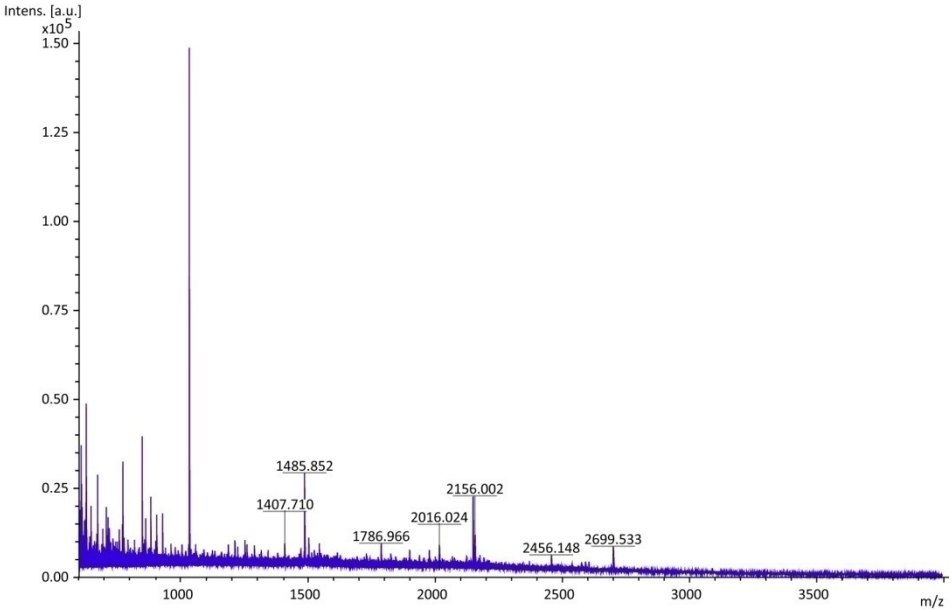


Figure 6.75 Positive ion reflector TOF - MALDI mass spectrum of 3_1_10

$[MH]^+$ 1407.710 Da	
Fragment masses	70,042; 84,061; 86,088; 101,088; 104,124; 110,082; 112,101; 115,105; 120,104; 129,129; 136,105; 139,124; 141,129; 143,149; 147,117; 151,126; 154,126; 157,147; 159,130; 167,135; 169,147; 171,154; 175,164; 181,150; 184,138;

	186,152; 189,158; 191,147; 195,153; 197,169; 200,177; 202,153; 205,146; 207,157; 209,170; 211,174; 213,173; 216,166; 219,153; 221,154; 226,180; 229,175; 232,187; 235,167; 237,180; 240,195; 243,187; 245,163; 247,174; 249,185; 251,180; 254,207; 257,193; 259,169; 261,184; 268,194; 271,227; 278,187; 280,193; 282,192; 284,199; 286,201; 292,190; 294,180; 296,208; 299,202; 308,194; 313,246; 316,184; 329,210; 331,225; 346,192; 373,174; 382,229; 400,247; 407,211; 442,251; 508,276; 529,272; 538,287; 555,321; 563,264; 597,356; 684,349; 726,353; 769,417; 796,377; 813,456; 847,385; 862,342; 879,439; 942,197; 966,496; 1032,491; 1083,657; 1306,702; 1331,102; 1336,370; 1341,686; 1343,772; 1352,183; 1355,275; 1358,502; 1360,659; 1362,819; 1366,123; 1381,383; 1385,888; 1388,487
T. atroviride	**Not related**
$[MH]^+$ 1485.852 Da	
Fragment masses	70,040; 84,076; 86,089; 98,079; 101,069; 104,111; 110,077; 112,092; 115,093; 120,089; 129,112; 136,094; 141,108; 143,137; 147,096; 155,103; 157,123; 159,103; 167,115; 172,125; 175,143; 181,125; 184,108; 186,136; 191,121; 195,112; 197,135; 199,130; 201,128; 211,143; 213,157; 215,139; 219,135; 226,155; 232,158; 235,133; 237,135; 240,148; 242,184; 244,141; 247,142; 249,153; 251,140; 254,160; 257,156; 259,130; 262,149; 266,147; 268,158; 271,176; 279,143; 286,158; 294,137; 296,169; 298,159; 304,149; 310,136; 313,199; 326,175; 328,177; 340,163; 345,196; 407,159; 442,184; 508,246; 525,161; 538,221; 555,250; 563,205; 597,262; 623,250; 847,255; 918,375; 942,206; 1015,401; 1032,403; 1097,669; 1286,590; 1302,708; 1404,780; 1422,716; 1431,148; 1434,322; 1436,486; 1441,836; 1459,151; 1465,544
T. atroviride	**FAD/FMN containing dehydrogenase R.IVLKNTGHDYLGR.S (NOT significant)**
$[MH]^+$ 1786.966 Da	
Fragment masses	70,064; 84,083; 86,098; 98,100; 101,084; 104,113; 110,087; 112,103; 115,104; 120,101; 129,121; 136,094; 143,140; 155,124; 157,126; 159,124; 167,132; 169,143; 172,130; 175,146; 181,128; 183,151; 185,142; 187,121; 195,126; 197,146; 200,156; 212,147; 214,168; 226,163; 229,154; 235,145; 313,226; 597,339; 764,315; 813,400; 847,407; 913,433; 1032,419; 1081,469; 1143,546; 1291,686; 1371,722; 1588,856; 1659,050; 1671,172; 1675,354; 1689,149; 1707,182; 1719,828; 1725,223; 1731,432; 1734,555; 1736,705; 1738,957; 1742,210; 1762,875
T. atroviride	**Not related**
$[MH]^+$ 2016.024 Da	
Fragment masses	70,047; 84,067; 86,086; 101,080; 110,073; 112,083; 115,088; 120,094; 129,105; 136,076; 143,118; 155,105; 157,117; 159,097; 167,093; 169,115; 172,106; 175,122; 181,111; 183,129; 185,113; 195,101; 197,129; 200,122; 212,125; 226,147; 252,131; 268,149; 284,143; 313,190; 590,248; 622,264; 813,359; 847,360; 879,317; 942,310; 1133,335; 1134,372; 1152,384; 1199,262; 1485,651; 1572,862; 1933,242; 1944,738; 1954,548; 1961,264; 1964,518; 1969,920; 1973,351; 1992,766
T. atroviride	**Not related**
$[MH]^+$ 2156.002 Da	
Fragment masses	70,050; 74,114; 84,081; 86,099; 98,091; 110,087; 112,105; 115,100; 120,098; 129,125; 136,096; 143,152; 155,114; 159,117; 169,129; 175,146; 181,143; 183,170; 187,131; 197,156; 230,160; 258,161; 270,154; 301,166; 341,203; 359,220; 409,197; 440,258; 610,432; 799,435; 845,446; 876,426; 892,370; 894,407; 910,372; 924,461; 942,471; 956,351; 1022,457; 1040,446; 1104,497; 1120,447; 1125,635; 1152,585; 1232,558; 1250,552; 1283,589; 1299,646; 1337,694; 1381,593; 1397,573; 1438,731; 1569,809; 1812,257; 1988,118; 2015,930; 2028,403; 2033,985; 2043,551; 2046,345; 2051,783; 2061,338; 2063,6432079,641 2097,244 2104,794 2112,374 2130,392
T. atroviride	**Not related**
$[MH]^+$ 2456.148 Da	
Fragment masses	70,019; 74,015; 84,043; 86,063; 110,044; 112,059; 115,052; 129,073; 136,046; 155,069; 157,075; 169,078; 175,084; 181,067; 186,073; 195,067; 197,086; 209,083; 212,090; 226,087; 228,104; 230,088; 255,093; 257,115; 268,107;

	272,090; 430,129; 442,154; 614,139; 810,242; 855,313; 954,361; 1070,371; 1151,366; 1208,440; 1285,485; 1387,420; 1502,514; 1511,656; 1582,538; 1738,653; 1829,414; 1859,800; 1886,657; 2014,884; 2341,248; 2382,688; 2385,612; 2391,605; 2396,733; 2401,244; 2407,960; 2415,063; 2424,750; 2429,401; 2434,425; 2438,558
T. atroviride	**Ran-binding domain containing protein R.DAKGDEEEAPESEDVHFEPVVK.L (NOT significant)**
$[MH]^+$ 2699.533 Da	
Fragment masses	110,041; 112,052; 129,074; 175,075; 216,082; 226,086; 242,101; 244,062; 268,108; 286,080; 313,106; 357,083; 398,116; 440,115; 563,108; 597,271; 640,172; 771,279; 810,246; 844,356; 1013,356; 1200,391; 1403,559; 1686,857; 1785,915; 1914,180; 2002,568; 2210,516; 2412,131; 2485,749; 2555,197; 2571,577; 2627,141; 2630,340; 2639,942; 2642,969; 2664,773; 2674,651
T. atroviride	**Not related**

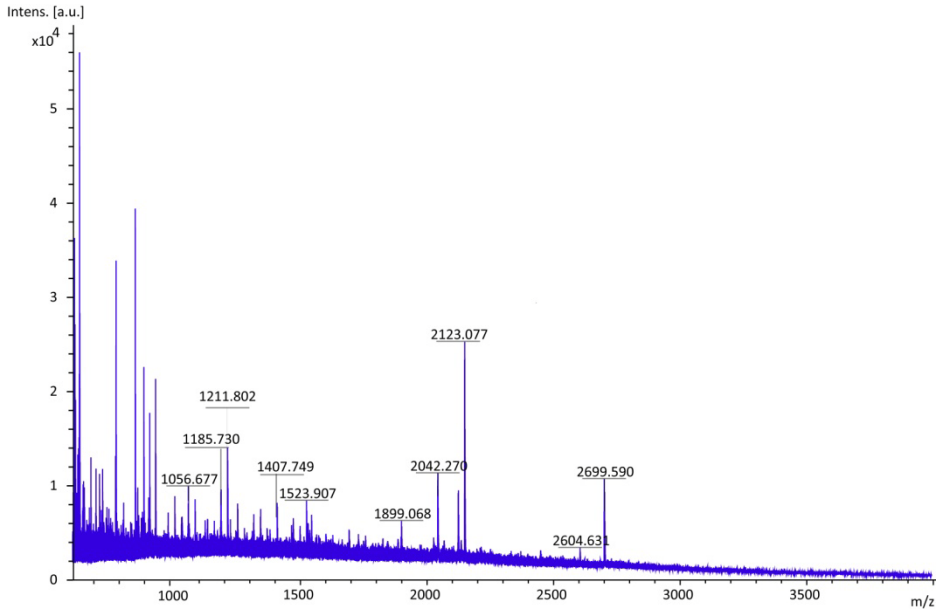


Figure 6.76 Positive ion reflector TOF - MALDI mass spectrum of 3_1_11

$[MH]^+$ 1056.677 Da	
Fragment masses	57,996; 60,011; 70,040; 84,056; 86,070; 95,053; 98,067; 101,060; 104,101; 107,056; 112,077; 115,077; 120,070; 123,094; 125,073; 129,095; 136,063; 141,091; 143,092; 153,089; 157,095; 161,087; 166,105; 169,086; 172,071; 175,107; 181,084; 184,086; 187,093; 191,073; 193,086; 195,088; 197,099; 199,101; 202,087; 209,089; 211,102; 213,100; 215,098; 217,087; 219,088; 226,099; 229,114; 231,092; 236,124; 240,115; 243,105; 245,107; 251,100; 254,124; 257,123; 259,088; 261,097; 268,108; 271,149; 279,113; 286,116; 289,114; 296,128; 302,134; 304,116; 313,169; 329,128; 331,153; 373,116; 385,186; 407,112; 425,130; 434,150; 442,151; 513,167; 529,146; 538,163; 555,208; 563,152; 597,230; 652,151; 711,403; 753,462; 858,738; 862,024; 883,750; 900,743; 990,283; 992,404; 995,735; 996,953; 999,023; 1001,939; 1005,056; 1008,269; 1011,570; 1013,807; 1016,016; 1029,982; 1032,080; 1034,540; 1036,755
T. atroviride	**Not related**
$[MH]^+$ 1185.730 Da	
Fragment masses	70,048; 84,051; 86,072; 99,065; 101,065; 104,103; 112,079; 115,084; 120,076; 129,097; 136,065; 141,084; 143,102; 147,066; 157,099; 167,089; 171,094; 175,102; 181,082; 184,070; 191,084; 193,098; 195,080; 197,096; 199,109; 202,089; 209,086; 212,095; 215,099; 217,072; 223,089; 226,087; 229,103; 231,094; 236,108; 240,103; 243,094; 245,068; 251,095; 254,116; 258,093; 268,093; 271,140; 278,093; 280,098; 286,098; 289,114; 294,074; 296,118; 313,159; 329,098; 331,132; 373,106; 383,123; 400,143; 407,085; 442,153;

	485,166; 513,172; 529,173; 538,182; 555,225; 563,155; 586,173; 597,257; 652,120; 684,195; 711,333; 739,120; 868,148; 882,518; 995,630; 1029,755; 1119,298; 1121,429; 1124,770; 1128,013; 1133,982; 1137,218; 1139,458; 1141,734; 1143,969; 1150,854; 1159,951; 1162,121; 1164,026; 1166,549; 1169,575
T. atroviride	**Not related**
$[MH]^+$ 1211.802 Da	
Fragment masses	70,042; 84,059; 86,079; 95,051; 98,074; 101,067; 104,109; 112,086; 115,085; 120,077; 123,097; 126,088; 129,105; 133,093; 136,077; 141,100; 143,109; 157,107; 167,090; 169,106; 172,095; 175,118; 181,089; 184,084; 187,084; 191,083; 193,097; 195,097; 197,108; 199,113; 201,095; 203,098; 209,103; 211,110; 214,109; 216,102; 223,097; 226,106; 229,110; 231,103; 236,130; 240,119; 244,114; 251,105; 254,130; 258,108; 260,094; 268,116; 271,155; 279,118; 286,120; 289,127; 294,094; 296,129; 304,118; 313,171; 329,130; 331,145; 400,152; 407,109; 442,164; 529,168; 538,205; 555,236; 563,158; 597,251; 995,838; 1037,869; 1055,881; 1128,064; 1131,418; 1147,550; 1153,108; 1155,430; 1161,210; 1163,395; 1165,584; 1170,079; 1178,050; 1184,958; 1188,256; 1192,944
T. atroviride	**Not related**
$[MH]^+$ 1407.749 Da	
Fragment masses	70,055; 84,070; 86,094; 98,096; 101,091; 104,129; 112,110; 115,107; 120,105; 129,130; 136,111; 140,120; 143,141; 147,120; 157,146; 167,136; 169,154; 171,155; 175,166; 181,149; 184,135; 186,163; 191,141; 193,153; 195,152; 197,160; 199,168; 202,155; 209,154; 211,173; 213,167; 216,165; 219,178; 226,177; 229,176; 231,167; 233,167; 237,187; 240,187; 244,178; 251,184; 254,203; 257,195; 259,173; 268,197; 271,228; 279,204; 286,202; 289,216; 296,214; 298,209; 304,209; 313,253; 329,222; 331,231; 373,220; 400,254; 407,217; 442,268; 513,308; 529,295; 538,310; 555,344; 561,386; 563,277; 580,331; 597,374; 682,286; 684,362; 726,393; 737,410; 753,423; 769,452; 771,429; 796,417; 813,477; 821,289; 837,402; 847,427; 862,398; 879,461; 966,518; 969,600; 1035,618; 1083,629; 1095,622; 1338,511; 1341,630; 1343,779; 1347,679; 1350,836; 1353,255; 1356,414; 1358,514; 1360,705; 1362,916; 1366,112; 1380,227; 1384,642; 1386,577
T. atroviride	**Not related**
$[MH]^+$ 1523.907 Da	
Fragment masses	70,063; 84,088; 86,089; 98,096; 101,087; 112,106; 115,109; 129,123; 136,100; 141,112; 143,133; 157,133; 169,134; 172,119; 175,150; 181,125; 184,115; 186,130; 189,132; 191,120; 193,115; 195,123; 197,151; 199,150; 201,132; 207,136; 209,130; 212,147; 214,160; 216,136; 219,157; 226,152; 229,158; 231,152; 233,145; 235,153; 237,158; 240,164; 243,159; 247,142; 251,158; 254,172; 258,156; 261,149; 268,171; 271,201; 278,160; 280,171; 286,168; 289,166; 296,190; 298,176; 304,158; 313,218; 324,170; 329,193; 331,197; 340,195; 353,175; 357,183; 373,185; 382,203; 399,211; 407,172; 442,223; 513,249; 529,253; 538,272; 555,308; 563,245; 597,334; 813,377; 847,345; 870,402; 904,358; 936,369; 1457,662; 1464,073; 1467,206; 1470,421; 1473,331; 1475,534; 1478,913; 1482,142; 1496,892
T. atroviride	**Not related**
$[MH]^+$ 1899.068 Da	
Fragment masses	70,070; 74,122; 84,090; 86,114; 98,125; 101,106; 110,107; 112,122; 115,124; 120,124; 129,145; 136,114; 141,151; 143,168; 155,161; 157,157; 167,155; 169,162; 175,177; 181,168; 183,186; 185,165; 197,192; 226,217; 313,302; 359,200; 400,275; 407,303; 441,359; 529,417; 555,396; 563,366; 597,466; 712,342; 813,526; 847,533; 879,515; 904,538; 936,508; 969,636; 1603,719; 1669,723; 1692,408; 1825,702; 1828,957; 1832,083; 1834,198; 1840,469; 1843,539; 1847,620; 1851,114; 1857,439
T. atroviride	**Not related**
$[MH]^+$ 2042.270 Da	
Fragment masses	70,038; 74,205; 84,067; 86,086; 98,088; 101,070; 110,069; 112,085; 115,081; 129,096; 136,064; 141,085; 143,109; 157,096; 159,084; 167,087; 169,101; 175,115; 181,112; 183,123; 186,115; 200,124; 209,108; 211,123; 213,107; 226,141; 230,119; 244,158; 254,127; 258,129; 313,173; 341,154; 357,200; 359,147; 456,273; 470,171; 529,251; 555,260; 563,243; 583,248; 597,318; 601,235; 672,358; 712,269; 771,383; 813,365; 825,319; 847,345; 954,337; 1137,342; 1155,324; 1896,694; 1968,352; 1971,885; 1975,184; 1978,090; 1981,326; 1984,427; 1987,610; 1992,964; 1996,119;

	1999,429; 2009,044; 2016,685; 2024,399
T. atroviride	**Not related**
$[MH]^+$ 2123.077 Da	
Fragment masses	70,032; 84,056; 86,077; 98,076; 110,052; 112,072; 115,071; 129,086; 143,103; 155,077; 159,063; 175,107; 187,066; 226,096; 244,117; 313,141; 316,109; 341,101; 357,147; 400,158; 415,144; 442,150; 456,199; 470,074; 529,182; 555,177; 571,229; 583,151; 601,199; 616,191; 654,239; 672,287; 681,144; 694,208; 712,196; 731,055; 745,238; 753,305; 771,346; 797,300; 807,234; 810,180; 825,257; 844,292; 858,349; 870,428; 923,265; 936,307; 954,296; 957,433; 987,382; 1054,427; 1068,364; 1071,492; 1137,369; 1149,489; 1155,372; 1200,543; 1210,468; 1236,445; 1253,352; 1313,639; 1336,571; 1353,539; 1442,695; 1555,773; 1799,113; 1819,129; 1914,231; 2007,441; 2010,484; 2025,330; 2043,363
T. atroviride	**Not related**
$[MH]^+$ 2604.631 Da	
Fragment masses	73,985; 84,067; 110,072; 112,084; 115,088; 129,107; 136,083; 155,106; 175,125; 181,116; 186,136; 189,168; 212,140; 215,137; 226,145; 268,168; 286,155; 2529,856; 2540,097; 2543,975; 2546,833; 2578,727
T. atroviride	**Not related**
$[MH]^+$ 2699.590 Da	
Fragment masses	74,049; 84,036; 86,048; 110,041; 112,034; 129,070; 175,076; 181,068; 189,126; 200,082; 203,105; 212,055; 216,081; 226,077; 240,092; 242,113; 244,078; 257,076; 266,080; 268,085; 270,085; 286,080; 311,077; 313,116; 325,091; 328,085; 339,114; 341,075; 344,110; 355,089; 357,093; 398,118; 440,116; 458,113; 511,174; 786,262; 1013,417; 1200,373; 1281,757; 1315,557; 1546,818; 1618,675; 1686,807; 1785,972; 1913,952; 2001,035; 2130,374; 2210,332; 2425,374; 2485,787; 2554,899; 2571,990; 2625,582; 2629,133; 2633,545; 2638,136; 2642,219; 2645,522; 2655,903; 2665,033; 2671,227; 2674,597; 2678,417; 2681,399
T. atroviride	**Not related**

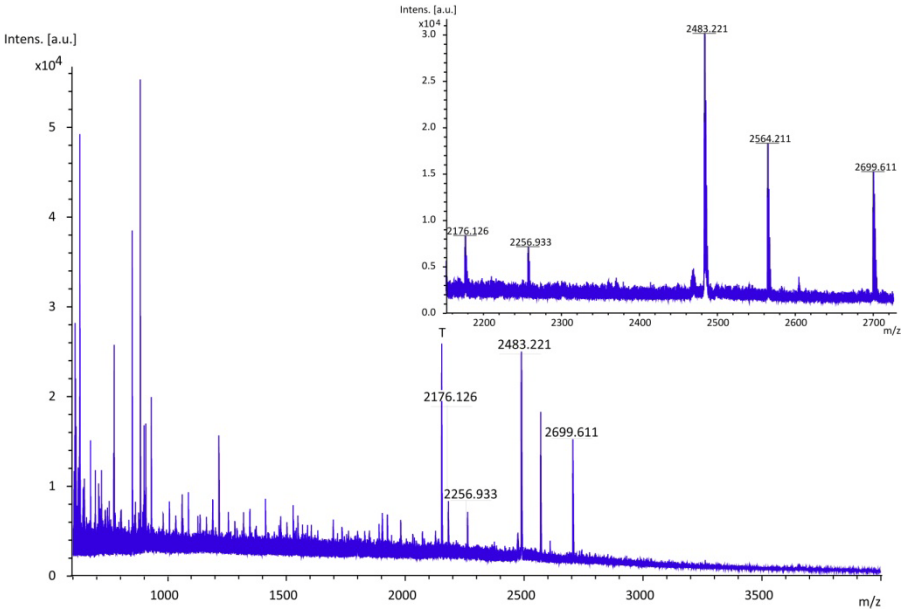


Figure 6.77 Positive ion reflector TOF - MALDI mass spectrum of 3_1_12

$[MH]^+$ 2176.126 Da	
Fragment masses	70,028; 84,053; 98,079; 101,063; 110,066; 112,078; 115,080; 120,070; 129,097; 136,072; 143,108; 152,094; 155,093; 157,106; 159,093; 169,117; 172,099; 175,114; 181,103; 183,123; 186,116; 195,105; 197,123; 200,117; 212,135;

