Supporting Information for Proteomics

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Proteomics identification of differentially expressed proteins in the muscle of dysferlin myopathy patients
TABLE 2.

Mascot search scores are shown for the top match and, in parenthesis, for the highest ranked hit to a non-homologous protein. "Matched peptides" column shows the number of peptides matching to the top-match protein and, in parenthesis, the number of unmatched peptides in the spectra. The percent of the total intensity of the spectrum corresponding to the matched peptides is shown in the last column.

<table>
<thead>
<tr>
<th>Spot N</th>
<th>Identification</th>
<th>Uni-Prot Access #</th>
<th>Mascot Score</th>
<th>Matched peptides</th>
<th>Sequence Coverage %</th>
<th>Intensity Coverage %</th>
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<tbody>
<tr>
<td>22669</td>
<td>Fructose-bisphosphate aldolase A (EC 4.1.2.13)</td>
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<td>119 (59)</td>
<td>15 (31)</td>
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<td>169 (65)</td>
<td>23 (46)</td>
<td>46.3</td>
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<td>22056</td>
<td>Hypothetical protein, similarity heat Shock Protein</td>
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<td>88 (45)</td>
<td>7 (13)</td>
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<td>114 (47)</td>
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<td>22522</td>
<td>Acyl-CoA dehydrogenase (EC 1.3.99.3)</td>
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<td>79 (59)</td>
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<td>MLE1_HUMAN</td>
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<td>12 (27)</td>
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<td>16 (32)</td>
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<td>Myosin alkali light chain, slow skeletal muscle</td>
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<td>Protein L-isoaspartate O-methyltransferase</td>
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<td>80 (58)</td>
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</table>
Table 1

**Spot 21920**
Match to: **JH0624** Score: 87 Expect: 0.00025
protein-L-isoaspartate(D-aspartate) O-methyltransferase (EC 2.1.1.77) splice form II - human

Nominal mass (M): **24835**; Calculated pI value: **6.05**
NCBI BLAST search of **JH0624** against nr
Unformatted sequence string for pasting into other applications
Taxonomy: **Homo sapiens**
Links to retrieve other entries containing this sequence from NCBI Entrez:
Q5VYC1 HUMAN from **Homo sapiens**
CAH72863 from **Homo sapiens**
AAH07501 from **Homo sapiens**
AAA90934 from **Homo sapiens**
BAA02991 from **Homo sapiens**
BAA05029 from **Homo sapiens**
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **24**
Number of mass values matched: **9**
Sequence Coverage: **43%**

**Spot 22000**
Match to: **MOHUSA** Score: 80 Expect: 0.0013
myosin alkali light chain, slow skeletal muscle - human

Nominal mass (M): **22864**; Calculated pI value: **5.56**
NCBI BLAST search of **MOHUSA** against nr
Unformatted sequence string for pasting into other applications
Taxonomy: **Homo sapiens**
Spot 22016
Match to: MYL3_HUMAN Score: 120 Expect: 1.3e-007
Myosin light polypeptide 3 (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1SB

Nominal mass (M): 21958; Calculated pI value: 5.03
NCBI BLAST search of MYL3_HUMAN against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 37
Number of mass values matched: 12
Sequence Coverage: 57%

Spot 22054
Match to: Q96A32_HUMAN Score: 91 Expect: 0.0001
Myosin regulatory light chain 2 (Myosin light chain 2).- Homo sapiens (Human).
Nominal mass (M,) : 19116; Calculated pl value: 4.91
NCBI BLAST search of Q96A32_HUMAN against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Links to retrieve other entries containing this sequence from NCBI Entrez:
AAK52797 from Homo sapiens
AAH12571 from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 27
Number of mass values matched: 8
Sequence Coverage: 52%

