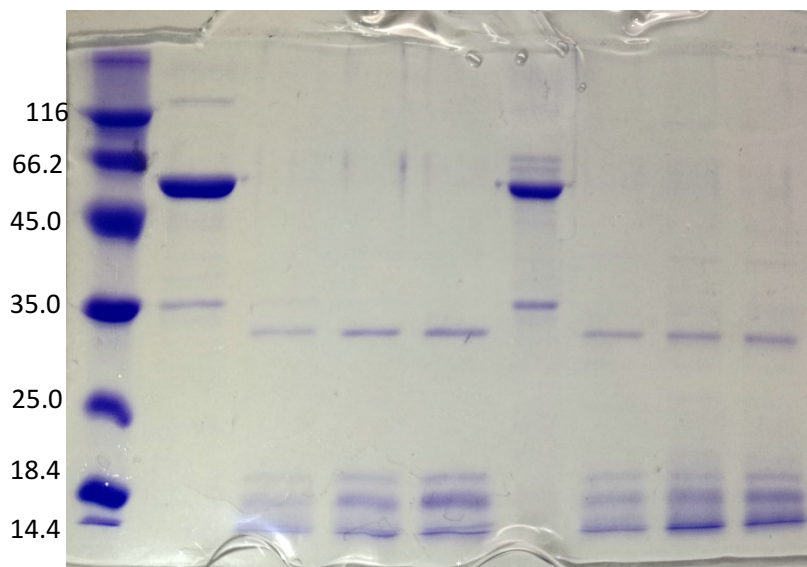
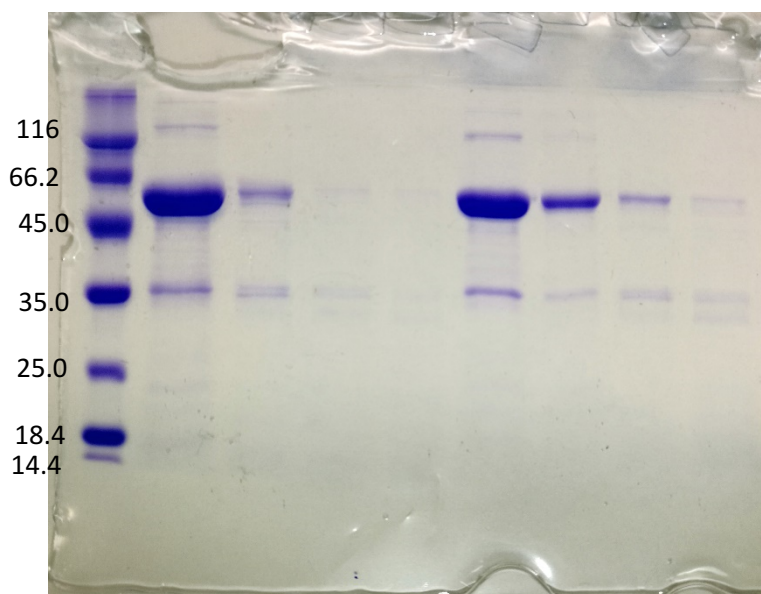


TRYPSIN DIGESTION REPORT- Nov. 2018

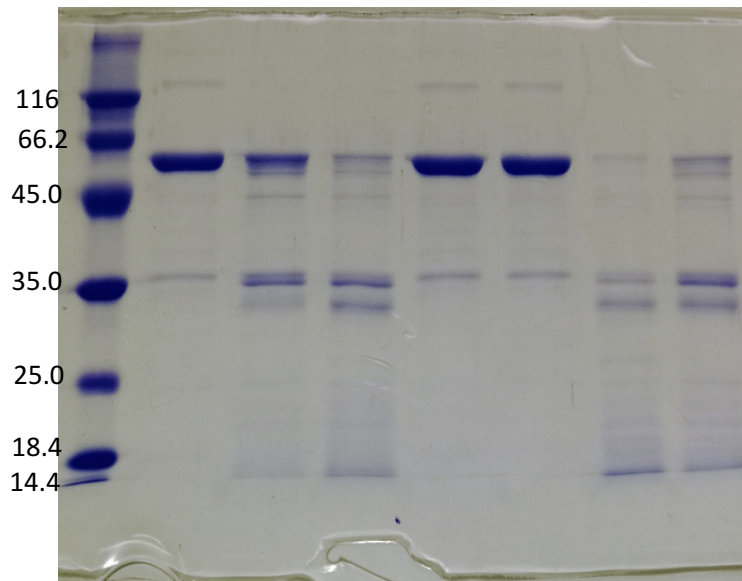
The students are separated into a total of 8 groups. Trypsin digestions were performed at 37 degree, and samples were taken at three different timepoint: 5min, 10min and 30min. Time 0 min was used as the control.