	226,141; 228,133; 230,153; 233,128; 240,148; 244,129; 254,149; 258,137; 268,157; 270,159; 275,157; 301,152; 341,199; 359,205; 440,231; 547,228; 564,246; 610,377; 693,280; 727,350; 804,323; 847,389; 904,374; 1084,530; 1483,453; 1987,828; 2130,549; 2141,985; 2146,673; 2158,931
T. atroviride	**Not related**
$[MH]^+$ 2256.933 Da	
Fragment masses	70,055; 84,087; 86,106; 98,117; 101,099; 110,098; 112,112; 115,116; 120,103; 129,133; 136,113; 143,159; 155,133; 157,143; 159,126; 169,146; 226,190; 449,163; 466,264; 547,198; 564,258; 693,282; 804,430; 813,455; 821,416; 847,486; 904,478; 921,449; 932,449; 949,489; 992,526; 1003,519; 1020,492; 1124,586; 1138,568; 1155,628; 1183,636; 1200,634; 1297,699; 1385,753; 1466,690; 1483,791; 1564,844; 1740,925; 1758,318; 1856,138; 1884,117; 1985,554; 2054,428; 2124,638; 2141,721; 2159,574; 2177,619; 2233,094
T. atroviride	**HMG-box protein K.RYEDEKQAYNADQEDESS.- + Phospho (significant)**
$[MH]^+$ 2483.221 Da	
Fragment masses	70,022; 84,045; 86,062; 98,069; 110,051; 112,066; 115,067; 129,091; 136,053; 141,080; 155,081; 157,100; 159,084; 169,090; 171,097; 175,110; 181,087; 186,099; 189,136; 197,111; 199,103; 209,099; 211,125; 227,097; 229,107; 235,104; 244,156; 252,120; 259,100; 286,151; 298,145; 300,137; 308,145; 315,178; 326,155; 358,148; 373,163; 397,198; 425,214; 430,176; 455,178; 457,201; 487,213; 526,217; 554,248; 574,256; 584,203; 586,238; 625,264; 655,277; 665,265; 673,303; 683,280; 698,240; 754,289; 782,328; 784,318; 795,244; 802,333; 812,244; 848,292; 853,321; 866,256; 883,272; 901,357; 911,352; 982,375; 1010,396; 1012,413; 1030,423; 1092,320; 1141,409; 1159,409; 1258,417; 1269,435; 1340,443; 1357,450; 1565,506; 1583,538; 1654,461; 1768,500; 2400,764; 2426,962; 2430,058; 2448,719; 2459,564; 2466,276
T. atroviride	**Not related**
$[MH]^+$ 2564.211 Da	
Fragment masses	70,029; 72,068; 74,038; 84,058; 98,059; 102,047; 110,071; 112,083; 115,080; 129,100; 136,066; 155,095; 157,118; 159,101; 169,102; 175,129; 186,110; 189,152; 195,094; 199,119; 201,109; 209,125; 211,120; 227,099; 244,157; 259,103; 298,145; 300,133; 315,183; 326,152; 331,116; 358,153; 373,145; 397,198; 407,198; 412,175; 425,198; 430,160; 455,159; 457,192; 487,187; 496,218; 511,205; 526,220; 541,188; 554,224; 558,186; 568,201; 574,220; 584,190; 586,233; 610,250; 625,245; 655,267; 665,278; 673,281; 683,261; 698,227; 754,310; 764,299; 767,262; 782,325; 784,310; 795,243; 802,330; 812,263; 838,285; 848,297; 853,355; 866,278; 883,289; 893,360; 901,390; 911,366; 964,332; 981,279; 992,433; 1010,434; 1013,424; 1030,442; 1079,455; 1081,463; 1092,367; 1097,472; 1109,390; 1123,473; 1141,499; 1159,491; 1169,517; 1191,444; 1208,447; 1210,445; 1240,528; 1251,537; 1258,573; 1269,525; 1290,484; 1307,506; 1322,587; 1340,584; 1357,648; 1486,688; 1547,729; 1565,741; 1583,789; 1636,778; 1654,858; 1703,786; 1751,481; 1756,446; 1768,946; 1847,491; 1866,127; 1883,059; 1943,263; 2012,183; 2141,305; 2240,449; 2260,262; 2338,617; 2355,662; 2431,738; 2438,785; 2448,751; 2457,298; 2466,733; 2484,738
T. atroviride	**Not related**
$[MH]^+$ 2699.611 Da	
Fragment masses	70,012; 74,019; 84,051; 98,056; 110,054; 112,085; 115,071; 129,092; 136,082; 143,109; 155,077; 157,099; 169,099; 171,108; 175,116; 181,083; 183,121; 186,101; 189,139; 195,088; 197,104; 199,094; 201,115; 203,112; 207,092; 209,107; 212,100; 216,111; 226,115; 229,120; 235,090; 237,102; 240,107; 242,137; 244,110; 252,096; 254,116; 257,137; 266,103; 268,117; 270,114; 272,112; 283,136; 286,117; 297,133; 313,144; 315,137; 323,126; 325,149; 328,144; 342,143; 344,159; 357,131; 359,131; 367,142; 369,148; 398,163; 440,165; 454,166; 458,156; 511,204; 1200,484; 1686,903; 1785,927; 2001,130; 2210,362; 2485,885; 2554,009; 2573,022; 2614,433; 2624,724; 2628,176; 2630,881; 2633,217; 2638,676; 2643,194; 2646,633; 2655,943; 2661,123; 2667,284; 2672,738; 2679,132
T. atroviride	**Not related**

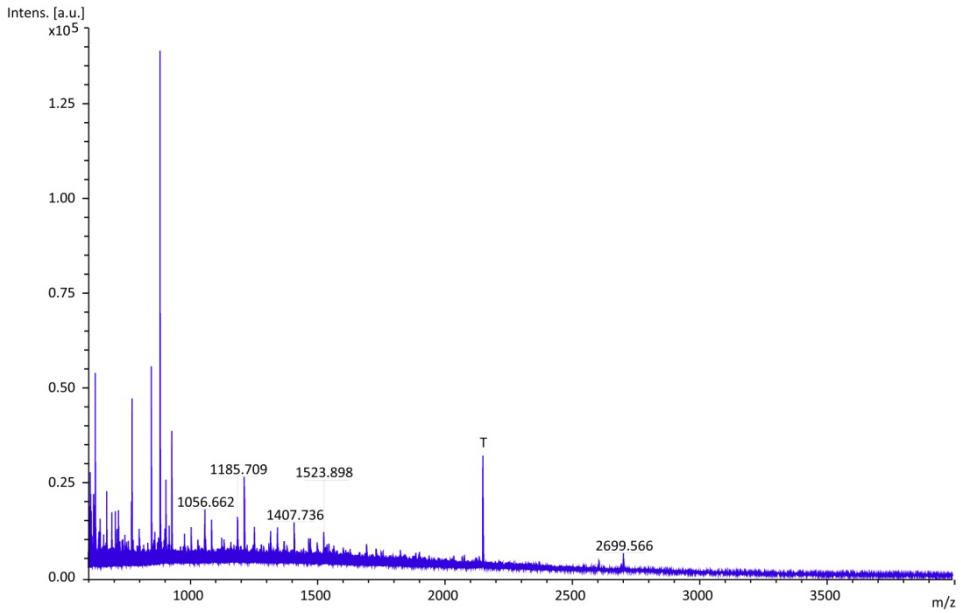


Figure 6.78 Positive ion reflector TOF - MALDI mass spectrum of 3_1_13

$[MH]^+$ 1056.662 Da	
Fragment masses	57,998; 60,022; 70,040; 73,040; 84,057; 86,077; 95,053; 98,068; 101,067; 104,105; 107,054; 112,080; 115,079; 120,075; 123,090; 126,083; 129,095; 133,076; 136,074; 139,088; 141,091; 143,101; 146,080; 152,074; 154,085; 157,099; 161,089; 166,101; 169,097; 171,099; 175,110; 181,089; 184,090; 187,090; 193,087; 195,096; 197,104; 199,104; 202,092; 206,087; 209,089; 211,105; 214,102; 216,098; 218,113; 226,106; 229,114; 231,105; 235,109; 237,116; 240,127; 244,113; 251,107; 254,131; 257,122; 260,114; 262,114; 268,119; 271,154; 279,123; 286,123; 289,128; 294,096; 296,137; 299,116; 313,176; 329,132; 331,160; 373,126; 400,178; 407,124; 434,164; 442,161; 538,181; 555,208; 563,163; 597,239; 652,170; 859,775; 863,934; 866,095; 882,684; 900,734; 981,016; 995,730; 997,944; 1007,211; 1009,335; 1012,698; 1014,905; 1017,156; 1022,846; 1033,211; 1035,716
T. atroviride	**Not related**
$[MH]^+$ 1185.709 Da	
Fragment masses	70,041; 84,059; 86,080; 95,051; 98,065; 101,066; 104,107; 112,078; 115,078; 120,073; 125,070; 129,095; 136,061; 139,082; 141,081; 143,094; 146,074; 148,075; 151,072; 154,085; 157,098; 167,080; 169,083; 172,075; 175,106; 181,074; 184,076; 187,074; 191,063; 193,095; 195,082; 197,094; 200,106; 207,079; 209,078; 212,093; 214,106; 216,081; 218,112; 226,092; 229,100; 231,079; 233,087; 237,096; 240,102; 243,104; 251,089; 254,114; 258,093; 268,097; 271,137; 286,103; 289,115; 296,119; 299,112; 313,156; 331,148; 400,132; 407,083; 442,145; 485,159; 529,182; 538,175; 555,220; 563,157; 586,191; 595,122; 597,251; 652,142; 739,133; 868,127; 996,483; 1029,764; 1119,319; 1125,935; 1128,144; 1138,318; 1141,764; 1143,970; 1151,778; 1159,962; 1163,176; 1167,378; 1169,714
T. atroviride	**Not related**
$[MH]^+$ 1407.736 Da	
Fragment masses	70,064; 84,078; 86,097; 98,091; 101,085; 104,127; 112,109; 115,113; 120,103; 129,132; 136,107; 141,137; 143,144; 157,156; 167,141; 169,147; 172,140; 175,162; 181,146; 184,135; 186,153; 191,146; 195,153; 197,170; 200,178; 209,167; 212,182; 214,168; 216,182; 218,185; 226,190; 229,177; 231,177; 237,195; 240,195; 243,192; 246,188; 251,186; 254,212; 258,202; 268,193; 271,234; 279,203; 286,207; 289,231; 294,188; 296,216; 299,214; 313,260; 329,228; 356,245; 373,235; 400,262; 407,226; 441,289; 443,251; 513,315; 529,314; 538,334; 555,370; 561,413; 563,308; 580,338; 597,397; 682,321;

	684,383; 726,416; 737,437; 753,473; 769,492; 796,440; 813,506; 821,311; 837,432; 847,472; 862,452; 879,492; 966,566; 969,645; 1035,620; 1083,686; 1095,664; 1336,267; 1339,481; 1343,718; 1351,370; 1354,331; 1357,483; 1361,775; 1366,102; 1368,583; 1382,509; 1386,018
T. atroviride	**Not related**
$[MH]^+$ 1523.898 Da	
Fragment masses	70,063; 84,084; 86,097; 98,088; 101,090; 112,101; 115,103; 120,098; 129,120; 136,095; 139,110; 141,125; 143,126; 146,102; 152,128; 157,131; 167,122; 169,132; 171,132; 175,144; 181,127; 185,138; 191,117; 193,144; 195,132; 197,146; 200,148; 202,145; 205,137; 209,137; 212,152; 215,151; 218,164; 221,144; 226,155; 229,157; 231,151; 233,151; 235,147; 237,156; 240,160; 243,165; 246,163; 249,150; 251,158; 254,180; 257,163; 259,156; 261,158; 268,174; 271,197; 278,160; 280,159; 283,168; 286,173; 289,173; 292,151; 294,166; 296,183; 298,172; 304,164; 308,165; 310,170; 313,225; 325,169; 327,186; 329,186; 331,205; 339,176; 341,184; 343,186; 373,183; 382,211; 400,222; 407,175; 442,236; 513,266; 529,249; 538,267; 555,296; 563,247; 597,328; 620,255; 684,289; 727,317; 753,310; 769,360; 771,361; 796,323; 813,353; 847,330; 870,390; 879,318; 904,362; 925,358; 936,362; 993,424; 1057,290; 1324,709; 1449,206; 1454,391; 1458,769; 1464,009; 1467,143; 1469,125; 1471,383; 1473,480; 1475,668; 1478,896; 1482,174; 1499,134; 1501,950
T. atroviride	**Not related**
$[MH]^+$ 2699.566 Da	
Fragment masses	73,951; 110,042; 112,047; 129,073; 175,057; 186,085; 189,095; 195,071; 197,086; 212,071; 216,074; 226,085; 229,081; 244,075; 252,072; 268,094; 271,096; 284,085; 286,080; 313,120; 398,138; 440,102; 597,205; 1013,413; 1200,372; 1617,817; 1686,778; 1785,639; 2001,051; 2211,534; 2485,768; 2555,044; 2573,134; 2656,945; 2671,625
T. atroviride	**Not related**

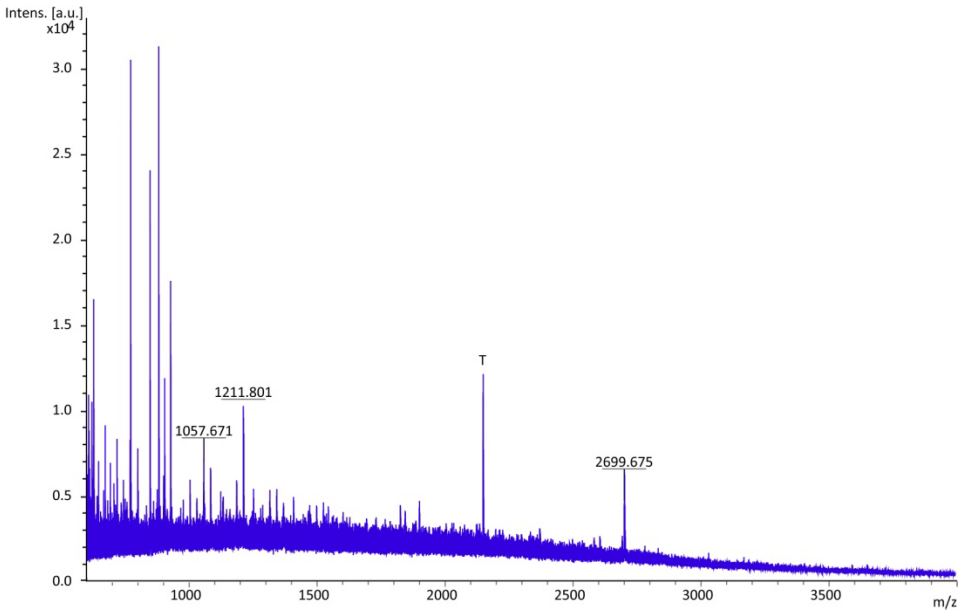


Figure 6.79 Positive ion reflector TOF - MALDI mass spectrum of 3_1_14

$[MH]^+$ 1057.671 Da	
Fragment masses	57,999; 60,034; 70,049; 84,059; 86,087; 95,067; 98,085; 101,068; 104,115; 107,070; 112,087; 115,089; 120,078; 123,107; 126,106; 129,105; 136,073; 140,091; 143,130; 154,086; 157,107; 166,129; 169,111; 172,096; 175,127; 181,102; 184,126; 187,098; 191,086; 193,123; 195,101; 197,111; 200,136;

	202,106; 209,109; 211,133; 214,122; 219,119; 226,121; 229,121; 231,106; 237,128; 240,136; 244,132; 251,124; 254,149; 258,134; 268,139; 271,171; 279,144; 286,142; 294,114; 296,166; 304,140; 313,199; 329,161; 331,193; 385,219; 400,195; 407,153; 434,188; 442,194; 555,266; 563,209; 597,275; 652,186; 711,394; 841,575; 883,668; 901,714; 997,845; 1006,134; 1008,202; 1010,391; 1012,629; 1014,782; 1017,022; 1022,770; 1033,050
T. atroviride	**Not related**
$[MH]^+$ 1211.801 Da	
Fragment masses	69,982; 112,012; 129,026; 157,026; 175,032; 226,009; 271,046; 286,005; 296,025; 329,012; 331,040; 400,040; 406,977; 434,012; 442,034; 529,031; 555,087; 563,021; 597,111; 620,033; 771,211; 978,551; 995,577; 999,368; 1013,518; 1037,623; 1055,654; 1127,783; 1131,099; 1136,978; 1146,200; 1152,855; 1162,033; 1166,452; 1169,820; 1177,829; 1185,727; 1189,030; 1192,096; 1194,310
T. atroviride	Not related
$[MH]^+$ 2699.675 Da	
Fragment masses	69,994; 74,001; 84,057; 98,074; 110,053; 112,079; 115,065; 129,094; 155,088; 157,096; 169,088; 171,087; 175,111; 181,092; 183,106; 185,089; 189,133; 195,094; 197,103; 200,112; 202,094; 209,088; 212,107; 215,103; 217,108; 226,114; 229,111; 231,112; 235,102; 237,121; 240,111; 242,128; 244,097; 252,111; 254,126; 257,123; 266,116; 268,121; 270,110; 272,122; 275,121; 278,110; 286,113; 297,126; 299,137; 301,122; 309,121; 311,139; 313,149; 315,131; 323,129; 325,149; 327,107; 329,118; 339,125; 341,120; 344,163; 355,117; 357,142; 359,127; 440,156; 1013,465; 1200,460; 1686,905; 1786,028; 2001,229; 2211,599; 2485,723; 2554,152; 2571,926; 2612,464; 2617,305; 2622,315; 2626,771; 2629,128; 2632,587; 2637,949; 2642,688; 2646,839; 2655,857; 2660,200; 2668,427; 2671,852; 2676,438
T. atroviride	**Not related**

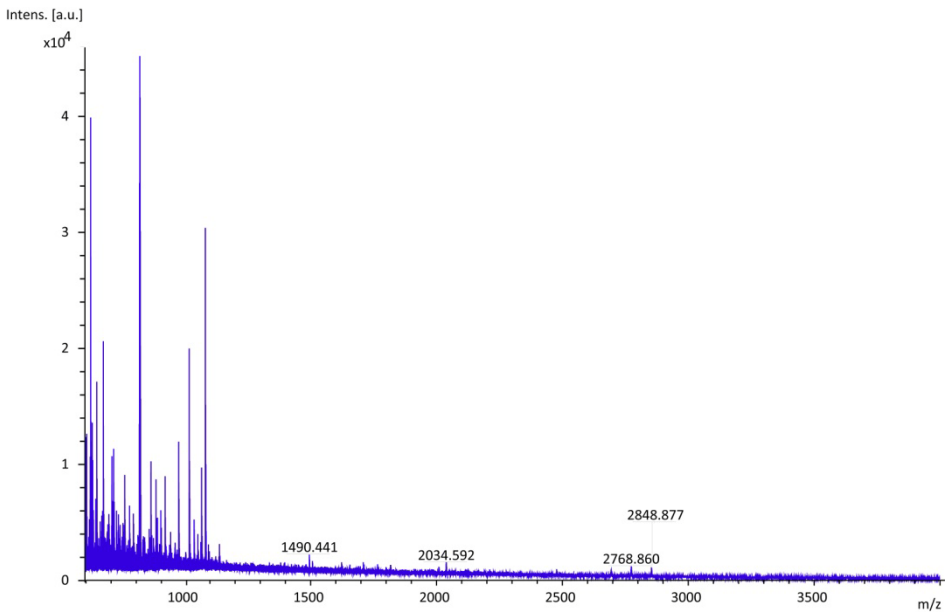


Figure 6.80 Positive ion reflector TOF - MALDI mass spectrum of 3_2_1

$[MH]^+$ 1490.441 Da	
Fragment masses	70,045; 84,055; 86,077; 110,063; 112,085; 115,089; 129,097; 136,074; 141,095; 143,106; 154,090; 159,099; 167,092; 171,122; 175,124; 185,115; 197,125; 212,133; 214,125; 217,105; 229,127; 257,139; 282,123; 288,166; 297,135; 331,141; 591,162; 902,195; 1032,256; 1297,856; 1375,754; 1392,759; 1410,884; 1440,468; 1445,875; 1462,381; 1466,309; 1468,578; 1471,439

T. atroviride	**Not related**
$[MH]^+$ 2034.592 Da	
Fragment masses	70,044; 74,182; 86,067; 110,042; 112,059; 115,064; 129,071; 154,052; 175,081; 181,052; 197,087; 226,073; 278,073; 690,148; 789,221; 864,202; 902,241; 963,219; 1016,276; 1046,260; 1062,317; 1103,317; 1147,380; 1191,282; 1232,401; 1246,424; 1307,148; 1345,451; 1458,381; 1555,605; 1634,763; 1652,731; 1735,809; 1753,567; 1928,512; 1936,072; 1954,143; 2007,008; 2011,650; 2014,495
T. atroviride	**Not related**
$[MH]^+$ 2768.860 Da	
Fragment masses	112,055; 175,078; 186,056; 195,050; 197,058; 246,093; 282,075; 297,093; 310,062; 375,100; 399,086; 490,113; 547,113; 591,151; 611,197; 769,256; 807,187; 883,250; 900,266; 1155,419; 1164,351; 1181,362; 1284,367; 1412,559; 1459,471; 1477,513; 1541,580; 1819,632; 1985,860; 2115,219; 2230,985; 2634,510; 2641,693; 2645,181; 2651,079; 2654,501; 2659,442; 2663,970; 2671,569; 2687,679; 2690,424
T. atroviride	**Plasma membrande H^+ - ATPase K.LGSSDDEAEEDEKEQEESALVSHR.A + Phospho (NOT significant)**
$[MH]^+$ 2848.877 Da	
Fragment masses	74,020; 167,070; 175,076; 195,041; 246,088; 357,099; 375,105; 455,076; 490,075; 547,102; 573,130; 591,133; 807,156; 883,232; 900,240; 1164,361; 1181,376; 1459,541; 1477,535; 1557,495; 1819,695; 2653,557; 2661,214; 2706,778; 2710,070; 2726,753; 2733,398; 2750,624; 2768,594; 2821,397
T. atroviride	**Not related**

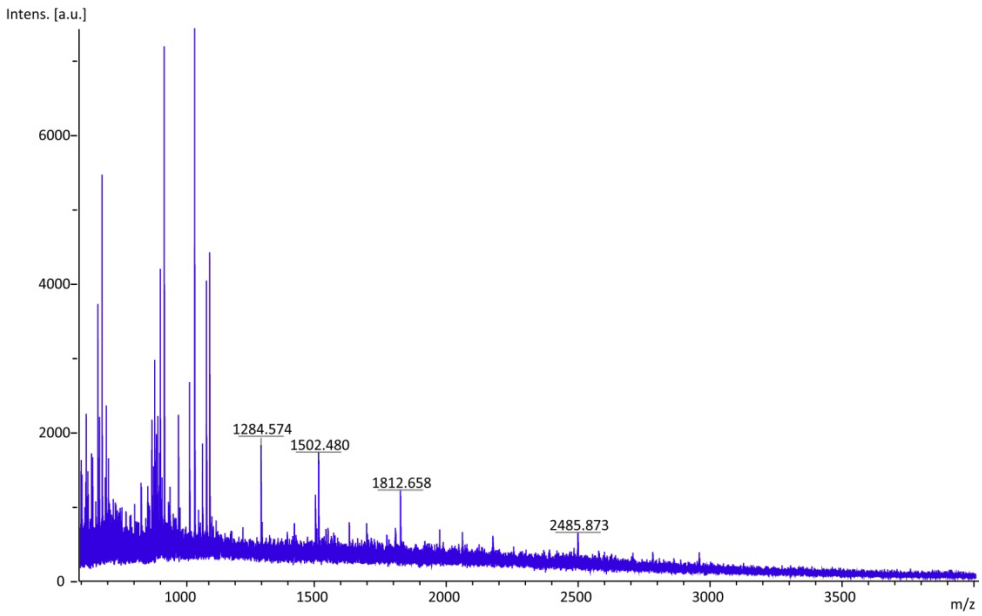


Figure 6.81 Positive ion reflector TOF - MALDI mass spectrum of 3_2_2

$[MH]^+$ 1284.574Da	
Fragment masses	70,025; 86,074; 110,060; 112,090; 115,080; 129,104; 132,083; 136,079; 141,105; 143,139; 147,075; 154,086; 157,091; 159,091; 163,084; 165,098; 167,096; 169,088; 171,115; 175,117; 181,093; 185,098; 187,089; 192,105; 197,120; 202,106; 207,082; 212,105; 214,107; 216,115; 227,105; 229,105; 232,119; 235,101; 240,130; 242,110; 244,101; 247,116; 252,106; 254,120; 258,111; 262,140; 268,129; 270,133; 272,125; 274,126; 279,116; 286,120; 288,153; 296,124; 304,122; 316,118; 331,137; 336,131; 346,126; 504,180; 508,223; 909,151; 946,810; 1031,007; 1047,973; 1087,677; 1089,766; 1092,943; 1096,167; 1121,685; 1185,615; 1220,521; 1229,876; 1236,398; 1239,726; 1242,975; 1254,769; 1257,809; 1259,816; 1262,628

T. atroviride	**Not related**
$[MH]^+$ 1502.480 Da	
Fragment masses	70,041; 84,105; 86,093; 110,067; 112,097; 129,116; 147,078; 154,095; 157,121; 167,099; 172,111; 175,129; 197,134; 202,098; 214,149; 232,140; 243,140; 260,132; 272,149; 288,157; 290,123; 343,172; 345,185; 355,171; 472,178; 508,241; 513,200; 518,189; 588,213; 606,185; 623,220; 787,233; 902,224; 1015,340; 1032,431; 1129,254; 1167,338; 1288,644; 1302,628; 1374,923; 1391,915; 1395,098; 1399,335; 1404,771; 1409,877; 1422,840; 1451,240; 1454,435; 1458,809; 1476,208
T. atroviride	**Not related**
$[MH]^+$ 1812.658 Da	
Fragment masses	70,049; 84,052; 86,088; 110,061; 112,080; 115,078; 129,097; 136,073; 158,102; 167,080; 175,112; 186,104; 195,072; 197,111; 212,107; 227,090; 272,148; 289,094; 528,229; 576,160; 761,304; 826,351; 854,328; 1032,322; 1089,441; 1145,473; 1650,008; 1688,535; 1706,532; 1715,089; 1717,201; 1724,448; 1741,781; 1753,094; 1760,423; 1766,037; 1771,168; 1783,016; 1795,008
T. atroviride	**Not related**
$[MH]^+$ 2485.873 Da	
Fragment masses	70,012; 110,037; 112,058; 129,069; 175,076; 197,070; 227,051; 232,080; 272,133; 275,112; 347,074; 386,120; 439,138; 503,153; 697,216; 715,221; 798,239; 816,266; 875,250; 935,289; 963,321; 1050,346; 1064,370; 1087,328; 1151,390; 1250,454; 1363,536; 1571,617; 1589,636; 1660,715; 1761,831; 1832,791; 1905,068; 2016,787; 2102,123; 2171,320; 2190,848; 2369,299; 2372,796; 2377,568; 2383,075; 2387,398; 2395,021; 2465,860; 2467,262
T. atroviride	**Translation initiation factor R.ESSPTAATAPEIVSTFTPDDIQK.V + Phospho (significant)**