Spot 22056
Match to: Q96C20_HUMAN Score: 88 Expect: 0.00019
Hypothetical protein (Fragment).- Homo sapiens (Human).
Nominal mass (M.): \textbf{21186}; Calculated pI value: \textbf{5.55}
NCBI BLAST search of \textbf{Q96C20 \_HUMAN} against \textbf{nr}
Unformatted sequence string for pasting into other applications
Taxonomy: \textbf{Homo sapiens}
Links to retrieve other entries containing this sequence from NCBI Entrez:
\textbf{AAH14920} from \textbf{Homo sapiens}
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: \textbf{20}
Number of mass values matched: \textbf{7}
Sequence Coverage: \textbf{35\%}

\underline{Spot 22113-1}
Match to: \textbf{CYHUAB} Score: \textbf{94} Expect: \textbf{6.3e-05}
\textbf{alpha-crystallin chain B [validated]} - \textbf{human}
Nominal mass (M.): \textbf{20146}; Calculated pI value: \textbf{6.76}
NCBI BLAST search of \textbf{CYHUAB} against \textbf{nr}
Unformatted sequence string for pasting into other applications
Taxonomy: \textbf{Homo sapiens}
Links to retrieve other entries containing this sequence from NCBI Entrez:
\textbf{CAH91560} from \textbf{Pongo pygmaeus}
\textbf{CAE93952} from \textbf{Homo sapiens}
\textbf{AAH07008} from \textbf{Homo sapiens}
\textbf{AAP35416} from \textbf{Homo sapiens}
\textbf{AAA52104} from \textbf{Homo sapiens}
\textbf{AAB23453} from \textbf{Homo sapiens}
\textbf{AAX41998} from \textbf{synthetic construct}
CRYAB_HUMAN from Homo sapiens
CRYAB_PONPY from Pongo pygmaeus
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 31
Number of mass values matched: 8
Sequence Coverage: 42%

Spot 22166
Match to: A24904 Score: 129 Expect: 1.6e-008
actin alpha, skeletal muscle - mouse
Nominal mass (M_r): 42366; Calculated pI value: 5.23
NCBI BLAST search of A24904 against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Mus musculus
Links to retrieve other entries containing this sequence from NCBI Entrez:
ATCH from Gallus gallus
ATHU from Homo sapiens
ATRT from Rattus norvegicus
JC5301 from Sus scrofa domestica
Q5R9O5_PONPY from Pongo pygmaeus
Q5U2A5_XENLA from Xenopus laevis
CAH91505 from Pongo pygmaeus
AAC48692 from Sus scrofa
AAF02694 from Homo sapiens
CAI19050 from Homo sapiens
AAH12597 from Homo sapiens
CAG38754 from Homo sapiens
CAG46595 from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 48
Number of mass values matched: 16
Sequence Coverage: 45%

Spot 22271

Match to: A24904 Score: 102 Expect: 8.2e-006
actin alpha, skeletal muscle - mouse

Nominal mass (M_r): 42366; Calculated pI value: 5.23
NCBI BLAST search of A24904 against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Mus musculus

Links to retrieve other entries containing this sequence from NCBI Entrez:
ATCH from Gallus gallus
ATHU from Homo sapiens
ATRT from Rattus norvegicus
JC5301 from Sus scrofa domestica
Q5R9O5_PONPY from Pongo pygmaeus
Q5U2A5_XENLA from Xenopus laevis
CAH91505 from Pongo pygmaeus
AAC48692 from Sus scrofa
AAFO2694 from Homo sapiens
CAI19050 from Homo sapiens
AAH12597 from Homo sapiens
CAG38754 from Homo sapiens
CAG46595 from Homo sapiens
AAB59376 from Homo sapiens
AAA60296 from Homo sapiens
AAH14877 from Mus musculus
AAH61974 from Rattus norvegicus
AAA37141 from Mus musculus
AAA37164 from Mus musculus
CAA24529 from Rattus norvegicus
AAH86161 from Xenopus laevis
CAA24753 from Gallus gallus
ACTS_BOVIN from Bos taurus
ACTS_CHICK from Gallus gallus
ACTS_HUMAN from Homo sapiens
ACTS_MOUSE from Mus musculus
ACTS_PIG from Sus scrofa
ACTS_RABIT from Oryctolagus cuniculus
ACTS_RAT from Rattus norvegicus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 36
Number of mass values matched: 10
Sequence Coverage: 42%