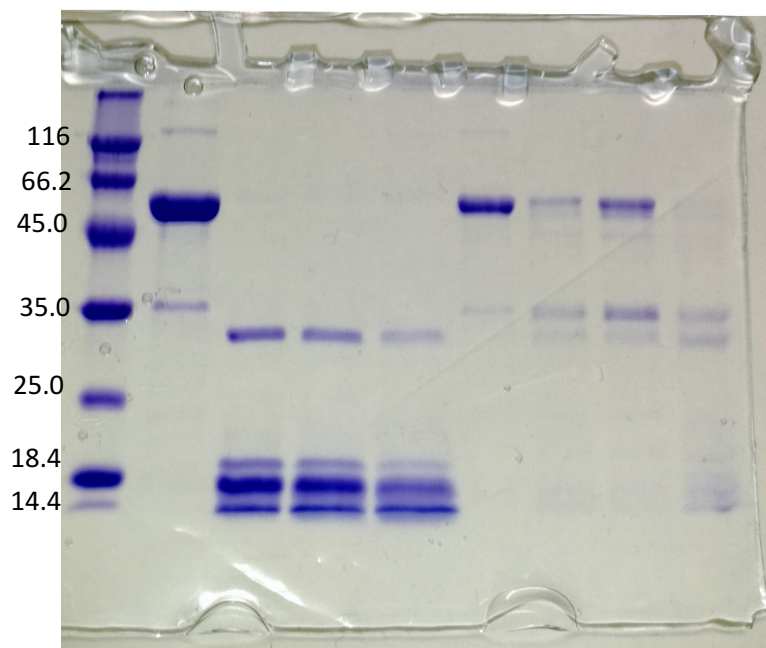
From left to right: Marker, 0 min (group 1), 5 min (group 1), 10min (group 1), 30min (group 1), 0min (group 2), 5 min (group 2), 10min (group 2), 30min (group 2)



From left to right: Marker, 0 min (group 3), 5 min (group 3), 10min (group 3), 30min (group 3), 0min (group 4), 5 min (group 4), 10min (group 4), 30min (group 4)



From left to right: Marker, 0 min (group 5), 5 min (group 5), 10min (group 5), 30min (group 5), 0min (group 6), 5 min (group 6), 10min (group 6), 30min (group 6)



From left to right: Marker, 0 min (group 7), 5 min (group 7), 10min (group 7), 30min (group 7), 0min (group 8), 5 min (group 8), 10min (group 8), 30min (group 8)

The smallest protein band observed for digestion carried out by most groups, is around 13-14 kDa. According to trypsin recognition sites (amino acids) this single band could be further digested into 4 smaller polypeptides with the following molecular masses (Da):

- 2568
- 2693
- 3931
- 4486

If you insert these peptide masses as a query in Mascot (Figure below):

- http://www.matrixscience.com/search_form_select.html

- peptide mass finger

(http://www.matrixscience.com/cgi/search_form.pl?FORMVER=2&SEARCH=PMF)

Home Mascot database search **Products** Technical support Training News Blog Newsletter Contact

Access Mascot Server | Database search help

Mascot database search > Access Mascot Server > Peptide Mass Fingerprint

MASCOT Peptide Mass Fingerprint

Your name Sheila **Email** sheila.sadeghi@unito.it

Search title _____

Database(s) Environmental_EST
Fungi_EST
Human_EST
Invertebrates_EST
Mammals_EST

Enzyme Trypsin

Allow up to 1 missed cleavages

Taxonomy Homo sapiens (human)

Fixed modifications --- none selected ---
Display all modifications

Variable modifications --- none selected ---

Protein mass _____ kDa

Peptide tol. ± 1.2 Da

Mass values MH⁺ M_r M-H⁻

Monoisotopic **Average**

Data file

Query
2568.000000
2693.000000
3931.000000
4486.000000

Decoy

Report top AUTO hits

Start Search ... Reset Form

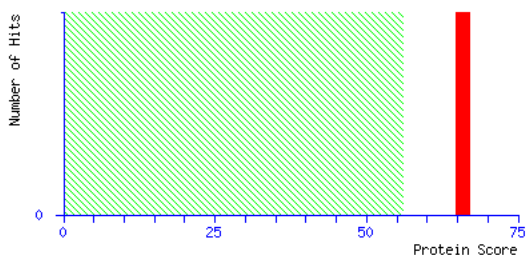
The output file generated (Figure below) identifies the protein as human FMO3 with a score of 66.

MATRIX SCIENCE Mascot Search Results

User : Sheila
 Email : sheila.sadeghi@unito.it
 Search title :
 Database : SwissProt 2018_09 (558590 sequences; 200544181 residues)
 Taxonomy : Homo sapiens (human) (20411 sequences)
 Timestamp : 6 Nov 2018 at 11:11:38 GMT
 Top Score : 66 for **FMO3_HUMAN**, Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens OX=9606 GN=FMO3 PE=1 SV=5

Mascot Score Histogram

Protein score is $-10 \cdot \log(P)$, where P is the probability that the observed match is a random event. Protein scores greater than 56 are significant ($p < 0.05$).



Concise Protein Summary Report

Format As [Help](#)
 Significance threshold p< Max. number of hits
 Preferred taxonomy

- [FMO3_HUMAN](#) Mass: 59994 Score: **66** Expect: 0.0052 Matches: 4
 Dimethylaniline monooxygenase [N-oxide-forming] 3 OS=Homo sapiens OX=9606 GN=FMO3 PE=1 SV=5

[HV10B_HUMAN](#) Mass: 12983 Score: 40 Expect: 2 Matches: 2
 Immunoglobulin heavy variable 1-8 OS=Homo sapiens OX=9606 GN=IGHV1-8 PE=3 SV=1

[MOTI_HUMAN](#) Mass: 12912 Score: 39 Expect: 2.5 Matches: 2
 Promotilin OS=Homo sapiens OX=9606 GN=MLN PE=1 SV=1

[DPRX_HUMAN](#) Mass: 21634 Score: 37 Expect: 4 Matches: 2
 Divergent paired-related homeobox OS=Homo sapiens OX=9606 GN=DPRX PE=3 SV=1