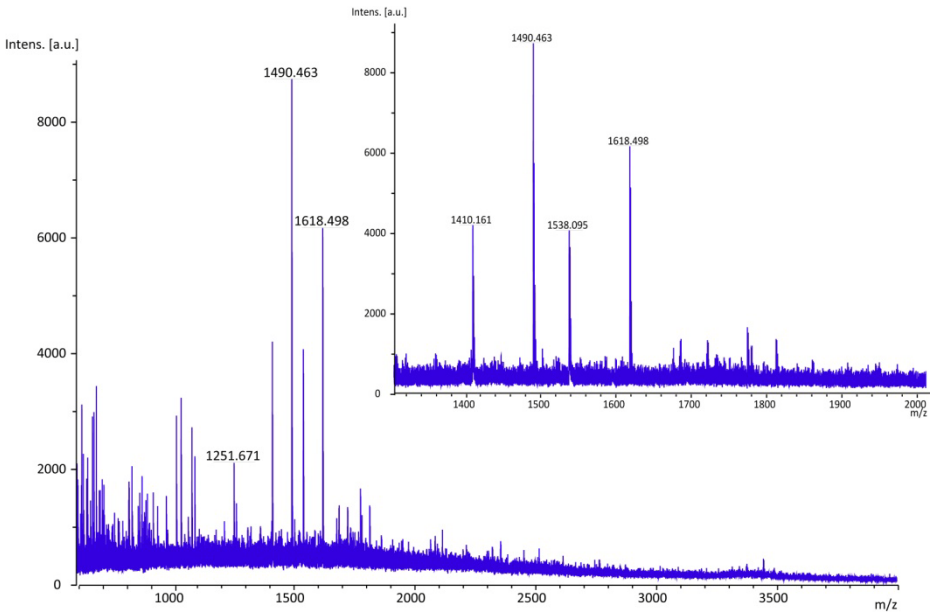


Figure 6.82 Positive ion reflector TOF - MALDI mass spectrum of 3_2_3

$[MH]^+$ 1251.671 Da	
Fragment masses	70,024; 84,049; 86,069; 102,030; 104,079; 110,049; 112,069; 115,061; 120,061; 129,085; 132,073; 136,055; 141,078; 143,098; 147,065; 154,068; 157,078; 159,072; 167,067; 169,089; 172,071; 175,097; 181,080; 183,090; 185,076; 187,076; 197,092; 201,076; 203,063; 205,067; 207,067; 209,080; 212,084; 214,099; 216,072; 219,064; 221,071; 223,090; 225,080; 227,082; 229,087; 232,092; 235,073; 237,091; 239,082; 242,104; 244,081; 246,088; 252,080; 254,092; 257,094; 259,076; 261,092; 264,088; 269,084; 272,107; 278,081; 280,083; 285,092; 288,111; 292,099; 294,077; 296,073;

	303,113; 306,080; 312,081; 314,096; 316,076; 331,098; 352,111; 369,116; 506,163; 633,201; 651,204; 746,354; 908,640; 1053,570; 1055,677; 1058,930; 1061,003; 1092,533; 1146,095; 1185,244; 1188,466; 1197,970; 1201,126; 1203,283; 1205,525; 1207,810; 1211,138; 1224,937; 1228,108; 1231,268; 1234,956
T. atroviride	**Not related**
$[MH]^+$ 1410.161 Da	
Fragment masses	70,069; 84,094; 86,110; 102,090; 110,106; 112,124; 115,129; 120,127; 129,152; 132,144; 136,133; 154,149; 157,175; 167,157; 169,184; 172,167; 175,186; 183,178; 185,175; 187,154; 197,194; 201,193; 203,151; 209,186; 214,205; 216,188; 219,186; 226,203; 229,199; 232,212; 235,191; 237,200; 239,204; 243,220; 245,187; 247,217; 249,198; 254,223; 257,220; 259,190; 262,211; 264,222; 266,210; 268,229; 270,234; 272,243; 275,220; 278,215; 280,220; 282,232; 284,219; 286,232; 288,235; 290,215; 298,241; 301,219; 303,250; 310,281; 313,233; 315,243; 318,225; 326,239; 332,226; 343,253; 353,271; 361,268; 369,254; 385,279; 387,261; 389,254; 413,258; 423,340; 427,286; 444,296; 455,278; 472,296; 526,314; 543,332; 554,311; 673,381; 690,378; 806,405; 885,319; 902,324; 920,544; 1032,394; 1146,359; 1164,768; 1215,869; 1261,504; 1279,362; 1298,071; 1301,350; 1306,541; 1310,916; 1317,349; 1341,540; 1344,545; 1348,920; 1356,239; 1358,386; 1360,533; 1362,699; 1365,926; 1368,222; 1374,806; 1381,339; 1384,408
T. atroviride	**Elongation factor 3 (EF-3) K.RGEEVFSDEDDL.- (NOT significant)**
$[MH]^+$ 1490.463 Da	
Fragment masses	70,047; 84,077; 86,080; 101,070; 110,076; 112,092; 115,087; 120,089; 129,109; 136,078; 139,102; 141,107; 154,101; 157,120; 167,092; 169,122; 172,111; 175,132; 181,109; 183,121; 187,096; 197,129; 201,118; 214,134; 217,113; 228,140; 230,120; 232,138; 235,125; 239,122; 242,148; 246,143; 249,138; 251,142; 253,142; 257,147; 259,106; 262,130; 266,140; 268,152; 270,137; 272,142; 274,153; 276,142; 284,140; 288,161; 290,157; 298,143; 312,120; 315,158; 343,150; 385,176; 413,146; 427,156; 444,172; 455,154; 472,173; 482,221; 508,212; 526,176; 543,209; 554,189; 571,214; 596,235; 690,260; 718,254; 787,283; 805,286; 822,252; 885,280; 902,334; 913,502; 920,353; 968,733; 1000,309; 1031,416; 1128,882; 1146,507; 1155,883; 1164,514; 1170,476; 1244,548; 1261,610; 1270,259; 1273,150; 1279,655; 1287,079; 1289,497; 1310,304; 1359,594; 1375,858; 1383,195; 1392,820; 1398,461; 1410,853; 1424,438; 1441,339; 1444,659; 1448,038; 1466,499
T. atroviride	**Elongation factor 3 (EF-3) K.RGEEVFSDEDDL.- + Phospho (significant)**
$[MH]^+$ 1538.095 Da	
Fragment masses	70,068; 84,085; 87,088; 101,096; 110,075; 112,091; 115,092; 120,091; 129,112; 132,092; 136,083; 139,098; 141,111; 147,097; 154,101; 157,119; 159,103; 167,104; 169,122; 172,114; 175,132; 179,119; 181,114; 185,123; 189,103; 191,105; 195,109; 197,132; 201,118; 205,130; 209,131; 213,116; 215,137; 217,117; 219,133; 221,120; 226,143; 229,132; 231,112; 235,126; 237,128; 240,149; 243,167; 246,151; 250,136; 252,125; 255,131; 257,145; 259,120; 262,145; 268,181; 272,153; 276,143; 278,130; 280,137; 282,140; 285,190; 288,161; 290,149; 292,147; 294,151; 296,140; 298,139; 301,142; 303,163; 306,143; 308,153; 310,153; 312,131; 316,123; 326,153; 328,141; 332,132; 337,160; 340,150; 342,160; 345,161; 352,175; 355,155; 358,158; 360,164; 362,144; 365,155; 367,177; 369,163; 372,161; 374,161; 382,170; 385,173; 387,167; 401,177; 413,183; 415,165; 429,145; 443,232; 455,191; 471,226; 508,233; 555,248; 572,250; 583,239; 600,258; 654,289; 671,294; 682,270; 818,302; 932,270; 958,277; 1015,326; 1030,224; 1032,305; 1048,481; 1089,475; 1162,643; 1274,162; 1292,747; 1341,644; 1389,246; 1407,116; 1414,269; 1425,959; 1430,075; 1432,237; 1435,532; 1439,864; 1450,215; 1458,011; 1466,359; 1469,509; 1474,825; 1486,269; 1488,416; 1492,914; 1496,047; 1510,024; 1512,981
T. atroviride	**Elongation factor 3 (EF-3) R.KRGEEVFSDEDDL.- (NOT significant)**
$[MH]^+$ 1618.498 Da	
Fragment masses	70,060; 84,071; 101,096; 110,068; 112,090; 115,086; 120,080; 129,106; 136,077; 141,110; 154,092; 157,113; 159,099; 167,102; 169,109; 172,108; 175,124; 181,103; 185,108; 195,095; 197,127; 201,117; 207,095; 209,111; 212,117;

	214,128; 226,128; 229,109; 235,112; 240,139; 243,158; 245,111; 250,136; 255,131; 258,131; 268,154; 272,142; 285,164; 288,169; 303,161; 312,132; 314,166; 316,109; 342,167; 443,204; 471,216; 572,266; 583,250; 600,263; 654,294; 671,354; 682,305; 699,324; 818,416; 846,400; 915,439; 933,434; 950,405; 1013,449; 1030,482; 1041,311; 1048,503; 1091,578; 1128,439; 1159,533; 1177,548; 1274,631; 1283,794; 1292,648; 1298,147; 1372,609; 1389,733; 1398,277; 1401,221; 1407,760; 1415,026; 1417,486; 1420,698; 1425,858; 1486,826; 1492,822; 1494,954; 1502,918; 1505,203; 1512,427; 1520,918; 1530,441; 1538,944; 1571,684; 1577,029
T. atroviride	**Elongation factor 3 (EF3) R.KRGEEVFSDEDDL.- + Phospho (significant)**

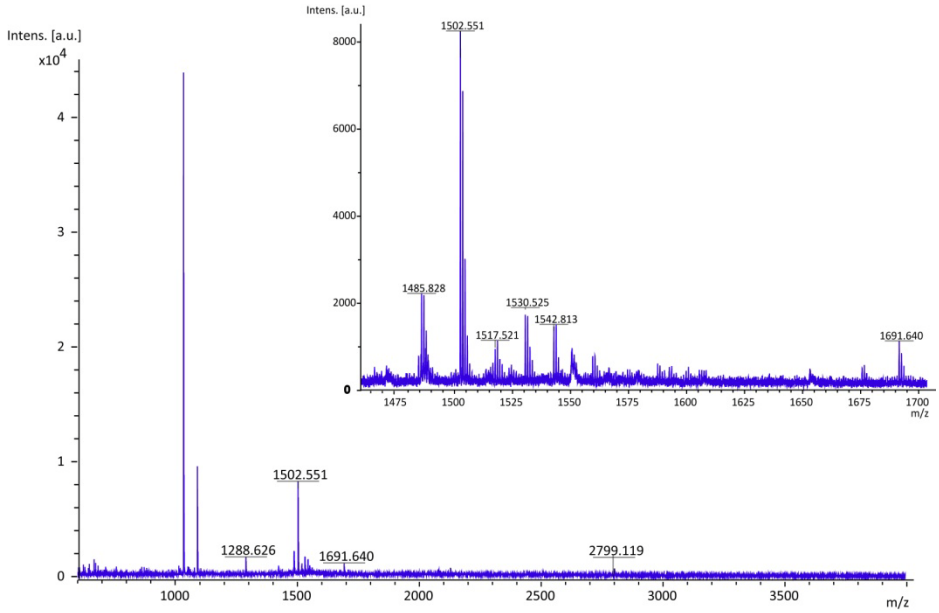


Figure 6.83 Positive ion reflector TOF - MALDI mass spectrum of 3_2_4

$[MH]^+$ 1288.626 Da	
Fragment masses	70,037; 84,052; 86,078; 101,061; 110,074; 112,093; 115,087; 129,109; 136,084; 141,082; 154,101; 158,105; 167,105; 171,116; 175,131; 181,114; 188,119; 190,127; 195,100; 197,128; 199,112; 201,115; 205,096; 207,076; 215,125; 229,119; 232,145; 240,141; 242,141; 244,116; 249,136; 253,102; 257,091; 262,125; 272,150; 275,111; 277,144; 279,111; 286,139; 288,161; 304,135; 310,115; 314,138; 328,170; 345,215; 349,119; 366,140; 382,146; 411,136; 508,299; 525,172; 566,189; 606,288; 623,312; 649,235; 666,253; 692,246; 701,222; 709,321; 764,281; 781,312; 899,414; 916,438; 919,332; 944,450; 1031,118; 1073,632; 1091,692; 1098,040; 1114,658; 1132,715; 1174,854; 1187,547; 1190,831; 1228,912; 1235,987; 1240,331; 1244,821; 1254,679
T. atroviride	**Not realted**
$[MH]^+$ 1485.828 Da	
Fragment masses	70,054; 84,073; 86,103; 110,079; 112,098; 115,096; 120,095; 129,119; 136,091; 141,102; 154,091; 158,112; 167,112; 172,123; 175,141; 181,114; 185,154; 188,134; 190,133; 195,110; 197,140; 199,129; 203,110; 205,126; 213,167; 215,132; 226,141; 232,153; 242,183; 245,115; 249,171; 253,114; 258,126; 272,148; 277,163; 279,125; 286,152; 288,160; 296,140; 310,126; 314,172; 328,191; 331,143; 345,220; 355,191; 361,177; 367,157; 369,157; 371,171; 373,129; 375,166; 382,175; 385,154; 387,122; 403,133; 411,160; 416,153; 453,123; 473,193; 491,188; 508,263; 518,224; 525,176; 588,225; 606,250; 623,278; 660,204; 688,219; 760,293; 817,333; 918,421; 977,288; 988,407; 1015,410; 1032,426; 1089,317; 1096,517; 1112,401; 1269,571 1285,696; 1288,594; 1302,719; 1344,826; 1361,735; 1369,761; 1377,104; 1381,270; 1383,486; 1386,732; 1390,031; 1393,285; 1399,303; 1404,735; 1408,018; 1421,845; 1423,770; 1432,997; 1438,595; 1441,801; 1450,752; 1457,753; 1459,901; 1461,982; 1466,753

T. atroviride	**FAD/FMN containing dehydrogenase R.IVLKNTGHDYLGR.S (significant)**
$[MH]^+$ 1502.551 Da	
Fragment masses	70,060; 84,060; 86,091; 112,094; 115,089; 129,112; 136,096; 154,089; 158,108; 167,106; 172,110; 175,130; 186,128; 195,097; 197,130; 199,107; 215,125; 226,132; 232,141; 242,151; 244,124; 249,152; 253,113; 277,142; 279,112; 286,136; 288,149; 292,136; 310,123; 328,169; 345,204; 355,179; 371,163; 373,122; 382,158; 410,146; 416,145; 473,163; 508,241; 518,224; 525,168; 588,221; 606,230; 623,251; 660,210; 688,197; 743,235; 801,266; 817,282; 918,277; 988,364; 1015,407; 1032,453; 1044,434; 1073,511; 1084,072; 1271,597; 1285,614; 1288,641; 1302,687; 1313,082; 1318,664; 1361,822; 1365,255; 1378,947; 1387,853; 1391,869; 1394,105; 1396,112; 1404,818; 1422,858; 1442,860; 1450,966; 1459,820; 1467,780; 1484,465
T. atroviride	**Not related**
$[MH]^+$ 1517.521 Da	
Fragment masses	70,037; 86,090; 101,079; 110,081; 112,094; 115,079; 120,084; 129,120; 136,092; 141,114; 154,114; 158,120; 167,109; 172,122; 175,149; 181,121; 185,133; 195,118; 197,144; 201,130; 213,165; 215,144; 226,151; 232,178; 240,140; 242,171; 244,143; 249,181; 253,134; 268,169; 270,173; 272,177; 277,160; 279,135; 288,180; 296,148; 310,145; 314,161; 345,254; 355,232; 367,175; 377,159; 382,192; 385,174; 410,190; 416,178; 473,200; 508,295; 518,261; 525,196; 588,253; 606,255; 623,277; 688,214; 918,270; 988,276; 1015,274; 1032,343; 1044,317; 1054,268; 1089,119; 1285,667; 1287,854; 1302,660; 1316,693; 1318,772; 1360,890; 1372,449; 1376,995; 1385,804; 1387,863; 1403,836; 1406,934; 1411,239; 1414,427; 1418,737; 1421,846; 1424,959; 1432,494; 1436,765; 1438,959; 1467,567; 1484,293; 1488,653
T. atroviride	**FAD/FMN containing dehydrogenase R.MIIKNTGHDYLGR.S (NOT significant)**
$[MH]^+$ 1530.525 Da	
Fragment masses	70,054; 84,064; 86,101; 110,087; 112,103; 115,105; 129,123; 136,095; 141,114; 147,098; 154,100; 158,118; 167,116; 172,129; 175,147; 181,114; 186,134; 195,118; 197,142; 213,157; 215,132; 226,143; 232,167; 253,126; 259,133; 266,134; 268,170; 272,165; 275,199; 277,162; 286,167; 288,173; 310,138; 314,157; 316,166; 328,191; 345,242; 355,209; 382,197; 392,165; 402,112; 410,183; 508,285; 518,230; 525,211; 533,250; 588,256; 606,263; 623,289; 634,254; 660,239; 688,227; 763,295; 801,291; 817,311; 842,361; 858,233; 892,357; 918,291; 946,396; 988,366; 1015,362; 1032,432; 1050,335; 1060,463; 1089,323; 1276,711; 1286,144; 1302,038; 1305,121; 1316,785; 1319,012; 1330,753; 1403,641; 1417,738; 1419,927; 1422,132; 1426,374; 1432,852; 1443,330; 1450,878; 1467,630; 1484,513; 1488,009; 1500,059; 1505,271
T. atroviride	**Not related**
$[MH]^+$ 1542.813 Da	
Fragment masses	70,060; 84,087; 86,112; 110,092; 112,103; 115,114; 120,086; 129,126; 136,106; 141,127; 154,117; 158,128; 167,120; 172,132; 175,147; 181,127; 186,143; 195,119; 197,149; 201,126; 213,169; 216,138; 226,153; 232,169; 242,175; 244,149; 246,160; 252,141; 258,152; 268,168; 270,157; 272,165; 277,152; 279,134; 282,173; 286,160; 288,178; 290,166; 301,169; 303,196; 310,150; 316,149; 328,188; 345,244; 355,200; 369,197; 402,159; 473,206; 508,297; 518,269; 525,219; 582,239; 588,258; 606,282; 623,302; 672,318; 688,256; 760,368; 801,273; 817,354; 858,412; 874,396; 918,375; 988,355; 1015,347; 1032,381; 1050,447; 1060,408; 1071,451; 1089,524; 1316,143; 1319,222; 1330,990; 1403,825; 1416,067; 1422,625; 1432,011; 1435,197; 1439,517; 1443,759; 1446,971; 1449,969; 1453,148; 1461,771; 1466,170; 1484,014; 1495,742; 1498,986; 1500,958; 1512,533; 1515,920; 1518,645; 1522,075
T. atroviride	**Not related**
$[MH]^+$ 1691.640 Da	
Fragment masses	70,042; 84,049; 86,074; 110,056; 112,066; 115,069; 120,071; 129,081; 133,056; 136,051; 141,082; 147,071; 154,067; 158,073; 167,066; 169,082; 175,096; 181,079; 185,086; 195,063; 197,100; 199,074; 201,073; 211,084; 213,072; 217,077; 223,111; 226,098; 230,078; 232,096; 235,078; 239,070; 242,074; 244,087; 251,097; 255,080; 272,103; 276,087; 289,087; 329,128; 345,131; 352,121; 387,092; 404,099; 432,117; 474,215; 508,189; 533,131; 551,149; 589,213; 642,201; 646,214; 649,159; 652,190; 659,183; 666,177; 670,181; 676,183; 755,259; 783,239; 909,256; 1000,327; 1014,265; 1022,378; 1032,261; 1089,253; 1141,405; 1159,442; 1202,145; 1260,559; 1403,653; 1484,034; 1492,760; 1501,053; 1510,794; 1518,887; 1568,194; 1573,723;

	1584,334; 1587,430; 1590,703; 1595,030; 1616,784; 1632,700; 1641,026; 1647,863; 1657,626; 1660,595
T. atroviride	**Heat shock 70 kDa protein K.STAGDTHLGGEDFDNR.L (significant)**
$[MH]^+$ 2799.119 Da	
Fragment masses	110,045; 129,100; 159,092; 175,111; 226,113; 231,087; 240,118; 244,098; 246,134; 257,132; 259,080; 266,101; 272,133; 284,104; 286,136; 303,164; 316,094; 357,106; 369,118; 386,161; 404,201; 413,141; 415,159; 431,112; 515,185; 532,230; 545,218; 599,196; 617,197; 661,253; 730,276; 732,322; 790,317; 819,310; 934,362; 937,388; 993,494; 1032,370; 1049,411; 1052,427; 1057,525; 1158,567; 1164,431; 1181,483; 1282,562; 1383,647; 1454,669; 1569,788; 1697,763; 1812,731; 1941,421; 2071,043; 2184,049; 2369,717; 2601,036; 2654,006; 2669,740; 2673,344; 2676,202; 2679,415; 2682,810; 2685,372; 2689,349; 2693,156; 2697,310; 2701,236; 2707,356; 2757,829; 2774,637
T. atroviride	**Molecular chaperone bip1 K.EATEWLEENGADATTEDFEEQKEK.L (significant)**

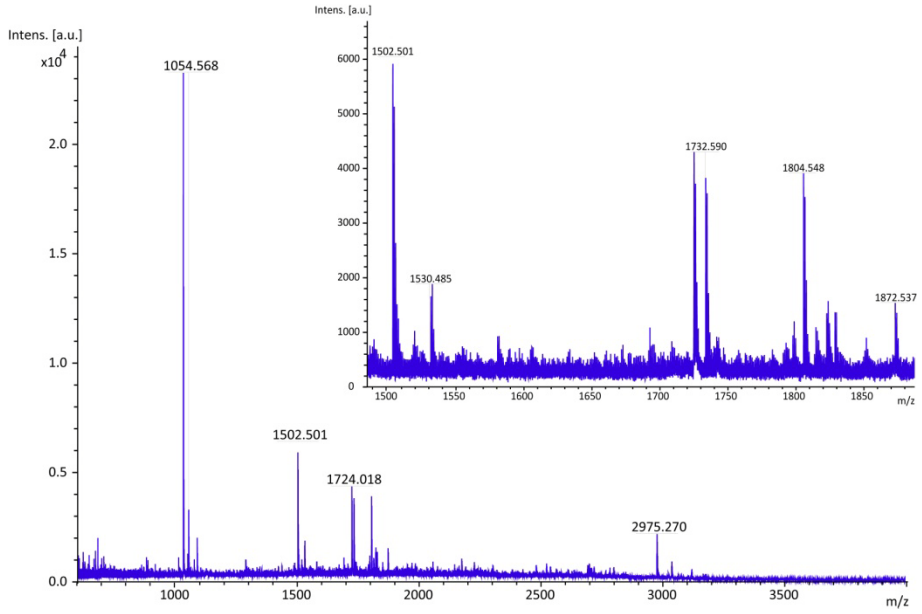


Figure 6.84 Positive ion reflector TOF - MALDI mass spectrum of 3_2_5

$[MH]^+$ 1054.568 Da	
Fragment masses	58,024; 70,048; 86,092; 101,075; 110,081; 113,089; 115,100; 120,094; 129,116; 132,100; 136,094; 141,120; 143,134; 147,093; 154,096; 159,091; 167,105; 171,118; 175,129; 179,113; 181,101; 184,126; 186,122; 195,104; 197,132; 200,131; 204,143; 207,121; 212,123; 216,113; 225,125; 227,119; 229,115; 232,144; 235,115; 238,133; 240,128; 245,114; 253,104; 261,122; 263,136; 270,134; 272,147; 275,124; 279,123; 286,157; 288,153; 294,127; 296,128; 310,123; 367,178; 379,177; 382,175; 393,155; 410,175; 421,146; 473,169; 508,150; 525,209; 530,257; 645,320; 660,301; 671,248; 688,313; 731,269; 782,455; 818,148; 823,423; 826,226; 839,509; 851,483; 860,967; 863,124; 865,147; 898,587; 908,571; 926,566; 940,643; 988,294; 994,262; 1006,257; 1009,547; 1013,109; 1015,194; 1031,558
T. atroviride	**FAD/FMN containing dehydrogenase R.NTGHDYYGK.S (NOT significant)**
$[MH]^+$ 1502.501 Da	
Fragment masses	70,062; 84,073; 86,092; 101,082; 110,077; 112,101; 115,094; 120,089; 129,120; 136,091; 147,118; 154,102; 158,113; 167,107; 169,120; 172,124; 175,136; 181,121; 185,105; 187,092; 195,113; 197,137; 201,118; 207,115; 212,139; 215,134; 217,132; 229,114; 232,148; 240,130; 242,140; 244,125; 253,116; 255,138; 272,166; 279,124; 286,146; 288,170; 290,145; 302,140; 304,170;