Spot 22522
Match to: DEHUCM Score: 79 Expect: 0.0018
acyl-CoA dehydrogenase (EC 1.3.99.3) precursor, medium-chain-specific, mitochondrial [validated]
Nominal mass (M_r): 47015; Calculated pI value: 8.61
NCBI BLAST search of DEHUCM against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Links to retrieve other entries containing this sequence from NCBI Entrez:
CAI22390 from Homo sapiens
AAH05377 from Homo sapiens
AAA51566 from Homo sapiens
AAA59567 from Homo sapiens
ACADM_HUMAN from Homo sapiens

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 50
Number of mass values matched: 13
Sequence Coverage: 32%

Spot 22669
Match to: **ALDOA_HUMAN** Score: **119** Expect: **1.6e-007**
**Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Muscle-type aldolase) (Lung cancer antigen NY-LU-1)**

Nominal mass (M_r): **39720**; Calculated pI value: **8.39**
NCBI BLAST search of **ALDOA_HUMAN** against nr
Unformatted sequence string for pasting into other applications
Taxonomy: **Homo sapiens**
Links to retrieve other entries containing this sequence from NCBI Entrez:
2ALDA from **Homo sapiens**
4ALD from **Homo sapiens**
1ALD from **Homo sapiens**
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **46**
Number of mass values matched: **15**
Sequence Coverage: **46%**

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**Spot 22761**

Match to: **MLE1_HUMAN** Score: **113** Expect: **6.5e-007**
**Myosin light chain 1, skeletal muscle isoform (MLC1F) (A1 catalytic) (Alkali myosin light chain 1).**

Nominal mass (M_r): **21058**; Calculated pI value: **4.97**
NCBI BLAST search of **MLE1_HUMAN** against nr
Unformatted sequence string for pasting into other applications
Taxonomy: **Homo sapiens**

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 39
Number of mass values matched: 12
Sequence Coverage: 45%

Spot 22772
Match to: ATCHSM Score: 81 Expect: 0.0011
actin gamma, smooth muscle - chicken

Nominal mass (M₀): 42249; Calculated pI value: 5.31
NCBI BLAST search of ATCHSM against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Gallus gallus
Links to retrieve other entries containing this sequence from NCBI Entrez:
A40261 from Homo sapiens
A32788 from Mus musculus
A31375 from Rattus norvegicus
AAH12617 from Homo sapiens
CAG46593 from Homo sapiens
BAA00546 from Homo sapiens
CAA34814 from Homo sapiens
AAH02042 from Mus musculus
AAH87689 from Rattus norvegicus
AA56841 from Mus musculus
AAA40672 from Rattus norvegicus
AAB27386 from Gallus gallus
ACTH CHICK from Gallus gallus
ACTH HUMAN from Homo sapiens
ACTH MOUSE from Mus musculus
ACTH RAT from Rattus norvegicus

Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **20**
Number of mass values matched: **7**
Sequence Coverage: **26%**

**Spot 22784**
Match to: **AAH22086** Score: **88** Expect: **0.00023**
**BC022086 NID:** - Homo sapiens

Nominal mass (M,): **35417**; Calculated pI value: **6.71**
NCBI BLAST search of **AAH22086** against nr
Unformatted sequence string for pasting into other applications
Taxonomy: **Homo sapiens**
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **29**
Number of mass values matched: **13**
Sequence Coverage: **24%**

**Spot 23349**
Match to: **S06756** Score: **169** Expect: **1.6e-012**
**phosphopyruvate hydratase (EC 4.2.1.11) beta - human**

Nominal mass (M,): **47285**; Calculated pI value: **7.05**
NCBI BLAST search of **S06756** against nr
Unformatted sequence string for pasting into other applications
Taxonomy: **Homo sapiens**
Links to retrieve other entries containing this sequence from NCBI Entrez:
**CAA34513** from **Homo sapiens**
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)  
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P  
Number of mass values searched: 69  
Number of mass values matched: 23  
Sequence Coverage: 46%  