	310,123; 316,134; 345,208; 347,151; 355,180; 358,144; 371,156; 373,155; 389,165; 508,256; 519,180; 525,181; 588,226; 605,231; 623,256; 1015,413; 1032,460; 1073,531; 1270,623; 1285,572; 1288,636; 1302,716; 1311,868; 1318,712; 1361,842; 1365,258; 1378,937; 1387,837; 1391,374; 1394,074; 1399,455; 1404,836; 1417,447; 1422,872; 1442,921; 1451,101; 1456,707; 1459,829; 1467,742
T. atroviride	**Not related**
$[MH]^+$ 1530.485 Da	
Fragment masses	70,053; 84,082; 86,094; 101,084; 110,078; 112,107; 115,099; 120,098; 129,123; 136,103; 147,097; 155,113; 159,113; 167,120; 169,125; 175,152; 181,132; 185,126; 187,126; 195,123; 197,145; 201,141; 215,146; 217,140; 226,154; 229,140; 232,169; 240,154; 244,147; 246,165; 253,138; 258,144; 262,174; 268,169; 270,166; 272,179; 276,178; 286,163; 288,188; 295,163; 312,175; 314,175; 316,173; 345,215; 355,198; 382,203; 402,146; 508,292; 519,241; 525,215; 588,249; 623,280; 1015,391; 1032,466; 1050,363; 1054,366; 1059,499; 1276,545; 1302,075; 1304,097; 1316,809; 1415,959; 1418,773; 1421,080; 1423,162; 1426,369; 1428,571; 1432,844; 1435,165; 1437,919; 1440,033; 1443,305; 1450,881; 1483,750; 1486,946; 1489,080; 1501,408; 1505,557
T. atroviride	**Not related**
$[MH]^+$ 1724.018 Da	
Fragment masses	70,052; 84,078; 86,088; 101,082; 110,073; 112,090; 115,088; 120,092; 129,106; 136,089; 139,096; 141,106; 147,124; 154,096; 157,107; 159,098; 167,096; 172,100; 175,122; 185,103; 187,088; 195,095; 197,124; 200,110; 213,119; 217,103; 221,127; 226,130; 228,123; 230,124; 235,107; 240,107; 242,143; 244,101; 249,111; 255,115; 258,118; 267,098; 270,149; 272,156; 276,127; 296,111; 305,176; 318,148; 332,128; 345,156; 370,147; 416,191; 434,216; 447,166; 482,153; 546,224; 562,253; 568,237; 584,343; 586,203; 611,205; 633,296; 668,221; 744,282; 761,342; 797,248; 816,298; 834,308; 902,386; 925,342; 1017,386; 1030,470; 1032,383; 1060,375; 1088,437; 1128,351; 1145,471; 1187,611; 1260,391; 1371,376; 1483,844; 1521,592; 1530,051; 1539,570; 1578,313; 1597,123; 1603,711; 1613,098; 1616,377; 1619,540; 1621,681; 1624,927; 1627,006; 1630,337; 1639,648; 1647,328; 1651,397; 1662,268; 1672,485; 1675,624; 1681,149; 1688,869; 1694,816; 1699,127; 1706,242
T. atroviride	**Ribosome-associated chaperone zuotin R.TFSEDDRIQAQESAK.N (NOT significant)**
$[MH]^+$ 1732.590 Da	
Fragment masses	70,047; 84,065; 86,078; 101,069; 110,059; 113,063; 115,076; 120,069; 129,087; 136,061; 147,101; 154,083; 157,101; 159,068; 167,083; 169,111; 172,076; 175,112; 183,096; 185,083; 187,071; 195,069; 197,111; 200,092; 217,080; 221,115; 226,100; 230,099; 242,135; 244,095; 249,090; 255,097; 258,100; 267,086; 272,137; 276,112; 305,177; 311,142; 315,088; 318,144; 329,162; 345,129; 370,126; 434,174; 454,152; 482,126; 546,203; 562,222; 581,182; 583,203; 586,212; 611,174; 633,263; 645,264; 668,201; 744,252; 769,235; 797,226; 808,317; 814,281; 834,269; 843,270; 897,287; 919,360; 925,280; 936,392; 1014,366; 1030,451; 1032,375; 1060,340; 1063,454; 1065,429; 1088,361; 1099,341; 1122,481; 1145,449; 1159,417; 1187,442; 1244,489; 1251,574; 1315,227; 1330,650; 1358,590; 1388,716; 1457,750; 1578,313; 1586,831; 1596,500; 1604,916; 1617,989; 1622,111; 1625,364; 1628,510; 1631,733; 1635,038; 1662,563; 1665,786; 1680,323; 1683,564; 1688,214; 1690,824; 1706,131
T. atroviride	**Rossmann-fold NAD(P)(+)-binding protein (FAD-binding domain containing proetein, FAD-Monooxygenase) R.DTQHEGEQYVGNVEK.H (significant)**
$[MH]^+$ 1804.548 Da	
Fragment masses	70,048; 84,073; 86,087; 101,076; 110,068; 112,082; 115,086; 120,080; 129,106; 136,079; 147,092; 157,099; 159,098; 167,092; 175,121; 183,131; 185,118; 200,112; 212,124; 221,094; 227,115; 272,167; 274,175; 305,152; 329,262; 345,218; 562,235; 568,186; 633,281; 751,492; 761,333; 773,427; 816,297;

	833,325; 851,350; 874,419; 887,442; 902,398; 910,484; 918,397; 946,394; 1013,520; 1015,502; 1024,491; 1030,527; 1074,448; 1110,522; 1128,562; 1145,576; 1162,518; 1216,602; 1225,559; 1243,562; 1246,589; 1260,634; 1389,746; 1402,759; 1452,551; 1458,784; 1560,811; 1578,969; 1589,948; 1596,015; 1606,617; 1633,999; 1663,127; 1666,602; 1671,045; 1673,337; 1677,079; 1680,559; 1684,023; 1689,159; 1691,425; 1694,322; 1697,444; 1700,759; 1707,149; 1718,809; 1725,175
T. atroviride	**Ribosome-associated chaperone zuotin R.TFSEDDRIQAQESAK.N + Phospho (significant)**
$[MH]^+$ 1872.537 Da	
Fragment masses	70,045; 84,065; 86,080; 101,071; 110,068; 112,089; 115,090; 120,085; 129,111; 136,090; 158,107; 167,098; 175,126; 181,114; 195,114; 197,137; 199,091; 226,129; 235,098; 245,104; 250,108; 262,125; 329,172; 364,127; 448,155; 514,109; 527,189; 563,193; 640,230; 661,296; 758,281; 775,284; 874,367; 989,413; 1032,508; 1118,488; 1145,553; 1233,540; 1512,373; 1709,016; 1716,342; 1759,243; 1763,480; 1768,750; 1773,070; 1776,392; 1779,522; 1781,604; 1791,121; 1794,434; 1804,989; 1808,124; 1820,616
T. atroviride	**Ribosome-associated chaperone zuotin R.SFEYLDEDVPDDGESR.D (significant)**
$[MH]^+$ 2975.270 Da	
Fragment masses	69,995; 73,993; 110,046; 112,041; 129,057; 169,076; 175,101; 212,079; 226,090; 232,107; 244,101; 256,085; 258,081; 267,080; 272,129; 295,109; 300,130; 303,144; 309,086; 313,105; 327,123; 341,124; 343,114; 355,112; 358,121; 360,147; 379,122; 386,125; 394,125; 396,113; 400,119; 414,125; 447,149; 460,136; 518,158; 534,161; 628,217; 640,161; 673,272; 697,201; 825,308; 981,350; 1034,441; 1051,442; 1069,587; 1122,528; 1209,539; 1296,615; 1367,608; 1383,634; 1454,619; 1592,669; 1608,785; 1679,799; 1767,935; 1934,937; 2037,504; 2122,993; 2347,661; 2516,839; 2521,880; 2732,887; 2846,003; 2850,498; 2855,628; 2861,368; 2865,389; 2867,731; 2873,115; 2875,835; 2903,877; 2931,829; 2945,677
T. atroviride	**Dihydrolipoamide acetyltransferase component K.KDSEPAPQSTPASAPQSSSAPEQYSSQGR.I (significant)**

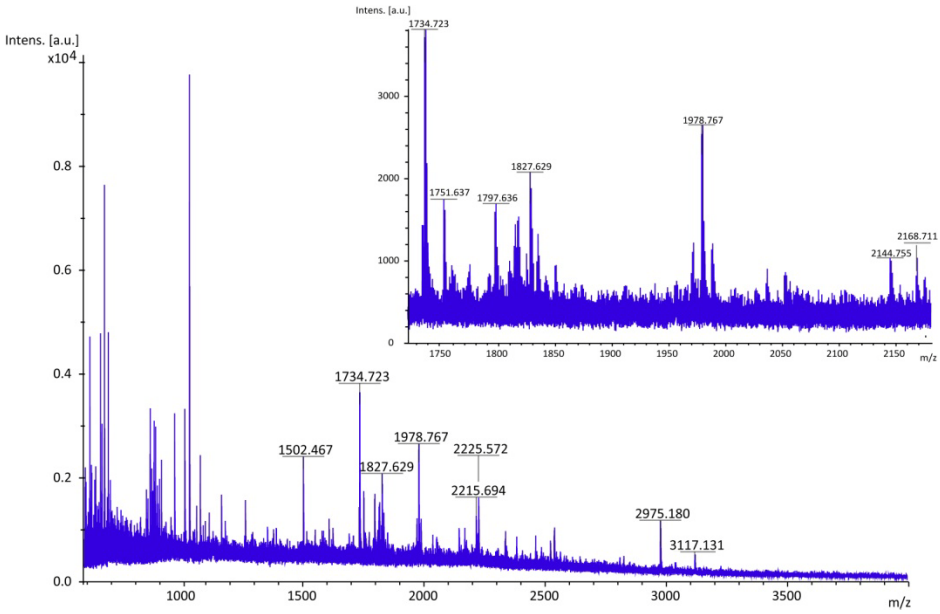


Figure 6.85 Positive ion reflector TOF - MALDI mass spectrum of 3_2_6

$[MH]^+$ 1502.467 Da	
Fragment masses	84,070; 86,094; 104,115; 112,107; 129,120; 136,091; 154,103; 158,121; 175,140; 195,102; 197,145; 215,136; 232,159; 244,125; 266,114; 268,142; 272,159; 274,155; 288,177; 341,164; 345,203; 355,183; 416,217; 508,269; 588,250;

	623,265; 694,303; 733,325; 885,391; 1032,477; 1271,756; 1288,698; 1302,720; 1308,769; 1312,896; 1361,944; 1387,875; 1392,070; 1399,495; 1404,857; 1422,882; 1454,546; 1458,909; 1476,159
T. atroviride	**Not related**
$[MH]^+$ 1734.723 Da	
Fragment masses	70,045; 74,118; 84,061; 98,082; 101,067; 110,053; 112,074; 115,075; 120,060; 129,087; 136,069; 143,101; 147,083; 154,079; 167,090; 175,103; 184,085; 187,107; 195,083; 197,116; 215,101; 223,105; 227,090; 240,093; 244,089; 251,089; 254,103; 258,099; 268,104; 272,119; 276,128; 286,089; 288,141; 344,138; 454,152; 482,173; 529,203; 546,226; 588,245; 611,195; 619,250; 671,251; 748,332; 797,252; 808,336; 845,333; 890,404; 907,410; 925,297; 936,364; 987,482; 1027,516; 1088,382; 1116,549; 1122,497; 1147,576; 1187,484; 1218,636; 1263,648; 1289,705; 1358,422; 1391,746; 1418,797; 1531,990; 1589,060; 1607,033; 1630,489; 1634,751; 1642,441; 1660,269; 1689,986
T. atroviride	**Not related**
$[MH]^+$ 1751.637 Da	
Fragment masses	70,050; 74,264; 84,065; 86,093; 98,095; 101,074; 110,073; 112,088; 115,098; 129,109; 143,132; 147,094; 154,096; 158,117; 167,097; 171,116; 175,134; 187,130; 195,111; 197,151; 213,117; 215,157; 226,146; 240,139; 258,167; 268,149; 272,181; 288,170; 543,217; 588,414; 628,341; 649,311; 736,349; 849,437; 903,328; 978,498; 987,499; 1027,511; 1032,425; 1106,620; 1147,508; 1219,471; 1243,539; 1364,685; 1391,849; 1404,654; 1637,170; 1641,376; 1644,558; 1647,604; 1651,925; 1659,505; 1701,595; 1707,007; 1731,532
T. atroviride	**Geranylgeranyl reductase family protein K.NGSTPSTQELSQLFNK.Y (NOT significant)**
$[MH]^+$ 1797.636 Da	
Fragment masses	70,051; 74,177; 84,088; 86,090; 110,060; 112,073; 115,064; 120,066; 129,093; 136,072; 154,081; 157,096; 167,085; 175,111; 195,107; 197,105; 232,128; 345,153; 502,181; 635,229; 640,198; 694,189; 773,296; 799,338; 887,333; 910,374; 960,391; 1007,413; 1015,441; 1024,427; 1086,489; 1162,498; 1250,574; 1277,553; 1337,602; 1390,641; 1452,792; 1597,863; 1689,443; 1694,776; 1699,067; 1745,448; 1753,138
T. atroviride	**Enolase K.KYDLDFKNPESDPTK.W (NOT significant)**
$[MH]^+$ 1827.629 Da	
Fragment masses	86,102; 110,087; 112,094; 115,092; 129,115; 154,112; 175,144; 342,196; 376,354; 428,170; 474,377; 488,276; 502,308; 505,267; 559,304; 717,391; 748,435; 785,397; 832,409; 947,476; 959,498; 1032,475; 1062,486; 1176,577; 1323,709; 1352,684; 1397,548; 1468,689; 1484,877; 1706,869; 1723,823; 1726,995; 1731,294; 1741,821; 1753,570; 1760,973; 1795,093
T. atroviride	**Rossmann-fold $NAD(P)^+$ binding protein (NADP binding domain containing protein, 6-phosphogluconate dehydrogenase) R.DILYFNDDDGTALVEK.I (NOT significant)**
$[MH]^+$ 1978.767 Da	
Fragment masses	70,054; 84,069; 110,061; 112,074; 115,079; 129,096; 136,064; 158,079; 167,062; 175,097; 197,091; 229,082; 272,114; 329,130; 331,174; 484,195; 532,295; 586,165; 718,296; 798,265; 1115,474; 1267,601; 1344,422; 1625,055; 1813,541; 1866,472; 1875,722; 1878,957; 1883,384; 1901,424; 1907,670; 1917,265; 1936,099; 1952,265
T. atroviride	**Not related**
$[MH]^+$ 2144.755 Da	
Fragment masses	70,052; 86,074; 110,063; 112,076; 129,092; 136,067; 158,086; 175,100; 651,303; 880,409; 949,480; 978,395; 995,502; 1010,452; 1032,406; 1092,490; 1149,528; 1189,555; 1549,858; 1583,720; 2030,417; 2034,586; 2038,664; 2048,377; 2100,174; 2114,849
T. atroviride	**Not related**
$[MH]^+$ 2168.711 Da	

Fragment masses	74,050; 84,055; 110,054; 112,066; 129,089; 175,105; 226,092; 272,119; 297,190; 369,032; 513,203; 523,149; 599,210; 728,328; 860,375; 880,474; 967,433; 1032,443; 1095,496; 1182,604; 1201,541; 1399,838; 1441,724; 1569,783; 1694,896; 1926,171; 2061,764; 2064,838; 2068,062; 2076,827; 2079,694; 2143,547
T. atroviride	**Dihydrolipoamide succinyltransferase K.EESKPQASESKPAAEPEEPK.S (NOT significant)**
$[MH]^+$ 2215.694 Da	
Fragment masses	70,066; 110,072; 112,105; 129,113; 175,148; 355,197; 546,298; 576,317; 615,316; 720,425; 731,405; 860,470; 888,488; 906,464; 975,499; 1003,492; 1021,500; 1032,564; 1119,695; 1131,633; 1149,585; 1278,683; 1310,716; 1317,675; 1862,303; 2109,708; 2115,293; 2119,473
T. atroviride	**Not related**
$[MH]^+$ 2225.572 Da	
Fragment masses	70,030; 110,069; 112,077; 129,099; 136,080; 158,074; 175,117; 244,145; 319,197; 355,222; 546,264; 603,276; 614,330; 674,318; 720,388; 731,344; 842,386; 860,408; 888,414; 906,501; 975,504; 1003,503; 1021,517; 1032,477; 1131,563; 1149,531; 1221,602; 1310,652; 1317,644; 1447,758; 1606,743; 1861,203; 1990,408; 2006,220; 2024,437; 2049,232; 2118,670; 2121,801; 2125,324; 2129,495; 2180,260; 2197,392
T. atroviride	**Rossmann-fold $NAD(P)^+$ binding protein (NADP binding domain containing protein, 6-phosphogluconate dehydrogenase) K.SDGEACCEWVGDEGAGHYVK.M (NOT significant)**
$[MH]^+$ 2975.180 Da	
Fragment masses	73,979; 175,087; 226,077; 244,086; 313,116; 327,106; 355,114; 360,120; 396,123; 447,170; 628,231; 697,285; 808,230; 825,341; 1041,561; 1051,457; 1122,459; 1209,544; 1272,725; 1296,590; 1383,616; 1484,659; 1512,592; 1608,761; 1631,837; 1680,736; 1695,755; 1935,021; 2517,261; 2732,922; 2867,691; 2874,612; 2904,154; 2932,064; 2945,612
T. atroviride	**Dihydrolipoamide acetyltransferase component K.KDSEPAPQSTPASAPQSSSAPEQYSSQGR.I (significant)**
$[MH]^+$ 3117.131 Da	
Fragment masses	175,176; 267,152; 396,207; 406,174; 525,224; 578,321; 640,283; 649,366; 720,400; 725,388; 730,362; 753,383; 791,454; 830,499; 866,465; 892,490; 963,510; 981,527; 1006,535; 1024,572; 1041,666; 1121,613; 1145,693; 1192,714; 1213,602; 1263,762; 1302,762; 1320,788; 1328,701; 1433,848; 1457,706; 1562,820; 1586,877; 1674,161; 1691,994; 1699,845; 1756,890; 1806,885; 1827,887; 1876,309; 1899,348; 1986,074; 2014,134; 2039,122; 2127,994; 2253,118; 2380,321; 2817,279; 2833,806; 2985,245; 2989,162; 3000,048; 3003,276; 3038,172
T. atroviride	**Not related**

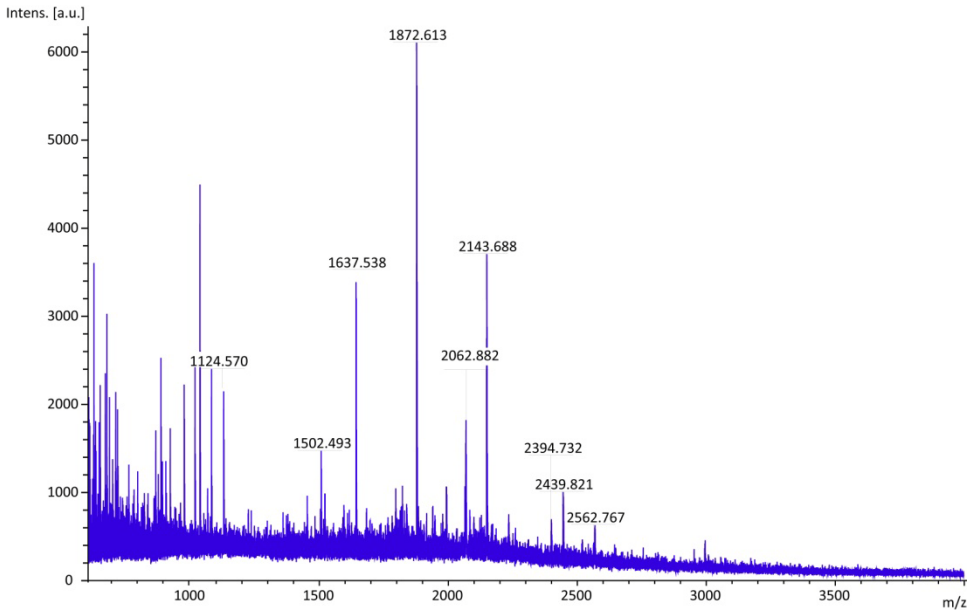


Figure 6.86 Positive ion reflector TOF - MALDI mass spectrum of 3_2_7

$[MH]^+$ 1124.570 Da	
Fragment masses	58,040; 70,081; 84,104; 86,122; 100,129; 102,116; 104,155; 110,119; 112,136; 115,134; 120,132; 123,132; 125,142; 129,164; 136,130; 143,188; 154,160; 157,174; 159,151; 167,157; 169,182; 171,184; 175,186; 186,184; 197,198; 199,189; 201,176; 203,181; 212,186; 214,202; 216,200; 221,177; 227,181; 230,158; 234,153; 240,222; 244,191; 246,212; 250,146; 252,199; 254,224; 257,213; 262,199; 265,216; 272,249; 275,219; 288,278; 300,242; 302,215; 304,237; 314,242; 346,261; 374,276; 377,261; 522,397; 531,398; 682,070; 735,876; 880,844; 885,014; 887,095; 889,167; 891,283; 908,731; 914,635; 918,704; 924,824; 927,911; 931,087; 933,158; 935,297; 938,469; 1009,920; 1021,632; 1061,701; 1076,589; 1079,654; 1082,073; 1097,028; 1100,652
T. atroviride	**Not related**
$[MH]^+$ 1502.493 Da	
Fragment masses	70,055; 84,054; 86,086; 110,076; 112,096; 115,089; 120,091; 129,115; 136,088; 154,107; 157,123; 159,106; 167,117; 172,118; 175,139; 185,126; 197,137; 201,119; 212,131; 214,132; 217,126; 219,149; 229,129; 232,151; 235,134; 237,134; 240,142; 242,147; 244,136; 252,150; 255,144; 258,128; 266,150; 268,164; 270,158; 272,151; 279,133; 288,166; 295,152; 301,131; 312,167; 314,171; 327,163; 338,181; 343,174; 345,202; 353,137; 369,179; 398,174; 508,259; 588,216; 623,206; 648,197; 852,393; 981,463; 1032,491; 1288,746; 1302,706; 1392,015; 1396,295; 1399,569; 1404,886; 1422,931; 1458,853; 1479,204
T. atroviride	**Not related**
$[MH]^+$ 1637.538 Da	
Fragment masses	70,040; 84,087; 110,068; 112,088; 115,085; 129,106; 136,076; 147,117; 154,095; 157,107; 172,108; 175,123; 193,100; 197,113; 201,127; 209,107; 221,083; 226,115; 229,111; 244,120; 264,104; 286,116; 310,142; 318,046; 320,085; 331,146; 336,107; 343,138; 421,177; 433,122; 448,180; 451,125; 611,307; 613,283; 629,272; 650,252; 653,199; 742,332; 757,370; 765,271; 872,391; 959,450; 1032,462; 1048,531; 1066,459; 1074,516; 1098,447; 1100,592; 1189,596; 1213,599; 1328,662; 1409,723; 1509,929; 1516,524; 1523,019; 1538,848; 1541,085; 1570,762; 1588,521; 1592,864
T. atroviride	**S-adenosylmethionine synthase K.DIGYDDSDKGFDYK.T (significant)**
$[MH]^+$ 1872.613 Da	
Fragment masses	70,067; 86,110; 101,101; 112,119; 115,122; 129,147; 133,101; 136,122; 141,140; 147,139; 154,140; 158,142; 167,156; 175,164; 195,136; 197,182; 199,214;

	209,158; 212,162; 216,155; 227,216; 244,163; 262,197; 283,231; 311,218; 326,282; 331,178; 343,235; 373,218; 380,259; 398,265; 405,210; 422,226; 444,172; 455,311; 472,231; 535,303; 569,334; 585,339; 623,330; 641,314; 698,446; 754,416; 778,396; 848,473; 865,441; 884,519; 964,529; 1008,632; 1032,619; 1061,575; 1078,632; 1095,685; 1158,613; 1175,656; 1286,758; 1304,794; 1338,842; 1401,805; 1418,879; 1512,489; 1547,975; 1647,176; 1690,338; 1757,475; 1759,439; 1762,600; 1764,644; 1769,063; 1775,490; 1791,328; 1793,536; 1803,997; 1821,773; 1826,077; 1837,331; 1843,504
T. atroviride	**Glycogen synthase kinase 3 K.ILVENEPNSYICSR.Y + Phospho (significant)**
$[MH]^+$ 2062.882 Da	
Fragment masses	70,026; 74,251; 84,041; 86,065; 110,041; 112,059; 115,063; 120,050; 129,075; 136,047; 155,063; 157,067; 167,071; 169,085; 175,084; 181,068; 185,071; 197,092; 212,061; 226,074; 240,091; 272,118; 285,071; 296,143; 343,168; 382,128; 424,100; 486,190; 500,105; 614,278; 628,164; 638,333; 729,306; 766,392; 888,386; 901,355; 1081,436; 1113,411; 1284,485; 1397,473; 1468,641; 1516,703; 1569,609; 1857,601; 1865,741; 1945,012; 1955,409; 1959,908; 1963,103; 2044,573
T. atroviride	**Not related**
$[MH]^+$ 2143.688 Da	
Fragment masses	70,050; 84,073; 86,085; 110,071; 112,085; 115,085; 120,078; 129,101; 136,072; 147,106; 167,083; 169,124; 175,110; 197,120; 219,078; 240,133; 258,108; 296,164; 325,153; 343,184; 379,181; 382,124; 424,225; 442,224; 450,135; 553,253; 638,366; 657,225; 739,329; 766,464; 781,237; 786,224; 895,517; 914,337; 1024,521; 1038,425; 1063,474; 1081,592; 1152,511; 1196,616; 1209,545; 1249,553; 1265,684; 1363,705; 1380,698; 1391,547; 1408,666; 1478,726; 1505,730; 1551,920; 1604,790; 1649,944; 1676,123; 1703,955; 1736,413; 1802,104; 1928,266; 2030,893; 2035,183; 2046,530; 2064,551; 2126,633
T. atroviride	**Elicitor protein R.FAYLGNDSDGEEKPVVPVK.T + Phospho (significant)**
$[MH]^+$ 2394.732 Da	
Fragment masses	74,024; 110,071; 112,092; 129,110; 175,114; 226,134; 232,136; 244,111; 303,153; 381,120; 452,222; 480,084; 595,083; 714,303; 829,317; 927,372; 944,403; 966,404; 1037,405; 1194,471; 1328,554; 1429,616; 1453,478; 1514,802; 1628,709; 1905,218; 2280,481; 2283,622; 2286,637; 2289,997; 2295,597; 2298,602; 2316,597; 2318,300; 2331,600; 2370,726; 2374,821
T. atroviride	**Cinnamyl-alcohol dehydrogenase family protein K.GGEHVDENKAYKWNCDETNK.L (NOT significant)**
$[MH]^+$ 2439.821 Da	
Fragment masses	110,059; 112,090; 129,101; 167,087; 175,111; 185,100; 197,094; 207,113; 232,121; 235,115; 244,107; 272,135; 288,167; 414,137; 531,206; 646,191; 657,284; 832,312; 995,412; 1124,455; 1196,351; 1252,533; 1316,491; 1365,696; 1422,570; 1526,047; 2127,278; 2325,129; 2334,809; 2339,384; 2342,514; 2349,079; 2380,894; 2416,209
T. atroviride	**Glutamate ammonia ligase K.ALEPHHTECIKEYGEDNELR.L (significant)**
$[MH]^+$ 2562.767 Da	
Fragment masses	110,058; 112,073; 129,082; 175,115; 195,083; 232,141; 252,086; 275,108; 301,146; 303,162; 416,149; 475,095; 557,266; 585,228; 643,395; 699,294; 758,349; 765,407; 781,285; 845,367; 862,438; 887,454; 991,438; 1059,512; 1089,410; 1106,415; 1219,422; 1283,444; 1303,602; 1308,523; 1418,659; 1584,743; 1615,791; 1713,484; 1731,789; 1959,811; 2144,217; 2400,338; 2406,858; 2417,491; 2447,589; 2452,345; 2462,321; 2464,368; 2466,387; 2482,397; 2497,401
T. atroviride	**Protein phosphatase PTC2 R.GPGVHHNYEDSDSGYDLDQESGGK.F (NOT significant)**

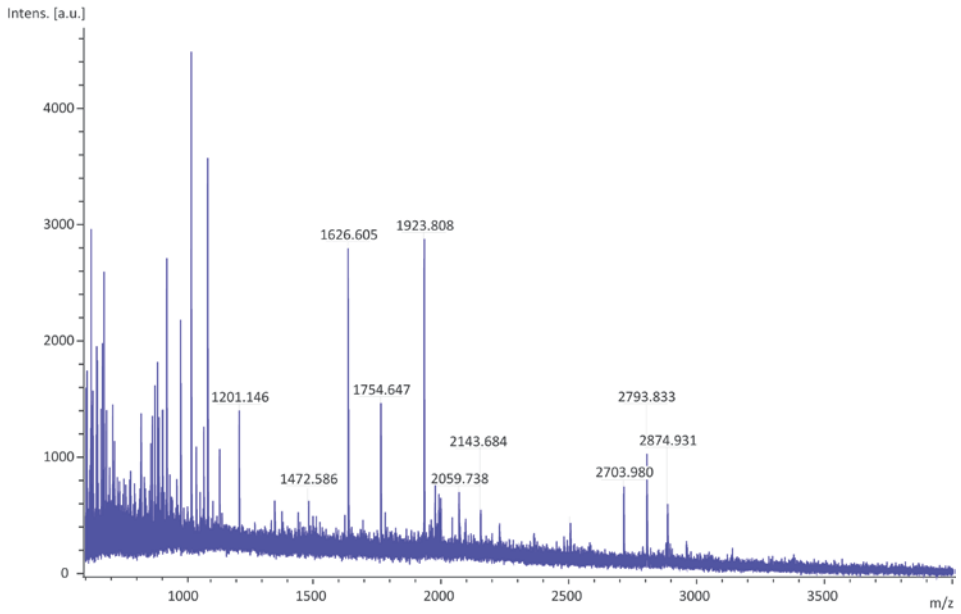


Figure 6.87 Positive ion reflector TOF - MALDI mass spectrum of 3_2_8

$[MH]^+$ 1201.146 Da	
Fragment masses	72,029; 84,039; 86,057; 110,037; 112,057; 115,061; 129,059; 132,066; 136,053; 154,047; 171,070; 175,071; 185,062; 197,067; 205,061; 212,080; 215,047; 227,062; 257,054; 259,046; 266,047; 268,083; 270,064; 288,104; 1002,523; 1004,603; 1006,791; 1010,009; 1012,223; 1101,648; 1121,488; 1151,149; 1153,514; 1157,235; 1160,085; 1174,885; 1178,118; 1181,263; 1184,239
T. atroviride	**Not related**
$[MH]^+$ 1472.658 Da	
Fragment masses	70,051; 84,068; 86,115; 101,097; 104,134; 110,084; 112,109; 115,109; 120,120; 129,135; 136,124; 141,136; 147,119; 154,133; 159,136; 167,133; 175,164; 181,150; 185,158; 197,182; 212,170; 217,170; 226,193; 228,186; 231,169; 240,196; 242,198; 244,173; 254,195; 266,180; 268,215; 273,194; 288,227; 357,238; 375,224; 387,218; 410,256; 446,283; 513,332; 524,231; 552,304; 577,344; 653,310; 688,371; 705,370; 768,337; 785,367; 798,367; 820,395; 896,448; 1027,581; 1032,474; 1098,704; 1129,869; 1210,703; 1278,072; 1368,562; 1375,057; 1379,484; 1381,626; 1401,546; 1404,773; 1419,388; 1422,563; 1425,766; 1446,109
T. atroviride	**Transaldolase like protein R.FDFNEDQMAVEK.L (NOT significant)**
$[MH]^+$ 1626.605 Da	
Fragment masses	70,067; 86,101; 101,066; 110,079; 113,076; 115,096; 129,109; 136,081; 154,091; 159,089; 172,114; 175,122; 181,105; 185,107; 197,132; 201,110; 209,102; 216,103; 225,107; 229,118; 240,140; 253,093; 273,111; 290,115; 315,170; 324,129; 331,107; 341,120; 343,154; 352,132; 359,116; 403,196; 413,168; 423,183; 426,187; 430,187; 437,191; 444,215; 454,196; 474,238; 484,222; 539,227; 552,234; 567,254; 569,241; 587,245; 594,284; 611,315; 638,276; 656,277; 674,281; 691,317; 709,325; 726,353; 825,435; 866,391; 953,489; 1023,539; 1040,561; 1138,609; 1153,593; 1155,661; 1224,734; 1268,780; 1426,558; 1434,924; 1452,870; 1497,994; 1521,499; 1570,327; 1575,341; 1580,857 1585,100; 1608,236
T. atroviride	**Transaldolase like protein K.EGGDIDSQVDHALDR.L (significant)**
$[MH]^+$ 1754.647 Da	
Fragment masses	70,082; 84,094; 86,095; 101,098; 110,079; 112,092; 115,092; 129,112; 136,100; 154,104; 167,104; 169,112; 172,124; 175,130; 181,121; 197,146; 209,110; 216,125; 253,119; 290,132; 324,150; 403,177; 437,178; 474,225; 487,197; 594,305; 611,297; 709,293; 715,337; 726,328; 819,432; 825,376; 846,384; 930,442; 953,449; 1023,486; 1040,527; 1144,600; 1155,530; 1253,698; 1268,742; 1281,565; 1324,657; 1352,773; 1498,038; 1581,098; 1680,127;

	1707,914
T. atroviride	**Transaldolase like proteinK.KEGGDIDSQVDHALDR.L (significant)**
$[MH]^+$ 1923.808 Da	
Fragment masses	70,044; 84,082; 86,095; 110,089; 112,099; 115,110; 129,121; 175,133; 186,136; 197,161; 211,119; 301,146; 368,244; 385,230; 415,188; 484,315; 496,272; 513,290; 528,251; 553,365; 570,357; 639,377; 668,386; 685,423; 784,484; 883,518; 996,684; 1041,567; 1093,762; 1295,929; 1752,521; 1818,981; 1822,152; 1825,349; 1857,066; 1878,204; 1880,695
T. atroviride	**Not related**
$[MH]^+$ 2059.738 Da	
Fragment masses	70,024; 74,077; 110,056; 112,072; 129,081; 175,102; 197,113; 340,101; 378,131; 486,198; 500,113; 610,268; 614,313; 628,168; 632,227; 645,261; 729,341; 747,281; 859,301; 876,309; 901,402; 977,382; 987,334; 1053,385; 1088,410; 1105,427; 1113,493; 1228,570; 1233,460; 1284,554; 1361,633; 1397,895; 1688,708; 1807,667; 1947,215; 1954,589; 1964,318; 1982,271
T. atroviride	**Fructose bisphosphate aldolase, class II K.DYVLTAIGNPDGDDKPNKK.Y (NOT significant)**
$[MH]^+$ 2143.684 Da	
Fragment masses	70,049; 110,071; 112,083; 129,100; 136,064; 154,084; 175,115; 197,115; 258,072; 296,085; 343,185; 382,067; 424,170; 528,228; 553,173; 605,182; 615,266; 638,339; 688,241; 739,340; 766,447; 895,471; 914,335; 1081,580; 1196,628; 1703,959; 1737,200; 1801,937; 2028,477; 2031,784; 2043,613; 2046,584; 2064,604; 2071,903; 2091,737
T. atroviride	**Elicitor protein R.FAYLGNDSDGEEKPVVPVK.T + Phospho (NOT significant)**
$[MH]^+$ 2703.980 Da	
Fragment masses	112,067; 175,093; 345,130; 361,094; 476,115; 545,153; 660,202; 692,169; 724,328; 789,179; 979,284; 1037,422; 1047,320; 1162,330; 1260,470; 1277,386; 1663,652; 1756,770; 2590,154; 2593,431; 2597,075; 2609,904; 2660,713
T. atroviride	**60S ribosomal protein L5 K.TFVGVEEADGEFTLTESAETDDGER.R (NOT significant)**
$[MH]^+$ 2793.833 Da	
Fragment masses	112,060; 169,073; 175,095; 201,073; 231,058; 240,102; 245,054; 257,125; 272,077; 274,145; 311,122; 316,071; 328,133; 330,103; 345,175; 357,091; 361,154; 369,141; 374,040; 387,117; 440,170; 445,120; 474,201; 476,149; 484,177; 486,109; 504,090; 545,257; 555,237; 615,165; 625,253; 643,251; 660,268; 670,200; 714,196; 789,311; 829,259; 900,306; 918,391; 1029,391; 1043,399; 1047,417; 1114,349; 1127,414; 1158,499; 1162,452; 1260,482; 1277,461; 1346,472; 1403,538; 1550,545; 1663,602; 1681,814; 1877,612; 1992,550; 2107,781; 2224,609; 2609,001; 2685,801; 2703,194; 2757,920; 2759,812; 2774,235; 2776,360
T. atroviride	**Not related**
$[MH]^+$ 2874.931 Da	
Fragment masses	112,062; 129,087; 141,081; 169,071; 175,104; 240,104; 257,121; 274,143; 311,110; 314,095; 316,087; 328,140; 330,085; 345,171; 369,132; 403,146; 440,172; 445,100; 457,141; 474,203; 484,178; 486,102; 504,113; 527,210; 545,225; 555,195; 601,230; 619,238; 625,229; 643,219; 660,254; 670,228; 714,219; 716,257; 771,300; 789,308; 829,253; 875,274; 882,307; 900,331; 918,372; 928,367; 972,391; 981,490; 987,426; 1005,419; 1029,424; 1043,374; 1047,433; 1057,424; 1114,408; 1127,456; 1144,462; 1162,477; 1242,486; 1259,508; 1277,511; 1346,582; 1375,544; 1403,576; 1444,424; 1501,481; 1550,711; 1646,713; 1648,539; 1663,762; 1675,319; 1681,773; 1761,697; 1778,797; 1877,906; 1888,537; 1895,741; 1975,810; 1989,710; 1992,862; 2003,225; 2011,016; 2081,152; 2090,900; 2108,047; 2178,447; 2205,301; 2223,032; 2277,824; 2321,089; 2609,623; 2617,766; 2623,609; 2707,504; 2741,999; 2747,473; 2749,999; 2759,859; 2777,787; 2795,813
T. atroviride	**Elongation factor 1 beta (EF1B) K.APAAEDDDDVLFGSDDEEEDAEAVR.I + Phospho (significant)**

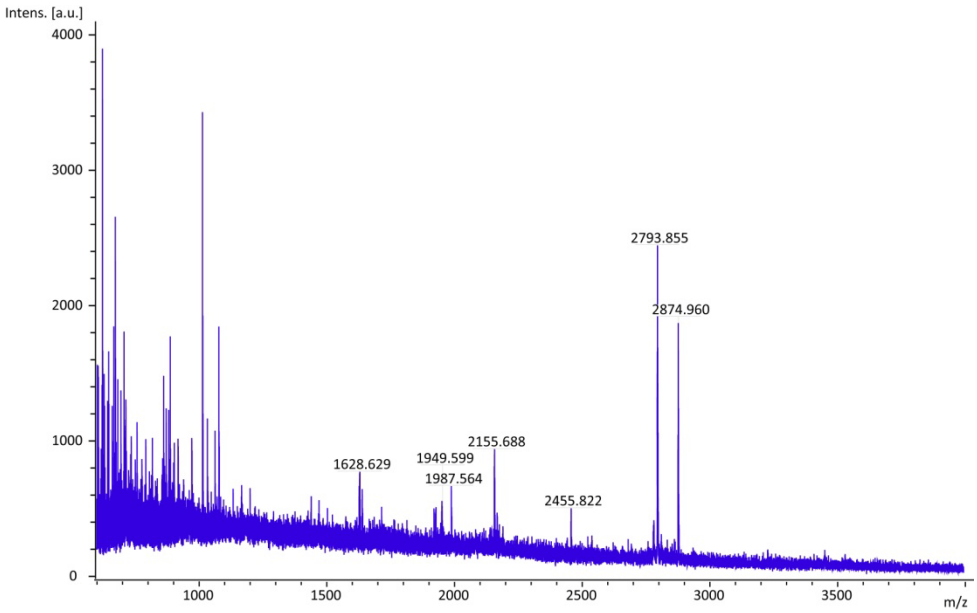


Figure 6.88 Positive ion reflector TOF - MALDI mass spectrum of 3_2_9

$[MH]^+$ 1628.629 Da	
Fragment masses	70,063; 84,058; 86,063; 110,054; 112,068; 115,083; 129,087; 136,057; 141,094; 154,074; 172,078; 175,098; 185,096; 192,097; 197,108; 202,071; 209,090; 215,108; 226,106; 229,111; 244,106; 253,083; 270,144; 272,109; 288,156; 383,136; 400,159; 435,167; 564,232; 611,251; 664,289; 778,350; 1040,455; 1149,489; 1285,769; 1424,413; 1426,486; 1428,530; 1432,781; 1521,379; 1559,507; 1575,293; 1578,451; 1581,789; 1585,069; 1598,050; 1601,304; 1604,750; 1608,555
T. atroviride	**Phosphotidylinositol transfer protein K.DNNSTFGDVDEFIR.W (NOT significant)**
$[MH]^+$ 1949.599 Da	
Fragment masses	70,036; 110,068; 112,088; 115,085; 120,081; 129,101; 154,089; 158,086; 175,108; 197,116; 272,135; 451,150; 580,179; 677,214; 694,251; 799,324; 882,289; 1068,363; 1137,334; 1183,410; 1320,521; 1506,678; 1843,538; 1861,732; 1880,772; 1900,725; 1906,017; 1931,789
T. atroviride	**Acetolactate synthase R.EISNGEHNGESTNEFER.T (NOT significant)**
$[MH]^+$ 1987.564 Da	
Fragment masses	70,046; 84,065; 110,061; 112,076; 129,085; 154,079; 175,102; 197,112; 259,072; 288,155; 345,145; 545,252; 586,166; 645,156; 774,213; 885,209; 903,222; 1018,263; 1147,324; 1267,472; 1276,335; 1333,408; 1480,567; 1537,695; 1594,640; 1683,037; 1707,867; 1855,040; 1877,329; 1881,875; 1883,846; 1895,452; 1899,596; 1909,349; 1962,721; 1968,421
T. atroviride	**60S acidic ribosomal protein K.KEEEEEEDEEGFGGLFD.- (significant)**
$[MH]^+$ 2155.688 Da	
Fragment masses	70,034; 110,053; 112,073; 115,072; 129,088; 136,063; 175,099; 185,077; 197,103; 244,103; 284,089; 301,104; 345,106; 384,148; 409,125; 416,109; 426,156; 487,140; 516,211; 539,234; 558,209; 587,249; 605,273; 687,386; 701,210; 720,300; 758,440; 781,302; 799,359; 813,438; 855,497; 892,450; 912,425; 943,333; 964,370; 997,444; 1012,493; 1068,554; 1108,487; 1125,575; 1240,579; 1320,628; 1329,628; 1337,641; 1438,698; 1569,777; 1812,216; 2025,285; 2028,256; 2041,539; 2046,498; 2049,792; 2064,715; 2078,703; 2111,285; 2114,520
T. atroviride	**Heme binding peroxidase R.DNDAAACTPDGRLPDASQGPK.H (significant)**
$[MH]^+$ 2455.822 Da	
Fragment masses	74,073; 110,072; 129,104; 175,111; 442,227; 513,278; 545,239; 558,180; 629,170; 657,214; 766,232; 794,283; 855,411; 954,464; 1070,495; 1285,540; 1502,733; 1511,741; 1582,994; 1711,800; 1738,833; 1886,069; 2015,127;

	2342,302; 2356,320
T. atroviride	**Ran binding domain containing protein R.DAKGDEEEAPESEDVHFEPVVK.L (NOT significant)**
$[MH]^+$ 2793.855 Da	
Fragment masses	112,037; 129,077; 141,090; 143,100; 158,072; 169,070; 171,074; 175,095; 187,062; 201,059; 215,073; 222,085; 229,088; 231,036; 240,101; 245,045; 257,124; 272,083; 274,142; 298,068; 300,067; 311,126; 316,071; 328,153; 345,179; 369,130; 374,072; 387,113; 399,106; 412,162; 427,078; 429,105; 431,090; 440,144; 445,122; 457,163; 461,056; 474,208; 484,169; 486,130; 503,153; 527,190; 542,124; 545,256; 555,176; 558,160; 560,140; 572,122; 590,130; 599,185; 615,167; 618,214; 625,194; 633,186; 643,256; 660,285; 670,205; 675,148; 689,173; 714,217; 732,222; 744,214; 771,283; 785,240; 789,330; 811,239; 829,249; 859,231; 875,261; 882,280; 900,300; 918,380; 928,332; 972,335; 999,352; 1029,387; 1043,336; 1047,398; 1057,392; 1096,357; 1114,369; 1127,380; 1144,386; 1162,437; 1242,413; 1260,423; 1277,485; 1346,467; 1403,510; 1550,498; 1663,530; 1681,671; 1761,394; 1778,624; 1877,562; 1895,850; 1987,545; 1992,499; 2079,703; 2107,488; 2222,853; 2592,237; 2608,492; 2690,376; 2732,010; 2747,118; 2756,657; 2758,895; 2775,323; 2777,585
T. atroviride	**Not related**
$[MH]^+$ 2874.960 Da	
Fragment masses	73,992; 112,062; 129,113; 141,086; 158,086; 169,100; 175,118; 201,092; 229,108; 240,119; 245,069; 257,146; 274,159; 284,129; 300,137; 311,139; 316,089; 328,172; 345,184; 355,147; 357,106; 369,141; 374,097; 387,119; 399,132; 427,101; 440,160; 443,144; 445,125; 456,214; 461,083; 474,194; 484,177; 486,121; 527,241; 545,250; 555,222; 560,145; 574,185; 599,225; 615,148; 625,244; 633,188; 643,243; 660,278; 670,257; 714,227; 732,258; 744,248; 771,329; 785,245; 789,336; 799,341; 804,236; 811,281; 829,279; 859,271; 875,301; 882,335; 900,353; 918,402; 928,379; 972,41; 1999,425; 1006,358; 1029,469; 1043,404; 1047,470; 1057,510; 1096,405; 1114,431; 1127,470 1144,499; 1162,509; 1227,521; 1242,504; 1259,535; 1277,551; 1328,534; 1346,591 1385,601; 1403,623; 1416,440; 1421,585; 1426,576; 1444,553; 1501,561; 1550,697 1562,701; 1645,891; 1648,665; 1663,829; 1675,360; 1681,817; 1743,835; 1761,770 1778,882; 1859,875; 1877,960; 1888,630; 1896,075; 1975,913; 1992,350; 2003,301 2010,052; 2081,518; 2090,941; 2108,106; 2117,872; 2178,169; 2206,004; 2223,168 2232,672; 2277,908; 2321,150; 2338,264; 2538,660; 2609,611; 2617,761; 2623,755 2628,004; 2707,620; 2732,392; 2737,968; 2742,488; 2748,146; 2751,414; 2757,028 2760,032; 2774,494; 2777,951; 2795,974
T. atroviride	**Elongation factor 1 beta (EF1B) K.APAAEDDDDVLFGSDDEEEDAEAVR.I + Phospho (significant)**