Spot 23352  
Match to: CAH3_HUMAN Score: 114 Expect: 5.2e-007  
Carbonic anhydrase III (EC 4.2.1.1) (Carbonate dehydratase III) (CA-III).- Homo sapiens (Human).  
Nominal mass (Mr): 29707; Calculated pI value: 6.94  
NCBI BLAST search of CAH3_HUMAN against nr  
Unformatted sequence string for pasting into other applications  
Taxonomy: Homo sapiens  
Fixed modifications: Carbamidomethyl (C)  
Variable modifications: Oxidation (M)  
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P  
Number of mass values searched: 37  
Number of mass values matched: 10  
Sequence Coverage: 37%  

Spot 23355  
Match to: MYL3_HUMAN Score: 97 Expect: 2.5e-005  
Myosin light polypeptide 3 (Myosin light chain 1, slow-twitch muscle B/ventricular isoform) (MLC1SB  
Nominal mass (Mr): 21958; Calculated pI value: 5.03
NCBI BLAST search of MYL3_HUMAN against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 13
Number of mass values matched: 7
Sequence Coverage: 38%

Spot 23360
Match to: Q5T8M7_HUMAN Score: 61 Expect: 0.13
Actin, alpha 1, skeletal muscle.- Homo sapiens (Human).
Nominal mass (M₀): 38142; Calculated pI value: 5.39
NCBI BLAST search of Q5T8M7_HUMAN against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Links to retrieve other entries containing this sequence from NCBI Entrez:
CAI19052 from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 26
Number of mass values matched: 5
Sequence Coverage: 13%
Mascot search scores are shown for the top match and, in parenthesis, for the highest ranked hit to a non-homologous protein. "Matched peptides" column shows the number of peptides matching to the top-match protein and, in parenthesis, the number of unmatched peptides in the spectra. The percent of the total intensity of the spectrum corresponding to the matched peptides is shown in the last column.

<table>
<thead>
<tr>
<th>Spot N</th>
<th>Identification</th>
<th>Swiss-Prot Access #</th>
<th>Mascot Score</th>
<th>Matched peptides</th>
<th>Sequence Coverage %</th>
<th>Intensity Coverage %</th>
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<td>Rho-GDP dissociation inhibitor ty-GDI</td>
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<td>8 (21)</td>
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<td>25.5</td>
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<td>Troponin T1, skeletal, slow</td>
<td>P13805</td>
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<td>11 (15)</td>
<td>19.9</td>
<td>66.2</td>
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<td>myosin regulatory light chain 2, ventricular/cardiac muscle isoform</td>
<td>P10916</td>
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<td>19 (38)</td>
<td>57.0</td>
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<td>21940</td>
<td>myosin regulatory light chain 2, skeletal muscle isoform</td>
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<td>146 (57)</td>
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<td>81.7</td>
<td>69.6</td>
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<td>Myotilin</td>
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<td>Hypothetical protein FLJ1664/TRIM72</td>
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<td>65.4</td>
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Table 2

Spot 21940
Match to: **Q96A32_HUMAN** Score: 146 Expect: 3.3e-010
*Myosin regulatory light chain 2 (Myosin light chain 2).- Homo sapiens (Human).*
Nominal mass (M_r): 19116; Calculated pI value: 4.91
NCBI BLAST search of **Q96A32_HUMAN** against nr
Unformatted sequence string for pasting into other applications
Taxonomy: *Homo sapiens*
Links to retrieve other entries containing this sequence from NCBI Entrez:
AAK52797 from *Homo sapiens*
AAH12571 from *Homo sapiens*
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 86
Number of mass values matched: 24
Sequence Coverage: 81%