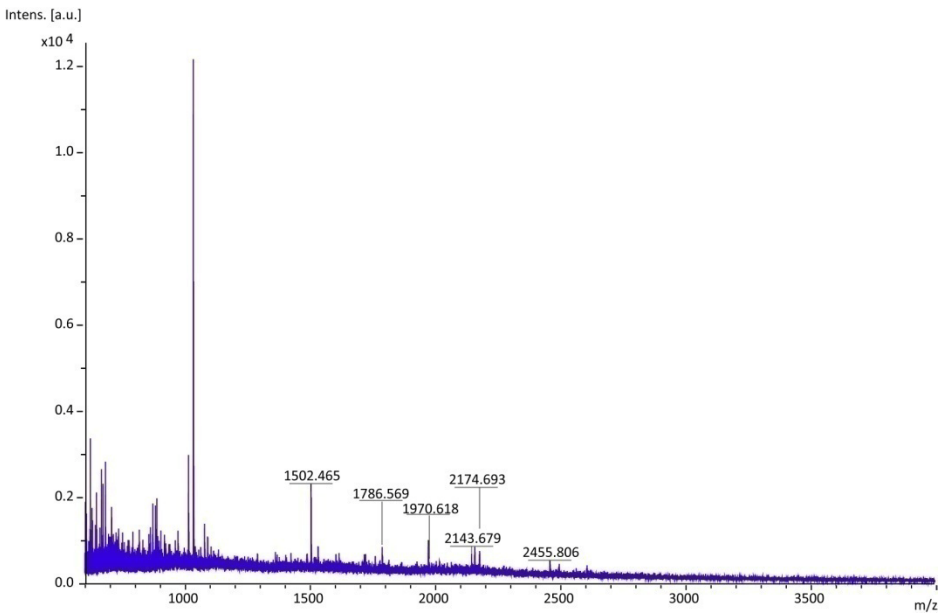


Figure 6.89 Positive ion reflector TOF - MALDI mass spectrum of 3_2_10

$[MH]^+$ 1502.465 Da	
Fragment masses	110,079; 112,094; 129,117; 136,091; 175,135; 195,127; 197,143; 232,147; 300,134; 345,216; 355,177; 508,256; 513,247; 518,236; 525,187; 588,247; 623,253; 942,226; 1032,491; 1040,196; 1152,394; 1302,732; 1404,936; 1423,007
T. atroviride	**Not related**
$[MH]^+$ 1786.569 Da	
Fragment masses	70,053; 84,078; 86,099; 110,085; 112,098; 115,101; 129,120; 154,117; 167,128; 175,145; 181,119; 197,155; 199,135; 250,106; 536,229; 608,312; 764,349; 776,411; 863,412; 913,464; 942,390; 1028,509; 1032,497; 1081,523; 1143,575; 1291,727; 1671,271; 1689,310; 1707,336
T. atroviride	**Not related**
$[MH]^+$ 1970.618 Da	
Fragment masses	70,050; 86,077; 110,063; 112,075; 129,098; 154,077; 167,072; 175,106; 181,093; 197,104; 250,087; 284,102; 376,075; 490,133; 865,263; 942,245; 1032,365; 1856,286
T. atroviride	**Necrosis inducing protein K.DGTEPEGILGHPYDWER.V (NOT significant)**
$[MH]^+$ 2143.679 Da	
Fragment masses	110,067; 112,080; 129,101; 175,118; 197,121; 244,162; 284,126; 397,190; 794,292; 811,316; 876,264; 878,354; 894,266; 909,299; 924,390; 942,398; 955,990; 960,402; 1004,370; 1022,359; 1040,371; 1055,466; 1088,424; 1104,403; 1119,418; 1134,517; 1152,518; 1164,574; 1232,469; 1250,491; 1283,530; 1381,504; 1397,541; 1438,651; 1495,513; 2028,477; 2032,351; 2046,430; 2080,280
T. atroviride	**Not related**
$[MH]^+$ 2174.693 Da	
Fragment masses	70,039; 110,061; 112,079; 129,100; 136,059; 155,082; 175,103; 272,130; 284,164; 799,406; 892,403; 910,356; 924,397; 942,429; 956,391; 1022,384; 1040,386; 1056,458; 1103,423; 1120,419; 1125,584; 1152,497; 1171,517; 1238,611; 1250,464; 1375,730; 2003,597; 2062,857; 2067,452; 2075,166; 2079,388; 2084,731; 2094,735; 2103,839; 2111,560
T. atroviride	**Not related**
$[MH]^+$ 2455.806 Da	
Fragment masses	110,066; 129,094; 175,119; 386,251; 414,104; 430,157; 442,239; 558,159; 614,204; 766,308; 810,340; 855,416; 945,334; 954,500; 1070,456; 1156,497; 1511,758; 2015,188
T. atroviride	**Ran binding domain containing protein R.DAKGDEEEAPESEDVHFEPVVK.L (NOT significant)**

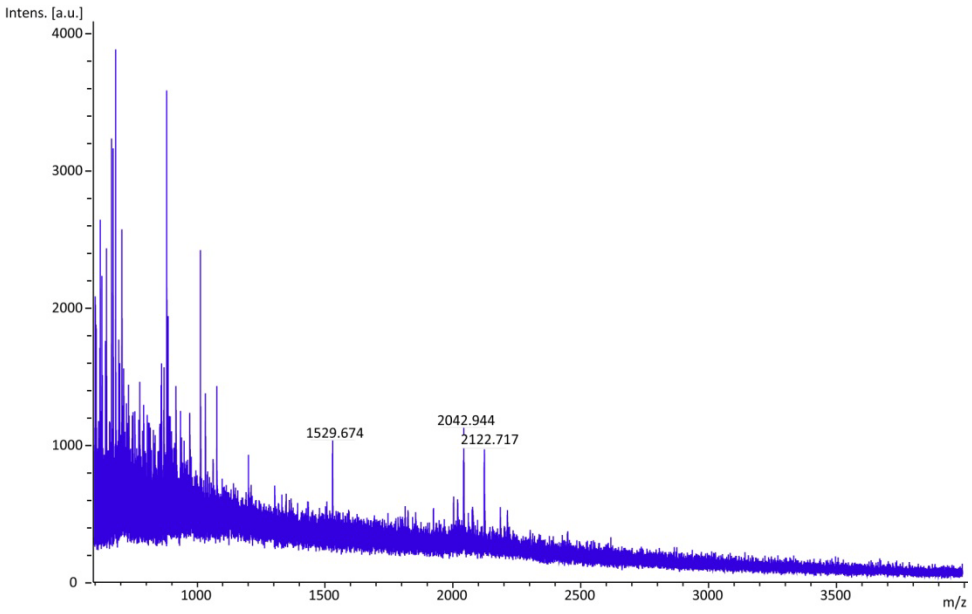


Figure 6.90 Positive ion reflector TOF - MALDI mass spectrum of 3_2_11

$[MH]^+$ 1529.674 Da	
Fragment masses	84,080; 86,072; 110,073; 112,095; 115,101; 129,109; 154,094; 163,096; 171,139; 175,122; 181,110; 186,135; 195,118; 197,131; 215,111; 227,110; 229,150; 232,143; 240,134; 242,147; 244,112; 268,132; 270,143; 288,146; 302,125; 309,156; 311,162; 313,135; 315,154; 333,168; 371,170; 379,165; 399,172; 413,169; 461,195; 513,291; 574,239; 590,228; 645,275; 699,274; 831,384; 1032,435; 1145,571; 1151,942; 1243,515; 1334,791; 1414,995; 1480,568; 1482,564; 1485,999; 1502,062; 1505,247; 1507,492; 1510,078; 1512,375
T. atroviride	**Cyclophilin K.DGKPTAEIKEQTGR.I (NOT significant)**
$[MH]^+$ 2042.944 Da	
Fragment masses	74,095; 110,070; 112,087; 129,111; 175,108; 244,167; 316,128; 341,139; 357,210; 456,301; 470,172; 488,162; 571,285; 583,267; 601,249; 672,401; 694,283; 712,311; 730,283; 771,434; 825,364; 954,364; 957,460; 1071,451; 1137,372; 1155,401; 1200,470; 1934,507; 2013,161; 2024,508
T. atroviride	**Not related**
$[MH]^+$ 2122.717 Da	
Fragment masses	86,086; 110,074; 129,100; 175,125; 226,120; 244,144; 341,088; 357,179; 415,213; 430,181; 456,232; 470,120; 486,210; 502,228; 528,256; 555,242; 568,158; 571,292; 583,214; 599,267; 601,241; 616,259; 627,290; 654,312; 672,339; 681,217; 694,271; 712,267; 730,433; 745,316; 753,389; 771,430; 797,357; 807,338; 810,293; 825,352; 844,385; 858,361; 870,487; 923,328; 936,362; 939,496; 954,399; 957,521; 987,469; 1068,467; 1071,592; 1137,457; 1149,655; 1155,473; 1200,636; 1236,543; 1253,465; 1313,735; 1353,579; 1442,857; 1555,925; 1799,247; 1819,420; 1914,403; 2007,632; 2010,812; 2017,839; 2025,476; 2043,468; 2063,832
T. atroviride	**Not related**

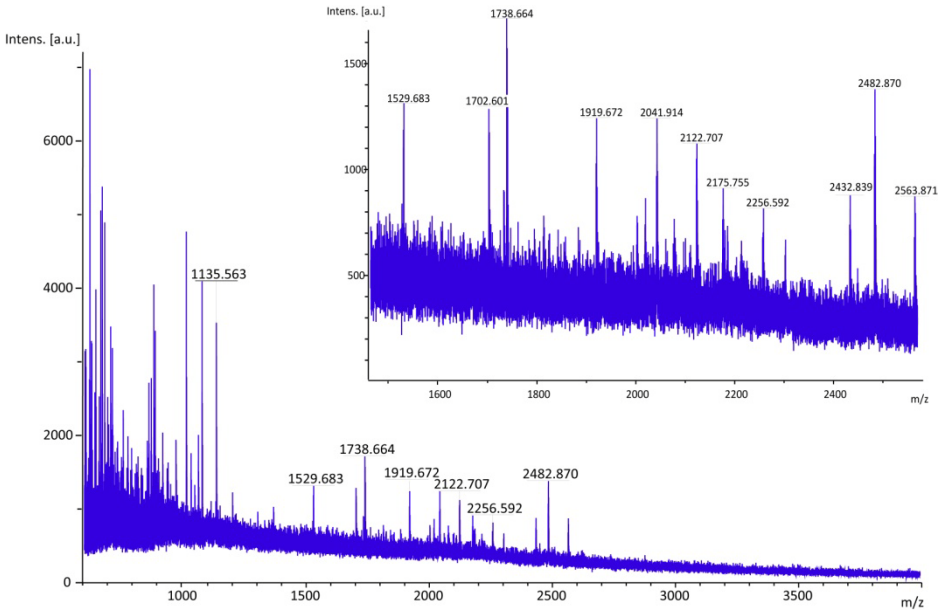


Figure 6.91 Positive ion reflector TOF - MALDI mass spectrum of 3_2_12

$[MH]^+$ 1135.563Da	
Fragment masses	58,013; 70,064; 72,084; 84,087; 86,110; 101,106; 112,127; 115,119; 129,140; 132,141; 136,121; 143,125; 147,137; 154,135; 158,139; 172,133; 175,168; 181,146; 187,131; 197,179; 200,158; 205,157; 209,157; 211,183; 216,153; 219,176; 221,167; 226,197; 228,168; 234,131; 242,162; 244,180; 246,190; 253,192; 255,171; 258,181; 269,192; 271,189; 274,182; 287,197; 302,186; 304,224; 309,213; 316,196; 327,207; 345,222; 359,221; 367,243; 373,223; 380,245; 397,267; 415,279; 432,289; 460,291; 467,281; 485,309; 488,289; 502,322; 519,366; 599,326; 617,331; 648,448; 681,872; 698,066; 704,454; 751,947; 817,541; 834,595; 880,530; 897,001; 901,150; 924,571; 928,608; 930,694; 934,805; 940,975; 945,205; 947,304; 949,421; 1015,242; 1020,892; 1039,418; 1069,385; 1072,566; 1074,960; 1080,733; 1083,263; 1085,784; 1087,443; 1089,653; 1091,917; 1095,159; 1097,436; 1113,319
T. atroviride	**40S ribosomal protein S12 K.DWGEESQER.S (NOT significant)**
$[MH]^+$ 1529.683 Da	
Fragment masses	110,084; 112,100; 115,100; 129,112; 154,101; 167,109; 172,115; 175,132; 187,104; 197,138; 209,109; 214,137; 226,120; 229,131; 232,121; 240,144; 244,117; 250,108; 252,127; 258,137; 268,136; 270,158; 272,167; 275,121; 288,167; 294,119; 303,157; 313,151; 326,143; 328,151; 330,125; 340,154; 356,161; 358,149; 362,171; 380,192; 397,176; 399,190; 459,225; 508,222; 513,288; 579,260; 688,295; 716,308; 811,344; 852,369; 879,373; 948,389; 1019,381; 1065,404; 1260,586; 1341,000; 1415,047; 1460,380; 1464,583; 1480,354; 1482,557; 1484,715; 1488,128; 1505,308; 1509,435
T. atroviride	**Not related**
$[MH]^+$ 1702.601 Da	
Fragment masses	110,074; 112,080; 129,110; 136,086; 154,096; 172,104; 175,115; 195,088; 197,126; 227,114; 288,176; 312,128; 358,132; 427,155; 513,260; 641,244; 770,293; 1039,550; 1046,494; 1391,693; 1659,107; 1675,280
T. atroviride	**40S ribosomal protein S15 K.HGYIGEFEEVDDHR.S (NOT significant)**
$[MH]^+$ 1738.664 Da	
Fragment masses	86,093; 101,077; 110,084; 129,113; 147,117; 154,108; 172,112; 175,142; 197,141; 200,144; 209,144; 213,127; 218,145; 237,139; 244,161; 257,160; 272,160; 285,155; 288,173; 294,160; 312,202; 315,178; 332,171; 389,208; 409,173; 494,275; 513,279; 517,264; 522,251; 556,259; 570,273; 579,271; 588,296; 611,326; 665,329; 693,351; 703,335; 778,441; 797,378; 804,398; 806,417; 819,452; 854,383; 925,427; 935,479; 1036,553; 1046,585; 1088,481; 1122,578; 1151,620; 1160,596; 1187,528; 1217,712; 1222,694; 1251,574; 1330,797; 1350,831; 1388,720; 1407,881; 1503,017; 1521,980; 1586,614; 1593,055; 1603,247; 1611,996; 1687,489; 1689,739; 1692,988
T. atroviride	**Copper/Zink superoxid dismutase R.HVGDLGNIETDAQGNAK.G (significant)**

$[MH]^+$ 1919.672 Da	
Fragment masses	70,052; 74,133; 84,097; 110,099; 112,116; 115,119; 129,142; 175,163; 186,160; 197,169; 226,173; 244,169; 272,273; 284,151; 513,296; 530,311; 547,281; 618,370; 765,507; 872,552; 1031,636; 1048,670; 1095,802; 1177,816; 1233,846; 1805,539; 1816,014
T. atroviride	**Plectin/S10 domain containing protein R.DAGEGKEGGAPGEFAPQFR.G (NOT significant)**
$[MH]^+$ 2041.914Da	
Fragment masses	110,052; 112,054; 129,076; 154,057; 175,090; 197,084; 513,175; 569,081; 690,101; 1034,417; 1191,628; 1419,393; 1563,387; 1798,498; 1846,940; 1947,635; 1992,604; 2020,303
T. atroviride	**Not related**
$[MH]^+$ 2122.707 Da	
Fragment masses	74,042; 84,044; 110,052; 112,054; 129,079; 136,059; 154,072; 172,061; 175,089; 197,100; 244,133; 513,206; 559,356; 864,439; 1089,446; 1166,589; 1281,489; 2025,177; 2099,787
T. atroviride	**Not related**
$[MH]^+$ 2175.755 Da	
Fragment masses	84,068; 110,069; 112,078; 115,078; 129,103; 136,081; 175,117; 195,076; 197,121; 240,150; 275,164; 466,238; 547,221; 564,255; 693,336; 710,360; 727,438; 804,416; 932,458; 1084,599; 1199,590; 1298,415; 1386,639; 1429,658; 1467,954; 1483,642; 1663,736; 1856,311; 1935,133; 2071,656; 2118,460; 2129,283; 2141,244; 2158,658
T. atroviride	**Not related**
$[MH]^+$ 2256.592 Da	
Fragment masses	70,071; 74,091; 84,085; 110,093; 112,108; 129,122; 136,095; 175,145; 275,141; 449,182; 459,247; 466,224; 492,181; 547,274; 564,241; 665,317; 693,323; 710,380; 804,420; 821,432; 918,486; 932,549; 949,503; 992,609; 1003,629; 1020,566; 1155,660; 1183,685; 1200,693; 1298,724; 1368,778; 1385,792; 1466,799; 1483,868; 1565,665; 1741,149; 1759,185; 1839,296; 1856,263; 1884,153; 1985,312; 2054,520; 2114,276; 2123,602; 2125,629; 2131,668; 2141,651; 2143,988; 2148,568; 2153,213; 2159,623; 2177,648; 2188,350
T. atroviride	**HMG-box protein K.RYEDEKQAYNADQEDESS.- + Phospho (significant)**
$[MH]^+$ 2432.839 Da	
Fragment masses	110,044; 112,048; 129,084; 175,080; 244,086; 303,064; 326,086; 416,151; 446,074; 455,081; 513,174; 677,219; 844,260; 861,334; 915,345; 932,369; 1030,353; 1047,366; 1144,401; 1275,499; 1679,675; 1762,661; 2004,118; 2247,487; 2331,011; 2388,344
T. atroviride	**Not related**
$[MH]^+$ 2482.870 Da	
Fragment masses	110,074; 175,108; 227,102; 229,122; 244,176; 259,097; 298,158; 315,212; 326,185; 358,162; 397,213; 407,230; 412,196; 425,254; 430,216; 455,188; 457,217; 473,138; 487,246; 496,283; 554,285; 574,300; 584,257; 586,268; 625,315; 655,348; 665,335; 673,356; 683,356; 698,304; 754,378; 782,398; 785,354; 795,331; 802,395; 812,345; 830,301; 848,334; 853,351; 866,357; 883,371; 901,420; 911,431; 982,469; 1010,483; 1012,530; 1030,509; 1092,422; 1141,523; 1159,542; 1258,595; 1269,562; 1340,594; 1357,625; 1565,614; 1583,733; 1654,690; 1768,839; 1883,753; 2049,478; 2431,828; 2448,716; 2451,490
T. atroviride	**Not related**
$[MH]^+$ 2563.871 Da	
Fragment masses	70,050; 110,072; 129,112; 227,115; 244,175; 259,120; 283,132; 298,166; 300,125; 310,190; 315,198; 326,166; 331,117; 358,159; 397,203; 407,211; 412,182; 425,227; 430,211; 455,184; 487,218; 496,255; 526,225; 536,276; 554,258; 558,211; 574,257; 584,220; 586,277; 610,305; 625,282; 655,314; 665,311; 673,338; 683,326; 698,265; 724,359; 737,344; 739,369; 754,367; 764,398; 767,317; 782,412; 785,367; 795,309; 802,393; 812,335; 830,307; 838,369; 848,316; 853,441; 866,349; 883,367; 893,472; 901,459; 911,447; 927,145; 964,414; 981,371; 992,491; 1010,534; 1013,481; 1030,521;1079,556; 1081,550; 1092,471; 1097,530; 1109,485; 1141,574; 1159,587; 1169,586; 1191,506; 1208,564; 1210,593; 1240,643; 1251,679; 1258,678; 1269,639; 1290,590; 1322,663; 1340,673; 1357,760; 1438,706; 1468,791; 1486,797; 1547,886;

	1565,823; 1583,903; 1636,975; 1654,956; 1704,284; 1751,002; 1757,380; 1769,047; 1847,626; 1883,193; 2012,284; 2141,340; 2240,508; 2260,193; 2355,738; 2432,586; 2437,687; 2447,013; 2449,866; 2455,384; 2458,645; 2466,831; 2484,867
T. atroviride	**Not related**

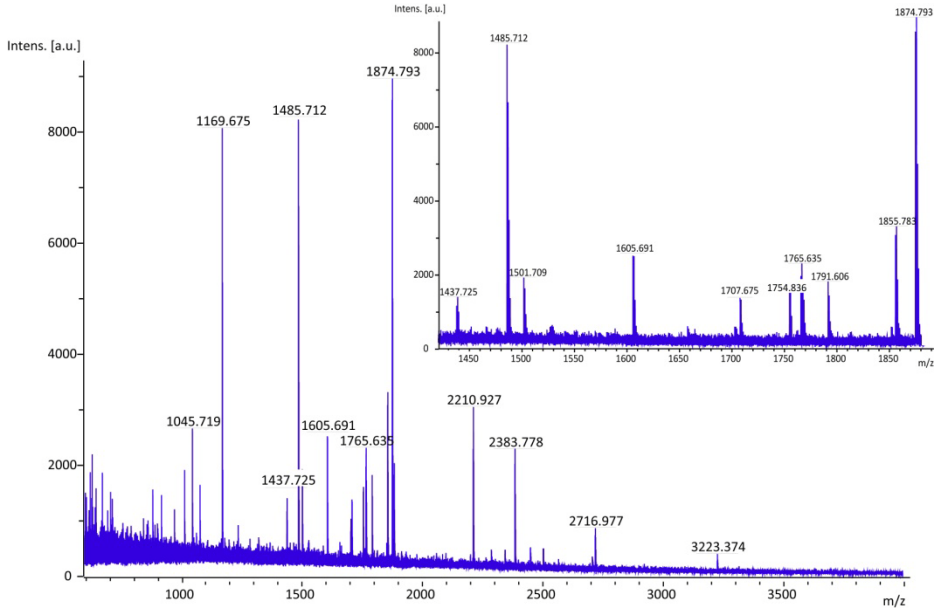


Figure 6.92 Positive ion reflector TOF - MALDI mass spectrum of 3_2_13

$[MH]^+$ 1045.719Da	
Fragment masses	58,021; 70,067; 72,072; 84,082; 86,098; 98,078; 100,088; 102,087; 110,085; 112,095; 115,100; 120,100; 123,113; 125,096; 127,114; 129,122; 132,125; 136,096; 139,116; 141,115; 143,133; 154,110; 157,137; 159,115; 161,122; 163,104; 165,113; 167,120; 169,128; 171,145; 175,144; 179,120; 181,122; 183,128; 185,129; 187,129; 191,112; 193,115; 195,124; 197,151; 201,126; 203,117; 212,139; 214,136; 216,133; 218,135; 227,134; 229,145; 232,151; 235,130; 238,155; 240,144; 242,168; 244,154; 246,158; 250,133; 252,159; 254,159; 257,145; 259,168; 262,166; 266,142; 268,163; 270,184; 272,169; 277,179; 283,162; 288,200; 294,148; 311,134; 339,181; 398,166; 534,265; 587,137; 651,139; 666,084; 713,192; 731,180; 811,140; 852,053; 854,162; 856,228; 916,773; 961,228; 982,461; 994,161; 997,381; 999,589; 1001,813; 1004,159; 1014,523; 1016,723; 1019,997; 1023,148
T. atroviride	**Not related**
$[MH]^+$ 1169.675 Da	
Fragment masses	58,013; 70,065; 72,072; 84,102; 86,117; 100,116; 102,115; 104,150; 110,115; 112,131; 115,134; 123,120; 125,149; 127,146; 129,159; 132,152; 136,138; 139,156; 141,157; 143,166; 154,154; 158,163; 167,166; 169,164; 171,167; 173,156; 175,178; 179,148; 181,161; 184,171; 186,178; 197,191; 202,172; 207,174; 209,185; 211,205; 214,207; 216,185; 218,193; 226,209; 228,203; 235,186; 240,214; 242,220; 244,198; 246,218; 249,198; 251,214; 254,223; 257,222; 259,208; 262,213; 273,212; 277,208; 284,236; 288,260; 294,205; 301,227; 311,250; 346,238; 1100,423; 1103,628; 1119,519; 1122,731; 1124,920; 1127,117; 1129,357; 1143,241; 1146,424
T. atroviride	**Not related**
$[MH]^+$ 1437.725 Da	
Fragment masses	86,088; 100,117; 110,083; 112,108; 115,105; 127,127; 129,125; 139,112; 141,128; 143,135; 154,126; 157,130; 167,131; 172,141; 175,158; 184,143; 186,146; 197,175; 201,160; 212,168; 214,188; 218,170; 224,200; 226,187; 228,178; 230,173; 234,175; 237,180; 240,201; 243,177; 246,195; 251,178;