Spot 21970
Match to: **Q5T458_HUMAN** Score: 120 Expect: 1.3e-007
*OTTHUMP00000059423.- Homo sapiens (Human).*
Nominal mass (M_r): 40006; Calculated pI value: 5.71
NCBI BLAST search of **Q5T458_HUMAN** against nr
Unformatted sequence string for pasting into other applications
Taxonomy: *Homo sapiens*
Links to retrieve other entries containing this sequence from NCBI Entrez:
CAI15461 from *Homo sapiens*
CAI14192 from *Homo sapiens*
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 12
Spot 22036
Match to: MLRV_HUMAN Score: 127 Expect: 2.6e-008
Myosin regulatory light chain 2, ventricular/cardiac muscle isoform (MLC-2) (MLC-2v).
Nominal mass (M_): 18646; Calculated pI value: 4.92
NCBI BLAST search of MLRV_HUMAN against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 57
Number of mass values matched: 19
Sequence Coverage: 56%

Spot 22148-A
Match to: AAH14006 Score: 80 Expect: 0.0014
BC014006 NTID: - Homo sapiens
Nominal mass (M_): 27815; Calculated pI value: 5.70
NCBI BLAST search of AAH14006 against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Links to retrieve other entries containing this sequence from NCBI Entrez:
CAB57866 from Homo sapiens
6PGL_HUMAN from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 37
Number of mass values matched: 8
Sequence Coverage: 36%

Spot 22063
Match to: A47742 Score: 91 Expect: 0.00011
Rho-GDP-dissociation inhibitor Ly-GDI - human
Nominal mass (M_r): 23031; Calculated pI value: 5.10
NCBI BLAST search of A47742 against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Links to retrieve other entries containing this sequence from NCBI Entrez:
AAM21075 from Homo sapiens
AAH09200 from Homo sapiens
CAA49280 from Homo sapiens
AAA59539 from Homo sapiens
GDIS_HUMAN from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 37
Number of mass values matched: 12
Sequence Coverage: 69%

Spot 21944
Match to: Q3B778_HUMAN Score: 121 Expect: 1.2e-07
Ankyrin repeat domain 2.- Homo sapiens (Human).
Nominal mass (M_r): 40006; Calculated pI value: 5.71
NCBI BLAST search of Q3B778_HUMAN against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Links to retrieve other entries containing this sequence from NCBI Entrez:
AAI07760 from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 19
Number of mass values matched: 11
Sequence Coverage: 26%

Spot 21984
Match to: **O43590_HUMAN** Score: **111** Expect: **1e-006**
**Actinin-associated LIM protein.- Homo sapiens** (Human).
Nominal mass (M): **39862**; Calculated pI value: **6.42**
NCBI BLAST search of **O43590_HUMAN** against **nr**
Unformatted sequence string for pasting into other applications
Taxonomy: **Homo sapiens**
Links to retrieve other entries containing this sequence from NCBI Entrez:
**AAB96665** from **Homo sapiens**
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **29**
Number of mass values matched: **12**
Sequence Coverage: **38%**

Spot 22062
Match to: **O43590_HUMAN** Score: **134** Expect: **5.2e-009**
**Actinin-associated LIM protein.- Homo sapiens** (Human).
Nominal mass (M): **39862**; Calculated pI value: **6.42**
NCBI BLAST search of **O43590_HUMAN** against **nr**
Unformatted sequence string for pasting into other applications
Taxonomy: **Homo sapiens**
Links to retrieve other entries containing this sequence from NCBI Entrez:
**Spot 22148-B**
Match to: **T09549**  Score: **68**  Expect: **0.02**
endoplasmic-reticulum-lumenal protein 28 - human
Nominal mass (Mz): **29032**; Calculated pI value: **6.77**
NCBI BLAST search of T09549 against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Links to retrieve other entries containing this sequence from NCBI Entrez:
CAG46468 from Homo sapiens
CAA64397 from Homo sapiens
ER29_HUMAN from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **29**
Number of mass values matched: **8**
Sequence Coverage: **42%**

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**Spot 23241**
Match to: **O43590_HUMAN**  Score: **85**  Expect: **0.00044**
**Actinin-associated LIM protein.** - Homo sapiens (Human).
Nominal mass (M_r): 39862; Calculated pI value: 6.42
NCBI BLAST search of O43590_HUMAN against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Links to retrieve other entries containing this sequence from NCBI Entrez:
AAB96665 from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 12
Number of mass values matched: 7
Sequence Coverage: 22%