	253,192; 255,191; 257,176; 261,176; 269,191; 272,213; 275,209; 282,215; 288,230; 292,189; 294,175; 297,217; 299,221; 310,198; 312,187; 328,231; 339,223; 395,262; 513,367; 610,274; 672,301; 759,304; 808,373; 896,347; 948,310; 1144,539; 1238,815; 1367,466; 1387,574; 1391,906; 1411,3571414,557 1416,599; 1419,093
T. atroviride	**Not related**
$[MH]^+$ 1485.712 Da	
Fragment masses	86,088; 98,055; 110,080; 112,085; 115,107; 127,113; 129,115; 136,091; 141,114; 143,105; 154,105; 157,111; 167,114; 169,129; 175,138; 185,138; 187,111; 190,150; 197,149; 200,135; 202,145; 208,140; 212,146; 214,145; 217,150; 226,161; 229,153; 241,147; 246,158; 249,165; 251,149; 253,130; 255,160; 257,159; 259,157; 262,156; 266,149; 268,168; 270,166; 272,154; 275,146; 277,160; 279,155; 282,158; 284,164; 286,162; 288,193; 292,167; 294,160; 311,156; 313,166; 315,186; 323,169; 326,169; 328,159; 335,162; 339,173; 341,156; 343,160; 345,174; 355,178; 383,191; 513,269; 1106,442; 1320,271; 1418,442; 1421,639; 1432,239; 1434,373; 1437,614; 1439,902; 1442,001; 1445,219; 1457,980; 1460,792; 1464,790
T. atroviride	**Not related**
$[MH]^+$ 1501.709 Da	
Fragment masses	84,072; 86,074; 110,069; 112,081; 115,076; 129,084; 141,085; 154,087; 157,102; 166,097; 175,119; 186,099; 197,115; 201,108; 207,113; 213,099; 217,102; 223,117; 226,129; 228,130; 230,103; 232,107; 234,106; 240,124; 242,130; 244,101; 246,155; 249,101; 253,082; 257,138; 262,108; 266,136; 268,140; 270,150; 272,114; 275,130; 278,109; 288,148; 290,127; 294,112; 301,109; 310,131; 312,136; 314,116; 327,134; 340,152; 343,147; 345,148; 351,125; 353,118; 355,127; 367,127; 369,129; 379,137; 393,123; 513,222; 529,202; 625,232; 641,287; 666,260; 683,251; 701,183; 746,280; 764,232; 781,282; 865,238; 1009,573; 1129,682; 1214,484; 1256,200; 1307,189; 1330,389; 1373,992; 1433,292; 1438,803; 1449,189; 1452,432; 1455,671; 1457,971; 1461,306; 1475,014; 1478,341; 1481,304; 1483,080
T. atroviride	**Not related**
$[MH]^+$ 1605.691 Da	
Fragment masses	86,067; 104,110; 110,057; 112,081; 115,074; 127,083; 129,094; 141,073; 154,082; 169,092; 171,105; 175,110; 195,094; 197,114; 201,106; 212,094; 214,119; 222,119; 224,116; 226,117; 239,134; 242,138; 244,103; 246,118; 252,119; 257,133; 259,120; 262,147; 269,125; 272,122; 276,087; 286,132; 288,170; 297,135; 312,154; 513,269; 1539,625; 1549,846; 1553,297; 1555,550; 1557,653; 1559,769; 1561,969; 1581,136
T. atroviride	**Not related**
$[MH]^+$ 1707.675 Da	
Fragment masses	86,080; 110,071; 112,073; 115,086; 129,103; 136,071; 154,082; 167,086; 175,118; 195,097; 197,115; 312,148; 358,140; 410,115; 427,182; 513,240; 542,241; 641,264; 657,228; 770,330; 899,290; 933,350; 1046,366; 1313,430; 1391,590; 1653,338; 1657,617; 1660,776; 1684,256
T. atroviride	**Not related**
$[MH]^+$ 1754.836 Da	
Fragment masses	110,076; 112,078; 115,081; 127,094; 129,101; 154,098; 167,095; 175,120; 197,139; 312,126; 369,123; 833,451; 1061,456; 1105,548; 1320,803; 1328,512; 1388,623; 1428,477; 1551,531; 1670,841; 1687,713; 1696,381; 1699,423; 1703,557; 1706,770; 1708,810; 1725,773
T. atroviride	**Not related**
$[MH]^+$ 1765.635 Da	
Fragment masses	74,222; 110,062; 112,073; 115,078; 129,095; 154,083; 167,082; 172,112; 175,109; 185,108; 195,107; 197,110; 226,124; 312,181; 369,224; 1715,606; 1718,970; 1723,131; 1745,038
T. atroviride	**Not related**
$[MH]^+$ 1791.606 Da	
Fragment masses	110,083; 112,097; 129,132; 154,106; 175,147; 197,144; 1732,248; 1738,611;

	1741,734; 1746,087; 1765,019
T. atroviride	**Not related**
$[MH]^+$ 1855.783 Da	
Fragment masses	70,051; 74,210; 110,088; 112,095; 115,105; 129,120; 154,133; 175,149; 197,166; 288,245; 369,322; 459,178; 918,523; 1144,645; 1458,643; 1748,392; 1800,484; 1805,782; 1809,165; 1812,258
T. atroviride	**Not related**
$[MH]^+$ 1874.793 Da	
Fragment masses	84,079; 110,090; 112,105; 129,127; 154,121; 175,147; 405,150; 448,136; 563,306; 677,397; 749,337; 806,510; 921,597; 1108,788; 1177,462; 1193,581; 1350,837; 1383,585; 1399,854; 1501,352; 1607,531; 1676,955; 1804,858; 1828,983
T. atroviride	**Not related**
$[MH]^+$ 2210.927 Da	
Fragment masses	86,079; 110,069; 112,087; 115,095; 129,120; 197,159; 1856,028 86,079; 110,069; 112,087; 115,095; 129,120; 197,159; 1856,028
T. atroviride	**Not related**
$[MH]^+$ 2383.778 Da	
Fragment masses	110,066; 129,094; 175,101; 2329,296; 2364,518
T. atroviride	**Not related**
$[MH]^+$ 2716.977 Da	
Fragment masses	74,166
T. atroviride	**Not related**
$[MH]^+$ 3223.374 Da	
Fragment masses	3172,265
T. atroviride	**Not related**

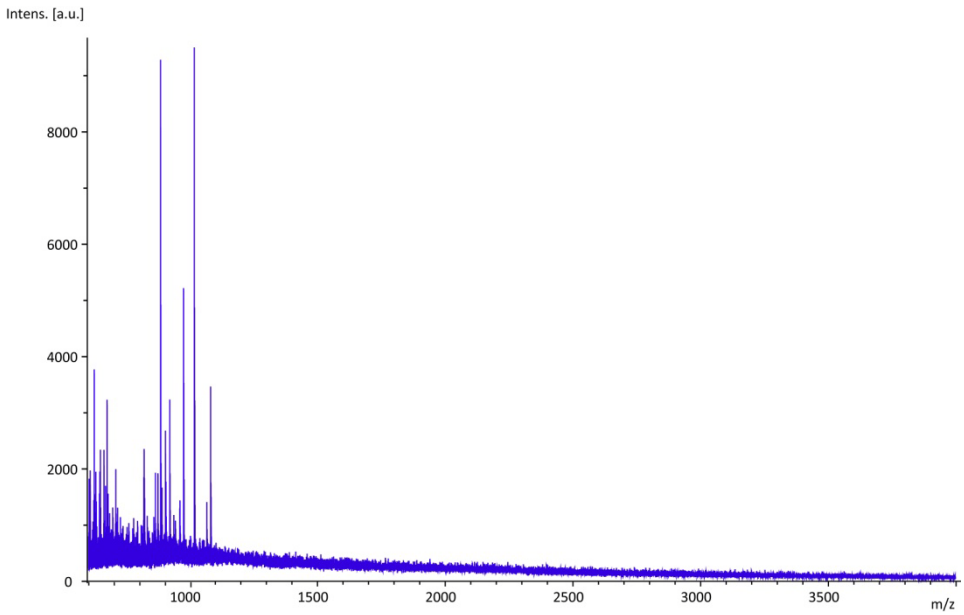


Figure 6.93 Positive ion reflector TOF - MALDI mass spectrum of 3_2_14

No relevant Peaks for PSD analysis

6.2.5 Details about Identifications and Statistics of the Detected Peptides

The attached files include tables that show the detected peptides and their possible functions as proteins. Detected peptides related to Trichoderma atroviride are written in bold and if they were detected carrying a phosphor group, they are written in bold red. The scores and thresholds (TH < 0.05), written in blue signal a significant identification. If the peptide is not related to Trichoderma atroviride, a BLAST search was carried out and the result is listed in the right column.

6.2.5.1 *Trichoderma atroviride* $_{wt}$ vs. *Trichoderma atroviride* $_{wt}$ (un-induced Mycoparasitism – self confrontation)

T_atroviride_wt_T_atrovirde_wt

T_atroviride_wt_T_atroviride_wt_Replicat

6.2.5.2 *Trichoderma atroviride* $_{wt}$ vs. Rhizoctonia solani (induced Mycoparasitism)

T_atroviride_wt_R_solani

T_atroviride_wt_R_solani_Replication

6.2.5.3 *Trichoderma atroviride* $_{tmk1}$ vs. Rhizoctonia solani (reduced Mycoparasitism)

T_atroviride_tmk1_R_solani

T_atroviride_tmk1_R_solani

6.2.6 MASCOT SEARCH RESULTS from the Identified Proteins

6.2.6.1 In *Trichoderma atroviride* $_{wt}$ (induced mycoparasitism)

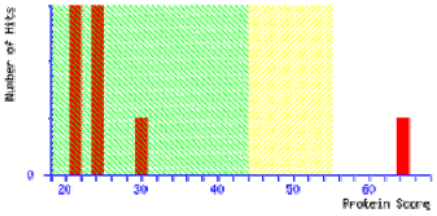
F-actin capping protein:

Mascot Search Results

```
User            : Bianca Bruckner
Email           : b.bruckner@live.at
Search title    :
MS data file    : DATA.TXT
Database        : NCBInr 20121013 (21019903 sequences; 7205775305 residues)
Taxonomy        : Fungi (1543708 sequences)
Timestamp       : 17 Oct 2012 at 09:44:44 GMT
Protein hits    : gi|46108688   hypothetical protein FG01226.1 [Gibberella zeae PH-1]
                  gi|402072429  hypothetical protein GGTG_14192 [Gaeumannomyces graminis var. tritici R3-111a-1]
                  gi|115386480  predicted protein [Aspergillus terreus NIH2624]
                  gi|403157993  hypothetical protein PGTG_00295 [Puccinia graminis f. sp. tritici CRL 75-36-700-3]
                  gi|367021024  hypothetical protein MYCTH_2297229 [Myceliophthora thermophila ATCC 42464]
                  gi|378727107  hypothetical protein HMPREF1120_01755 [Exophiala dermatitidis NIH/UT8656]
                  gi|154270111  hypothetical protein HCAG_09099 [Ajellomyces capsulatus NAm1]
                  gi|115399342  predicted protein [Aspergillus terreus NIH2624]
```

Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate peptides with significant homology.
Individual ions scores > 55 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.05 | Max. number of hits 20

Standard scoring ◉ MudPIT scoring ○ | Ions score or expect cut-off 0 | Show sub-sets 0

Show pop-ups ◉ Suppress pop-ups ○ | Sort unassigned Decreasing Score | Require bold red ☐

Preferred taxonomy All entries

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query-
-Accession- -Sequence-

Hit:	1	2	3	4	5
☑ 2235.0113 (1+)	●	●	●	●	●

Select All | Select None | Search Selected | ☐ Error tolerant

1. gi|46108688 Mass: 31135 Score: 65 Matches: 1(1) Sequences: 1(1)
hypothetical protein FG01226.1 [Gibberella zeae PH-1]
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2235.0113	2234.0041	2234.0564	-0.0523	0	65	0.0065	1	U	R.QVEQDLPVENDDSHIANVGR.L

Proteins matching the same set of peptides:
gi|302925610 Mass: 30218 Score: 65 Matches: 1(1) Sequences: 1(1)
predicted protein [Nectria haematococca mpVI 77-13-4]
gi|340517396 Mass: 31265 Score: 65 Matches: 1(1) Sequences: 1(1)
predicted protein [Trichoderma reesei QM6a]
gi|358388781 Mass: 30441 Score: 65 Matches: 1(1) Sequences: 1(1)
hypothetical protein TRIVIDRAFT_166999 [Trichoderma virens Gv29-8]
gi|358395844 Mass: 31312 Score: 65 Matches: 1(1) Sequences: 1(1)
hypothetical protein TRIATDRAFT_299923 [Trichoderma atroviride IMI 206040]

2. gi|255956451 Mass: 85988 Score: 26 Matches: 1(0) Sequences: 1(0)
Pc21g19870 [Penicillium chrysogenum Wisconsin 54-1255]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2235.0113	2234.0041	2233.8517	0.1523	1	26	51	3	U	K.SKQPPSSTVDDHSIMPPR.T + Oxidation (M); 3 Phospho (S

3. gi|296809996 Mass: 176942 Score: 23 Matches: 1(0) Sequences: 1(0)
P-type ATPase [Arthroderma otae CBS 113480]

Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2235.0113	2234.0041	2233.8752	0.1288	1	27	45	2	U	R.HSYVFSDKTGTLTDNSMR.F + Oxidation (M); Phospho (ST

4. gi|315043941 Mass: 57394 Score: 19 Matches: 1(0) Sequences: 1(0)
hypothetical protein MGYG_05893 [Arthroderma gypseum CBS 118893]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2235.0113	2234.0041	2234.0804	-0.0764	2	19	2.4e+02	8	U	K.RSVNSIHSRGAVEAVSPSSSK.K + Phospho (ST)

5. gi|429863679 Mass: 67420 Score: 19 Matches: 1(0) Sequences: 1(0)
arginine deiminase type-3 [Colletotrichum gloeosporioides Nara gc5]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2235.0113	2234.0041	2233.9422	0.0618	1	19	2.5e+02	10	U	K.VHLDLSPAGTDELLSKSGR.S + 3 Phospho (ST)

Search Parameters

Type of search : MS/MS Ion Search
Enzyme : Trypsin
Fixed modifications : Carbamidomethyl (C)
Variable modifications : Gln->pyro-Glu (N-term Q),Oxidation (M),Phospho (ST),Phospho (Y)
Mass values : Monoisotopic
Protein Mass : Unrestricted
Peptide Mass Tolerance : ± 0.8 Da
Fragment Mass Tolerance: ± 0.5 Da
Max Missed Cleavages : 2
Instrument type : MALDI-TOF-TOF
Number of queries : 1

MATRIX SCIENCE MASCOT Search Results

Protein View: gi|358395844

hypothetical protein TRIATDRAFT_299923 [Trichoderma atroviride IMI 206040]

Database:	NCBInr
Score:	65
Nominal mass (M_r):	31312
Calculated pI:	4.75
Taxonomy:	Trichoderma atroviride IMI 206040

Sequence similarity is available as an NCBI BLAST search of gi|358395844 against nr.

Search parameters

MS data file:	DATA.TXT
Enzyme:	Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications:	Carbamidomethyl (C)
Variable modifications:	Gln->pyro-Glu (N-term Q), Oxidation (M), Phospho (ST), Phospho (Y)

Protein sequence coverage: 7%

Matched peptides shown in ***bold red***.

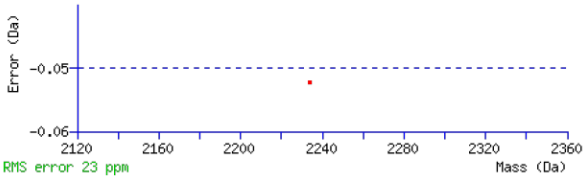
```
  1 MAADPFDSAL DLLRRLNPKH TSEHLSAIIS LAPDLTEDLL SSVDQPLTVK
 51 RCRQTGRDYL LCDYNRDGDS YRSPWSNQFD PPLDEGGVGG VGPGSNDGAG
101 EGAIPNERVR KMEIKANEAF DIYRELYYEG GVSSVYLWNL DDGFAGVVLV
151 KKSATPGSNT EGVWDSIHVF EAIERGRTTH YKLTSTVILS LSTNVESTVG
201 DMDLSGNMTR QVEQDLPVEN DDSHIANVGR LVEDMELKMR NLLQDVYFGK
251 AKDVVGDLRS VGSLSDGAKE RETQRELIGS MKR
```

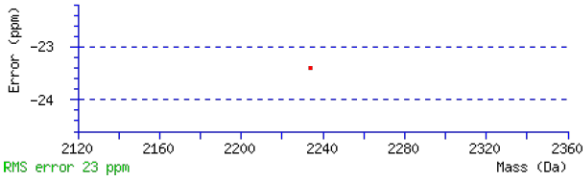
Unformatted sequence string: 283 residues (for pasting into other applications).

Sort peptides by ⊙ Residue Number ○ Increasing Mass ○ Decreasing Mass

Show predicted peptides also

Query	Start – End	Observed	Mr(expt)	Mr(calc)	Delta	M	Score	Expect	Rank	U	Peptide
1	211 – 230	2235.0113	2234.0041	2234.0564	-0.0523	0	65	0.0065	1	U	R.QVEQDLPVENDDSHIANVGR.L






```
LOCUS       EHK45231                 283 aa            linear   PLN 29-NOV-2011
DEFINITION  hypothetical protein TRIATDRAFT_299923 [Trichoderma atroviride IMI
            206040].
ACCESSION   EHK45231
VERSION     EHK45231.1  GI:358395844
DBSOURCE    accession ABDG02000024.1
KEYWORDS    .
SOURCE      Trichoderma atroviride IMI 206040
  ORGANISM  Trichoderma atroviride IMI 206040
            Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
            Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae;
            Hypocrea; mitosporic Hypocrea; Trichoderma.
COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..283
                     /organism="Trichoderma atroviride IMI 206040"
                     /strain="IMI 206040"
                     /db_xref="taxon:452589"
     Protein         1..283
                     /product="hypothetical protein"
     Region          5..255
                     /region_name="F_actin_cap_B"
                     /note="F-actin capping protein, beta subunit; pfam01115"
                     /db_xref="CDD:144634"
     CDS             1..283
                     /locus_tag="TRIATDRAFT_299923"
                     /coded_by="complement(join(ABDG02000024.1:1850565..1850959
                     ,ABDG02000024.1:1851036..1851463,
                     ABDG02000024.1:1851610..1851638))"
                     /note="GO_component: GO:8290 - F-actin capping protein
                     complex;
                     GO_function: GO:3779 - actin binding;
                     GO_process: GO:30036 - actin cytoskeleton organization and
                     biogenesis"
                     /db_xref="InterPro:IPR001698"
                     /db_xref="JGIDB:Triat2_299923"
```

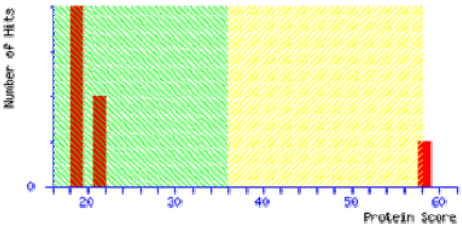
P23 hB-ind1 like protein:

MATRIX SCIENCE Mascot Search Results

```
User            : Sandra Stranzinger
Email           : b.bruckner@live.at
Search title    :
MS data file    : DATA.TXT
Database        : NCBInr 20130503 (25052984 sequences; 8638475353 residues)
Taxonomy        : Fungi (1852781 sequences)
Timestamp       : 7 May 2013 at 10:14:54 GMT
Protein hits    : gi|358388995 hypothetical protein TRIVIDRAFT_120772, partial [Trichoderma virens Gv29-8]
                  gi|331251085 hypothetical protein PGTG_19709 [Puccinia graminis f. sp. tritici CRL 75-36-700-3]
                  gi|366992932 hypothetical protein NCAS_0D02890 [Naumovozyma castellii CBS 4309]
                  gi|471906443 TRIAD3 [Rhizoctonia solani AG-1 IB]
                  gi|322701867 DNA repair protein Rad18, putative [Metarhizium acridum CQMa 102]
                  gi|367020172 hypothetical protein MYCTH_2136960 [Myceliophthora thermophila ATCC 42464]
                  gi|299746030 hypothetical protein CC1G_08698 [Coprinopsis cinerea okayama7#130]
```

Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 36 indicate peptides with significant homology.
Individual ions scores > 58 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.05 | Max. number of hits 20

Standard scoring ◉ MudPIT scoring ○ | Ions score or expect cut-off 0 | Show sub-sets 0

Show pop-ups ◉ Suppress pop-ups ○ | Sort unassigned Decreasing Score | Require bold red ☐

Preferred taxonomy All entries

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query- | -Accession- | -Sequence-

Hit:	1	2	3	4	5	6	7
☑ 2602.6472 (1+)	●	●	●	●	●	●	●

Select All | Select None | Search Selected | ☐ Error tolerant

```
1.   gi|358388995    Mass: 20511    Score: 58    Matches: 1(1)  Sequences: 1(1)
     hypothetical protein TRIVIDRAFT_120772, partial [Trichoderma virens Gv29-8]
   ☐ Check to include this hit in error tolerant search

     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score Expect Rank Unique  Peptide
       1    2602.6472  2601.6399  2602.0289  -0.3890   1    58   0.058   1     U    K.TDFDKWVDEDEQNEAADDDMSK.F

     Proteins matching the same set of peptides:
     gi|358396009    Mass: 23459    Score: 58    Matches: 1(1)  Sequences: 1(1)
     hypothetical protein TRIATDRAFT_169917, partial [Trichoderma atroviride IMI 206040]

2.   gi|331251085    Mass: 50559    Score: 21    Matches: 1(0)  Sequences: 1(0)
     hypothetical protein PGTG_19709 [Puccinia graminis f. sp. tritici CRL 75-36-700-3]
   ☐ Check to include this hit in error tolerant search

     Query   Observed   Mr(expt)   Mr(calc)    Delta Miss Score  Expect Rank Unique  Peptide
       1    2602.6472  2601.6399  2602.0325  -0.3926   1    21  3.1e+02   2     U    K.VPKTEASPGCSQHGDAPSLATPR.G + 3 Phospho (ST)
```

3. gi|366992932 Mass: 55574 Score: 21 Matches: 1(0) Sequences: 1(0)
hypothetical protein NCAS_0D02890 [Naumovozyma castellii CBS 4309]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2602.6472	2601.6399	2601.1248	0.5151	0	21	3.2e+02	3	U	M.AGAPVIPVVSDEDSESESQIVTGR.E + 2 Phospho (ST)

4. gi|471906443 Mass: 58970 Score: 20 Matches: 1(0) Sequences: 1(0)
TRIAD3 [Rhizoctonia solani AG-1 IB]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2602.6472	2601.6399	2602.0842	-0.4443	1	20	3.9e+02	10	U	R.QAMHKTVDFTQTVRPFVEGR.D + Oxidation (M); 3 Phospl

5. gi|322701867 Mass: 132952 Score: 19 Matches: 1(0) Sequences: 1(0)
DNA repair protein Rad18, putative [Metarhizium acridum CQMa 102]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2602.6472	2601.6399	2601.1621	0.4778	2	21	3.2e+02	5	U	K.YQSVLKQTQDVDETIMLMKR.A + Oxidation (M); Phospho

6. gi|367020172 Mass: 42774 Score: 19 Matches: 1(0) Sequences: 1(0)
hypothetical protein MYCTH_2136960 [Myceliophthora thermophila ATCC 42464]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2602.6472	2601.6399	2602.0577	-0.4178	2	21	3.3e+02	7	U	-.MPRNFLPTPASSTDIKGQDGSK.M + Oxidation (M); 3 Phos

7. gi|299746030 Mass: 60760 Score: 19 Matches: 1(0) Sequences: 1(0)
hypothetical protein CC1G_08698 [Coprinopsis cinerea okayama7#130]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2602.6472	2601.6399	2602.0780	-0.4381	1	20	3.6e+02	9	U	-.MAASPHVVVSSSFSSSTATMRMR.T + Oxidation (M); 2 Ph

Search Parameters

```
Type of search          : MS/MS Ion Search
Enzyme                  : Trypsin
Fixed modifications     : Carbamidomethyl (C)
Variable modifications  : Gln->pyro-Glu (N-term Q),Oxidation (M),Phospho (ST),Phospho (Y)
Mass values             : Monoisotopic
Protein Mass            : Unrestricted
Peptide Mass Tolerance  : ± 0.8 Da
Fragment Mass Tolerance: ± 0.5 Da
Max Missed Cleavages    : 2
Instrument type         : MALDI-TOF-TOF
Number of queries       : 1
```

MATRIX SCIENCE MASCOT Search Results

Protein View: gi|358396009

hypothetical protein TRIATDRAFT_169917, partial [Trichoderma atroviride IMI 206040]

Database:	NCBInr
Score:	58
Nominal mass (M_r):	23459
Calculated pI:	4.44
Taxonomy:	Trichoderma atroviride IMI 206040

Sequence similarity is available as an NCBI BLAST search of gi|358396009 against nr.

Search parameters

MS data file:	DATA.TXT
Enzyme:	Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications:	Carbamidomethyl (C)
Variable modifications:	Gln->pyro-Glu (N-term Q), Oxidation (M), Phospho (ST), Phospho (Y)

Protein sequence coverage: 10%

Matched peptides shown in ***bold red***.

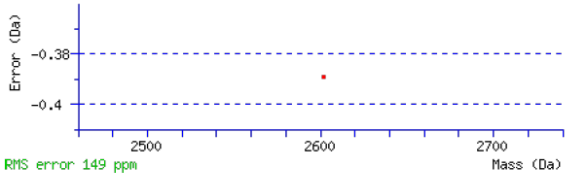
```
  1 VLWAQRSSVA DATKNFVYLT ISVPDVAKDD LKLDVQPTKV TFTGKSATLK
 51 NTYHVELELF AEIDPAESKI NHTAKNVEMK LQKKELKEEY WPRLLKENKK
101 LHFLKTDFDK WVDEDEQNEA ADDDMSKFGD MGKDQSHETN NLLSLLGGDF
151 GGIDFSKLGG GAGGMPDMSA MGLEGMPDLS SSGVPDSDSD DDDEDIPDLE
201 GEEKKEGEAA PKA
```

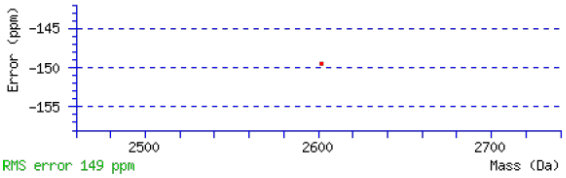
Unformatted sequence string: 213 residues (for pasting into other applications).

Sort peptides by ◉ Residue Number ○ Increasing Mass ○ Decreasing Mass

Show predicted peptides also

Query	Start – End	Observed	Mr(expt)	Mr(calc)	Delta	M	Score	Expect	Rank	U	Peptide
1	106 – 127	2602.6472	2601.6399	2602.0289	-0.3890	1	58	0.058	1	U	K.TDFDKWVDEDEQNEAADDDMSK.F






```
LOCUS       EHK45396                 213 aa            linear   PLN 29-NOV-2011
DEFINITION  hypothetical protein TRIATDRAFT_169917, partial [Trichoderma
            atroviride IMI 206040].
ACCESSION   EHK45396
VERSION     EHK45396.1  GI:358396009
DBSOURCE    accession ABDG02000024.1
KEYWORDS    .
SOURCE      Trichoderma atroviride IMI 206040
  ORGANISM  Trichoderma atroviride IMI 206040
            Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
            Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae;
            Hypocrea; mitosporic Hypocrea; Trichoderma.
COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..213
                     /organism="Trichoderma atroviride IMI 206040"
                     /strain="IMI 206040"
                     /db_xref="taxon:452589"
     Protein         <1..>213
                     /product="hypothetical protein"
     Region          1..112
                     /region_name="p23_hB-ind1_like"
                     /note="p23_like domain found in human (h) butyrate-induced
                     transcript 1 (B-ind1) and similar proteins. hB-ind1
                     participates in signaling by the small GTPase Rac1. It
                     binds to Rac1 and enhances different Rac1 effects
                     including activation of nuclear factor (NF)...; cd06465"
                     /db_xref="CDD:107222"
     Site            order(5,24..25,71,76,92,103,105..106,108..109,111)
                     /site_type="other"
                     /note="Hsp90 binding site"
                     /db_xref="CDD:107222"
     CDS             1..213
                     /locus_tag="TRIATDRAFT_169917"
                     /coded_by="complement(join(ABDG02000024.1:<2422876..242311
                     6,ABDG02000024.1:2423255..>2423652))"
                     /db_xref="InterPro:IPR017447"
                     /db_xref="JGIDB:Triat2_169917"
```

6.2.6.2 In *Trichoderma atroviride*$_{tmk1}$ (reduced mycoparasitism)

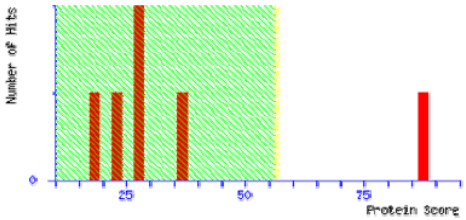
Glutamate ammonia ligase:

Mascot Search Results

```
User            : Bianca Bruckner
Email           : b.bruckner@live.at
Search title    :
MS data file    : DATA.TXT
Database        : NCBInr 20121118 (21581546 sequences; 7400919093 residues)
Taxonomy        : Fungi (1569831 sequences)
Timestamp       : 22 Nov 2012 at 11:00:07 GMT
Protein hits    : gi|358397635 glutamate-ammonia ligase [Trichoderma atroviride IMI 206040]
                  gi|342881716 hypothetical protein FOXB_06914 [Fusarium oxysporum Fo5176]
                  gi|367018656 hypothetical protein MYCTH_2087375 [Myceliophthora thermophila ATCC 42464]
                  gi|389644446 hypothetical protein MGG_03997 [Magnaporthe oryzae 70-15]
                  gi|400597511 PX domain-containing protein [Beauveria bassiana ARSEF 2860]
                  gi|385302790 urea amidolyase [Dekkera bruxellensis AWRI1499]
```

Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 56 indicate peptides with significant homology.
Individual ions scores > 57 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.05 | Max. number of hits 20

Standard scoring ◉ MudPIT scoring ○ | Ions score or expect cut-off 0 | Show sub-sets 0

Show pop-ups ◉ Suppress pop-ups ○ | Sort unassigned Decreasing Score | Require bold red ☐

Preferred taxonomy All entries

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query- | -Accession- | -Sequence-

Hit:	1	2	3	4	5	6
☑ 2439.8210 (1+)	●	●	●	●	●	●

Select All | Select None | Search Selected | ☐ Error tolerant

1. gi|358397635 **Mass:** 40508 **Score:** 87 **Matches:** 1(1) **Sequences:** 1(1)
glutamate-ammonia ligase [Trichoderma atroviride IMI 206040]
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2439.8210	2438.8138	2439.1124	-0.2987	1	87	5e-05	1	U	K.ALEPHHTECIKEYGEDNELR.L

2. gi|342881716 **Mass:** 154158 **Score:** 37 **Matches:** 1(0) **Sequences:** 1(0)
hypothetical protein FOXB_06914 [Fusarium oxysporum Fo5176]
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2439.8210	2438.8138	2438.9467	-0.1329	1	39	3.4	2	U	R.TNSEATQAKIQEATMEYLR.V + Oxidation (M); 2 Phospho

3. gi|367018656 Mass: 88223 Score: 27 Matches: 1(0) Sequences: 1(0)
hypothetical protein MYCTH_2087375 [Myceliophthora thermophila ATCC 42464]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2439.8210	2438.8138	2439.1965	-0.3827	2	31	21	5	U	K.DENARVTTNFPISYADRMALR.G

4. gi|389644446 Mass: 77181 Score: 25 Matches: 1(0) Sequences: 1(0)
hypothetical protein MGG_03997 [Magnaporthe oryzae 70-15]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2439.8210	2438.8138	2439.1812	-0.3674	1	25	78	6	U	K.QGQVAPTLVITVASDPATDKLR.K + 2 Phospho (ST)

5. gi|400597511 Mass: 107848 Score: 23 Matches: 1(0) Sequences: 1(0)
PX domain-containing protein [Beauveria bassiana ARSEF 2860]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2439.8210	2438.8138	2438.1045	0.7093	1	23	1.3e+02	8	U	K.MVELMMVSGIGTTSGFEERIR.F + Oxidation (M); Phospho

6. gi|385302790 Score: 18 Matches: 1(0) Sequences: 1(0)
urea amidolyase [Dekkera bruxellensis AWRI1499]
Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2439.8210	2438.8138	2438.0361	0.7776	0	22	1.6e+02	10	U	R.QALNETVFFGVVTNIDYLR.S + 2 Phospho (ST); Phospho

Search Parameters

```
Type of search         : MS/MS Ion Search
Enzyme                 : Trypsin
Fixed modifications    : Carbamidomethyl (C)
Variable modifications : Gln->pyro-Glu (N-term Q),Oxidation (M),Phospho (ST),Phospho (Y)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 0.8 Da
Fragment Mass Tolerance: ± 0.8 Da
Max Missed Cleavages   : 2
Instrument type        : MALDI-TOF-TOF
Number of queries      : 1
```

MASCOT Search Results

Protein View: gi|358397635

glutamate-ammonia ligase [Trichoderma atroviride IMI 206040]

Database: NCBInr
Score: 87
Nominal mass (M_r): 40508
Calculated pI: 5.40
Taxonomy: Trichoderma atroviride IMI 206040

Sequence similarity is available as an NCBI BLAST search of gi|358397635 against nr.

Search parameters

MS data file: DATA.TXT
Enzyme: Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Gln->pyro-Glu (N-term Q), Oxidation (M), Phospho (ST), Phospho (Y)

Protein sequence coverage: 5%

Matched peptides shown in ***bold red***.

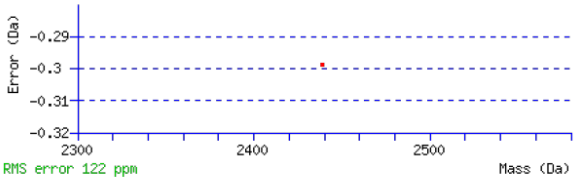
```
  1 MAVNQTSTSP SEIQKYLQLD QKNKIMAEYV WIDAGGETRS KSRTLDAKDV
 51 EYTPDNLPVW NFDGSSTGQA AGHDSDVYLR PCAVYPDPFR GSPNIIVLSE
101 CWNSDGTPNK YNFRHECAKV MEANAEREPW FGLEQEYTFL GQDDRPYGWP
151 VGGYPAPQGP YYCGVGAGKV VLRHVVDAHY KACLYAGINI SGTNAEVLPG
201 QWEFQVGPCV GISMGDELWI SRFFLARIAE EFGIKVTLHP KPIQGPWNGS
251 GLHSNFSTKD MRAEGGMKYI EEAIKALEPH HTECIKEYGE DNELRLTGEY
301 ETGSIEKFSW GVANRGTSIR VPRETAARGC GYFEDRRPAS NADPYRITKV
351 LMTSIFGKI
```

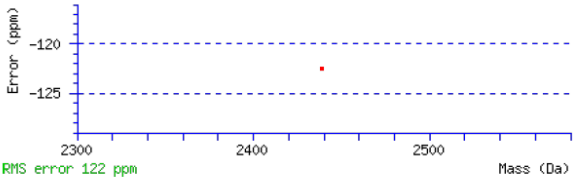
Unformatted sequence string: 359 residues (for pasting into other applications).

Sort peptides by ⦿ Residue Number ○ Increasing Mass ○ Decreasing Mass

Show predicted peptides also

Query	Start – End	Observed	Mr(expt)	Mr(calc)	Delta	M	Score	Expect	Rank	U	Peptide
1	276 – 295	2439.8210	2438.8138	2439.1124	-0.2987	1	87	5e-05	1	U	K.ALEPHHTECIKEYGEDNELR.L






```
LOCUS       EHK47003                 359 aa            linear   PLN 29-NOV-2011
DEFINITION  glutamate-ammonia ligase [Trichoderma atroviride IMI 206040].
ACCESSION   EHK47003
VERSION     EHK47003.1  GI:358397635
DBSOURCE    accession ABDG02000021.1
KEYWORDS    .
SOURCE      Trichoderma atroviride IMI 206040
  ORGANISM  Trichoderma atroviride IMI 206040
            Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;
            Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae;
            Hypocrea; mitosporic Hypocrea; Trichoderma.
COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..359
                     /organism="Trichoderma atroviride IMI 206040"
                     /strain="IMI 206040"
                     /db_xref="taxon:452589"
     Protein         1..359
                     /product="glutamate-ammonia ligase"
     Region          20..355
                     /region_name="PLN02284"
                     /note="glutamine synthetase"
                     /db_xref="CDD:177922"
     Region          23..103
                     /region_name="Gln-synt_N"
                     /note="Glutamine synthetase, beta-Grasp domain; pfam03951"
                     /db_xref="CDD:202826"
     Region          111..352
                     /region_name="Gln-synt_C"
                     /note="Glutamine synthetase, catalytic domain; pfam00120"
                     /db_xref="CDD:201016"
     CDS             1..359
                     /gene="glnA"
                     /locus_tag="TRIATDRAFT_298830"
                     /coded_by="complement(join(ABDG02000021.1:629456..629982,
                     ABDG02000021.1:630042..630124,
                     ABDG02000021.1:630199..630539,
                     ABDG02000021.1:631123..631212,
                     ABDG02000021.1:631296..631331,
                     ABDG02000021.1:631401..631403))"
                     /note="Glutamate-ammonia lyase or syn. glutamine
                     synthetase(GS) plays an essential role in the metabolism
                     of nitrogen by catalyzing the condensation of glutamate
                     and ammonia to form glutamine;
                     GO_function: GO:4356 - glutamate-ammonia ligase activity;
                     GO_process: GO:6807; glutamine biosynthetic process  -
                     nitrogen compound metabolic process  [PMID 6542]"
                     /db_xref="InterPro:IPR008146"
                     /db_xref="InterPro:IPR008147"
                     /db_xref="JGIDB:Triat2_298830"
```

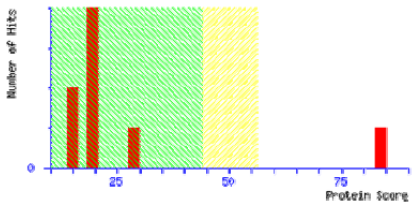
Molecular chaperon bip1:

Mascot Search Results

```
User            : Bianca Bruckner
Email           : b.bruckner@live.at
Search title    :
MS data file    : DATA.TXT
Database        : NCBInr 20121118 (21581546 sequences; 7400919093 residues)
Taxonomy        : Fungi (1569831 sequences)
Timestamp       : 21 Nov 2012 at 18:05:23 GMT
Protein hits    : gi|358387310 molecular chaperone bip1 [Trichoderma virens Gv29-8]
                  gi|154276968 suppressor of stem-loop protein 1 [Ajellomyces capsulatus NAm1]
                  gi|328354767 Peptide methionine sulfoxide reductase msrA/msrB Includes: RecName: Full=Thioredoxin; Includes: RecName:
                  gi|240275963 conserved hypothetical protein [Ajellomyces capsulatus H143]
                  gi|116193991 hypothetical protein CHGG_06713 [Chaetomium globosum CBS 148.51]
                  gi|115442968 hypothetical protein ATEG_09669 [Aspergillus terreus NIH2624]
                  gi|346327345 hypothetical protein CCM_01600 [Cordyceps militaris CM01]
                  gi|46137241  hypothetical protein FG10136.1 [Gibberella zeae PH-1]
```

Mascot Score Histogram

Ions score is -10*Log(P), where P is the probability that the observed match is a random event.
Individual ions scores > 44 indicate peptides with significant homology.
Individual ions scores > 56 indicate identity or extensive homology (p<0.05).
Protein scores are derived from ions scores as a non-probabilistic basis for ranking protein hits.



Peptide Summary Report

Format As | Peptide Summary | Help

Significance threshold p< 0.05 | Max. number of hits 20

Standard scoring ◉ MudPIT scoring ○ | Ions score or expect cut-off 0 | Show sub-sets 0

Show pop-ups ◉ Suppress pop-ups ○ | Sort unassigned Decreasing Score | Require bold red ☐

Preferred taxonomy All entries

Overview Table

Click on column header to jump to entry in results list.
Move mouse over any indicator to highlight identical peptides.
Click on an indicator to see details of individual match.
Use check boxes to select sub-set of queries for new search.

Mouse over: -Query- | -Accession- | -Sequence-

Hit:	1	2	3	4	5	6	7	8
☑ 2799.1189 (1+)	●	●	●	●	●	●	●	●

Select All | Select None | Search Selected | ☐ Error tolerant

1. gi|358387310 Mass: 72513 Score: 84 Matches: 1(1) Sequences: 1(1)
molecular chaperone bip1 [Trichoderma virens Gv29-8]
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2799.1189	2798.1117	2798.2042	-0.0926	1	86	5.6e-05	1	U	K.EATEWLEENGADATTEDFEEQKEK.L

Proteins matching the same set of peptides:
gi|340516513 Mass: 72660 Score: 82 Matches: 1(1) Sequences: 1(1)
predicted protein [Trichoderma reesei QM6a]
gi|358398848 Mass: 72450 Score: 82 Matches: 1(1) Sequences: 1(1)
molecular chaperone bip1 [Trichoderma atroviride IMI 206040]

2. gi|154276968 Mass: 55848 Score: 27 Matches: 1(0) Sequences: 1(0)
suppressor of stem-loop protein 1 [Ajellomyces capsulatus NAm1]
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2799.1189	2798.1117	2798.3375	-0.2259	1	27	45	2	U	R.TWETLVESADGTISATVEDLLGAGKR.K + Phospho (ST)

Proteins matching the same set of peptides:
gi|225554656 Mass: 51495 Score: 27 Matches: 1(0) Sequences: 1(0)
transcription factor TFIIH complex subunit Ssl1 [Ajellomyces capsulatus G186AR]

gi|240277005 **Mass:** 55906 **Score:** 27 **Matches:** 1(0) **Sequences:** 1(0)
transcription factor TFIIH complex subunit Ssl1 [Ajellomyces capsulatus H143]

3. gi|328354767 **Mass:** 13798 **Score:** 20 **Matches:** 1(0) **Sequences:** 1(0)
Peptide methionine sulfoxide reductase msrA/msrB Includes: RecName: Full=Thioredoxin; Includes: RecName: Full=Peptide methionine
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2799.1189	2798.1117	2797.4853	0.6263	0	20	2.2e+02	6	U	K.VFTLVAELIINMATVILSFSQPVGR.E + Phospho (ST)

4. gi|240275963 **Mass:** 44069 **Score:** 20 **Matches:** 1(0) **Sequences:** 1(0)
conserved hypothetical protein [Ajellomyces capsulatus H143]
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2799.1189	2798.1117	2797.3842	0.7275	2	20	2.3e+02	8	U	K.QKNSNSTTTSSPAPQPVDEENAIVKR.L

5. gi|116193991 **Mass:** 38303 **Score:** 20 **Matches:** 1(0) **Sequences:** 1(0)
hypothetical protein CHGG_06713 [Chaetomium globosum CBS 148.51]
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2799.1189	2798.1117	2797.4110	0.7007	2	20	2.4e+02	9	U	R.ASVQGTTSLLASALAESKKGSQEDVLK.S + Phospho (ST)

6. gi|115442968 **Mass:** 72942 **Score:** 18 **Matches:** 1(0) **Sequences:** 1(0)
hypothetical protein ATEG_09669 [Aspergillus terreus NIH2624]
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2799.1189	2798.1117	2798.1047	0.0069	0	20	2.3e+02	7	U	K.VTDSMIYASGEALSTALTAEEIDR.G + Oxidation (M); 2 Ph

7. gi|346327345 **Mass:** 16814 **Score:** 16 **Matches:** 1(0) **Sequences:** 1(0)
hypothetical protein CCM_01600 [Cordyceps militaris CM01]
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2799.1189	2798.1117	2798.3479	-0.2362	2	19	3.1e+02	10	U	-.MLYTAIAAVAFAATVAAAPSAETKKR.A + Oxidation (M); P

8. gi|46137241 **Score:** 15 **Matches:** 1(0) **Sequences:** 1(0)
hypothetical protein FG10136.1 [Gibberella zeae PH-1]
☐ Check to include this hit in error tolerant search

Query	Observed	Mr(expt)	Mr(calc)	Delta	Miss	Score	Expect	Rank	Unique	Peptide
1	2799.1189	2798.1117	2797.7404	0.3713	1	21	1.9e+02	5	U	R.RSSQTTTATSVSSTVNDSSSR.R + 8 Phospho (ST)

Proteins matching the same set of peptides:
gi|408398044 **Score:** 15 **Matches:** 1(0) **Sequences:** 1(0)
hypothetical protein FPSE_02630 [Fusarium pseudograminearum CS3096]

Search Parameters

```
Type of search          : MS/MS Ion Search
Enzyme                  : Trypsin
Fixed modifications     : Carbamidomethyl (C)
Variable modifications  : Gln->pyro-Glu (N-term Q),Oxidation (M),Phospho (ST),Phospho (Y)
Mass values             : Monoisotopic
Protein Mass            : Unrestricted
Peptide Mass Tolerance  : ± 0.8 Da
Fragment Mass Tolerance: ± 0.8 Da
Max Missed Cleavages    : 2
Instrument type         : MALDI-TOF-TOF
Number of queries       : 1
```

MASCOT Search Results

Protein View: gi|358398848

molecular chaperone bip1 [Trichoderma atroviride IMI 206040]

Database: NCBInr
Score: 82
Nominal mass (M_r): 72450
Calculated pI: 4.84
Taxonomy: Trichoderma atroviride IMI 206040

Sequence similarity is available as an NCBI BLAST search of gi|358398848 against nr.

Search parameters

MS data file:	DATA.TXT
Enzyme:	Trypsin: cuts C-term side of KR unless next residue is P.
Fixed modifications:	Carbamidomethyl (C)
Variable modifications:	Gln->pyro-Glu (N-term Q), Oxidation (M), Phospho (ST), Phospho (Y)

Protein sequence coverage: 3%

Matched peptides shown in ***bold red***.

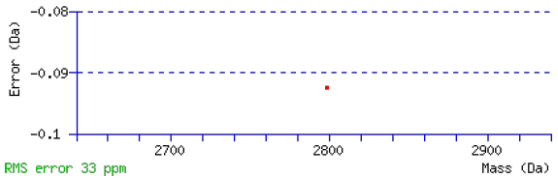
```
  1 MARSRSSLAL GLGLLCWITL LFAPLAFVGK VNASDDADNY GTVIGIDLGT
 51 TYSCVGVMQK GKVEILVNDQ GNRITPSYVA FTDEERLVGD SAKNQAAANP
101 TNTIFDIKRM IGRKFAEKDI QADMKHFPYK VIDKDGKPIV QVQVNGEKKQ
151 FTPEEISAMI LGKMKEVAES YLGKKVTHAV VTVPAYFNDN QRQATKDAGI
201 IAGLNVLRIV NEPTAAAIAY GLDKTDGERQ IIVYDLGGGT FDVSLLSIDN
251 GVFEVLATAG DTHLGGEDFD QRVINYLAKA YNKKNSVDIS KDLKAMGKLK
301 REAEKAKRTL SSQMSTRIEI EAFFEGNDFS ETLTRAKFEE LNMDLFKKTL
351 KPVEQVLKDA NVKKSEVDDI VLVGGSTRIP KVQSLIEEYF GGKKASKGIN
401 PDEAVAFGAA VQAGVLSGEE GTEEIVLMDV NPLTLGIETT GGVMTKLIPR
451 NTPIPTRKSQ IFSTAADNQP VVLIQVFEGE RSMTKDNNIL GKFELTGIPP
501 APRGVPQIEV SFELDANGIL KVSAHDKGTG KQESITITND KGRLTQEEID
551 RMVAEAEKFA EEDKATRERI EARNGLENYA FSLKNQVNDD EGLGGKIDEE
601 DKETILDAVK EATEWLEENG ADATTEDFEE QKEKLSNVAY PITSKMYQGA
651 GGEDDGDFHD EL
```

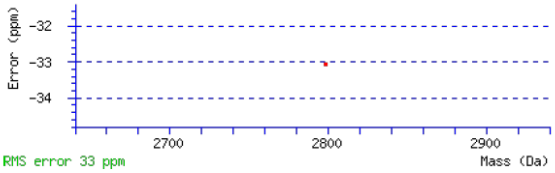
Unformatted sequence string: 662 residues (for pasting into other applications).

Sort peptides by: Residue Number, Increasing Mass, Decreasing Mass

Show predicted peptides also

Query	Start – End	Observed	Mr(expt)	Mr(calc)	Delta	M	Score	Expect	Rank	U	Peptide
1	611 – 634	2799.1189	2798.1117	2798.2042	-0.0926	1	86	5.6e-05	1	U	K.EATEWLEENGADATTEDFEEQKEK.L






```
LOCUS       EHK48199                 662 aa            linear   PLN 29-NOV-2011
DEFINITION  molecular chaperone bip1 [Trichoderma atroviride IMI 206040].
ACCESSION   EHK48199
VERSION     EHK48199.1  GI:358398848
DBSOURCE    accession ABDG02000019.1
KEYWORDS    .
SOURCE      Trichoderma atroviride IMI 206040
  ORGANISM  Trichoderma atroviride IMI 206040
            Eukaryota; Fungi; Dikarya; Ascomycota; Pezizomycotina;

             Sordariomycetes; Hypocreomycetidae; Hypocreales; Hypocreaceae;
             Hypocrea; mitosporic Hypocrea; Trichoderma.
COMMENT     Method: conceptual translation.
FEATURES             Location/Qualifiers
     source          1..662
                     /organism="Trichoderma atroviride IMI 206040"
                     /strain="IMI 206040"
                     /db_xref="taxon:452589"
     Protein         1..662
                     /product="molecular chaperone bip1"
     Region          41..403
                     /region_name="HSPA5-like_NBD"
                     /note="Nucleotide-binding domain of human HSPA5 and
                     similar proteins; cd10241"
                     /db_xref="CDD:212681"
     Region          43..648
                     /region_name="HSP70"
                     /note="Hsp70 protein; pfam00012"
                     /db_xref="CDD:200927"
     Site            order(47,49..52,108,184,212,235..240,242,266..267,304,
                     307..308,374..376,378..379,402)
                     /site_type="other"
                     /note="nucleotide binding site [chemical binding]"
                     /db_xref="CDD:212681"
     Site            order(70,86,90,93..94,170..171,294,297..298,301,305,319,
                     321..322)
                     /site_type="other"
                     /note="putative NEF/HSP70 interaction site [polypeptide
                     binding]"
                     /db_xref="CDD:212681"
```

```
Site            order(189..190,192..193,208..209,211,253..256)
                /site_type="other"
                /note="SBD interface [polypeptide binding]"
                /db_xref="CDD:212681"
CDS             1..662
                /gene="bip1"
                /locus_tag="TRIATDRAFT_298376"
                /coded_by="join(ABDG02000019.1:1061293..1061430,
                ABDG02000019.1:1061489..1061673,
                ABDG02000019.1:1061739..1061979,
                ABDG02000019.1:1062046..1063293,
                ABDG02000019.1:1063356..1063532)"
                /note="highsimilarity to bip1 of H. jecorina and bipA of
                Aspergillus niger; ATPase involved in protein import into
                the ER, also acts as a chaperone to mediate protein
                folding in the ER and may play a role in ER export of
                soluble proteins; regulates the unfolded protein response
                via interaction with Ire1 in Saccharomyces cerevisiae."
                /db_xref="InterPro:IPR013126"
                /db_xref="JGIDB:Triat2_298376"
```