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**Spot 21949**
Match to: Q6ZMU5_HUMAN  Score: 168  Expect: 2.1e-012

**Hypothetical protein FLJ16664.** - Homo sapiens (Human).
Nominal mass (M_r): 53613; Calculated pI value: 5.97
NCBI BLAST search of Q6ZMU5_HUMAN against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Links to retrieve other entries containing this sequence from NCBI Entrez:
BAD18630 from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 79
Number of mass values matched: 25
Sequence Coverage: 65%
Spot 22029
Match to: **TFHUP** Score: **258** Expect: **2.1e-021**
*transferrin precursor [validated] - human*
Nominal mass (M_r): **79280**; Calculated pI value: **6.81**
NCBI BLAST search of **TFHUP** against nr
Unformatted sequence string for pasting into other applications
Taxonomy: **Homo sapiens**
Links to retrieve other entries containing this sequence from NCBI Entrez:
AAK77664 from Homo sapiens
AAP45055 from Homo sapiens
AAA61140 from Homo sapiens
AAB22049 from Homo sapiens
TRFE_HUMAN from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: **86**
Number of mass values matched: **36**
Sequence Coverage: **48%**

Spot 22091
Match to: **Q9UBF9_HUMAN** Score: **74** Expect: **0.0051**
*Myotilin (Titin-like protein).- Homo sapiens (Human).*
Nominal mass (M_r): **55760**; Calculated pI value: **9.12**
NCBI BLAST search of **Q9UBF9_HUMAN** against nr
Unformatted sequence string for pasting into other applications
Taxonomy: **Homo sapiens**
Links to retrieve other entries containing this sequence from NCBI Entrez:
AAD29051 from Homo sapiens
AAD44754 from Homo sapiens
AAH05376 from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 35
Number of mass values matched: 10
Sequence Coverage: 21%

Spot 22228
Match to: AAH22086 Score: 68 Expect: 0.023
BC022086 NID: - Homo sapiens
Nominal mass (Mz): 35417; Calculated pI value: 6.71
NCBI BLAST search of AAH22086 against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 26
Number of mass values matched: 11
Sequence Coverage: 19%
Spot 23345
Match to: 2HMB Score: 104 Expect: 5.2e-006
Fatty acid binding protein (holo form, human muscle) (m-fabp) - human
Nominal mass (M_r): 14704; Calculated pI value: 6.34
NCBI BLAST search of 2HMB against nr
Unformatted sequence string for pasting into other applications
Taxonomy: Homo sapiens
Links to retrieve other entries containing this sequence from NCBI Entrez:
1HMR from Homo sapiens
1HMS from Homo sapiens
1HMT from Homo sapiens
Fixed modifications: Carbamidomethyl (C)
Variable modifications: Oxidation (M)
Cleavage by Trypsin: cuts C-term side of KR unless next residue is P
Number of mass values searched: 15
Number of mass values matched: 7
Sequence Coverage: 49%
**Date:** 2007-06-18

**User Name:** Carolina de la Torre

**Digestion:** Triptic Digestion (ZipPlate)

**Enzyme:** Trypsin

**Proteomics Facility-Universitat Pompeu Fabra**

**Operator:** Manuel Rodríguez

**Mass spectrometer:** MALDI-TOF Voyager STR (Applied Biosystems, 2001)

**Calibration type:** External and Internal Calibration

**Estimated Accuracy:** 50 ppm

**SPECTRUM PARAMETRES**

**Plate Type:** Sunyx

**Matrix composition:** ACH

**Deposition techniques:** Dried Droplet + finishing solution

**Grid Voltages:** 66%

**Acceleration voltages:** 20000 V

**Laser Type:** Nitrogen laser 337nm
Sample Name: E082 1 (spot 8326)

Spectrum

MASCOT IDENTIFICATION

Protein name: slow cardiac myosin regulatory light chain 2
Accession number: gi|94981553
Database: NCBInr
Taxonomy: Homo sapiens
MASCOT score: 129
Sequence Coverage: 76%
RMS error: 5 ppm

Sample Name: E082 2 (Spot 8330)

Spectrum

MASCOT IDENTIFICATION

Protein name: cardiac ventricular myosin light chain-2
Accession number: gi|34846
Database: NCBInr
**Taxonomy:** Homo sapiens  
**MASCOT score:** 93  
**Sequence Coverage:** 62%  
**RMS error:** 12 ppm

**Sample Name:** E082 3 (spot 8331)  
**Spectrum**

**MASCOT IDENTIFICATION**  
**Protein name:** myosin light chain 2  
**Accession number:** gi|28372499  
**Database:** NCBInr
Taxonomy: Homo sapiens
MASCOT score: 97
Sequence Coverage: 55%
RMS error: 8 ppm

Sample Name: E082 4 (spot 8636)

MASCOT IDENTIFICATION

Protein name: tropomyosin 2 (beta) isoform 1
Accession number: gi|42476296
Database: NCBInr
Taxonomy: Homo sapiens  
MASCOT score: 74  
Sequence Coverage: 16%  
RMS error: 1 ppm

Sample Name: E082 5 (spot 8635)
Spectrum

MASCOT IDENTIFICATION

Protein name: skeletal muscle tropomyosin  
Accession number: gi|339956  
Database: NCBInr  
Taxonomy: Homo sapiens  
MASCOT score: 84  
Sequence Coverage: 18%
RMS error: 17 ppm

*To confirm the results we apply the technique of MS/MS for identification of the protein

Sample Name: E082 10
Spectrum

MASCOT IDENTIFICATION

Protein name: Troponin T, slow skeletal muscle (TnTs) (Slow skeletal muscle troponin T) (sTnT)
Accession number: TNNT1_HUMAN
Database: SwissProt
Taxonomy: Homo sapiens
MASCOT score: 59
To confirm the results we apply the technique of MS/MS for identification of the protein.

Sample Name: E082 11

Spectrum

Voyager Spec #1 MC [BP = 1183.6, 8500]

**MASCOT IDENTIFICATION**
Protein name: Troponin T, slow skeletal muscle (TnTs) (Slow skeletal muscle troponin T) (sTnT)
Accession number: TNNT1_HUMAN
Database: SwissProt
Taxonomy: Homo sapiens
MASCOT score: 59
Sequence Coverage: 14%
To confirm the results we apply the technique of MS/MS for identification of the protein.

Sample Name: E082 17

Spectrum

MASCOT IDENTIFICATION

Protein name: Troponin T, slow skeletal muscle (TnTs) (Slow skeletal muscle troponin T) (sTnT)
Accession number: TNNT1_HUMAN
Database: SwissProt
Taxonomy: Homo sapiens
MASCOT score: 59
Sample Name: E082 12 (Spot 6549)

**Sequence Coverage:** 14%
**RMS error:** 17 ppm

**MASCOT IDENTIFICATION**

**Protein name:** Troponin T, slow skeletal muscle (TnTs) (Slow skeletal muscle troponin T) (sTnT)

**Accession number:** TNNT1_HUMAN

**Database:** SwissProt

**Taxonomy:** Homo sapiens

**MASCOT score:** 78

**Sequence Coverage:** 17%
Sample Name: E082 20 (Spot 6547)

MASCOT IDENTIFICATION

Accession number: HSPB1_HUMAN
Database: SwissProt
Taxonomy: Homo sapiens
MASCOT score: 60
Sequence Coverage: 17%
RMS error: 5 ppm

Sample Name: E082 23 (Spot 7566)
Spectrum

MASCOT IDENTIFICATION

Protein name: Homeobox protein TGIF2LY (TGFB-induced factor 2-like protein, Y-linked) (TGF(beta)induced transcription factor 2-like protein) (TGIF-like on the Y)
Accession number: TF2LY_HUMAN
Database: SwissProt
Taxonomy: Homo sapiens
MASCOT score: 63
Sequence Coverage: 20%
RMS error: 39 ppm
Sample Name: E082 29 (Spot 8328)
Spectrum

MASCOT IDENTIFICATION

Protein name: Myosin regulatory light chain 2, skeletal muscle isoform (Fast skeletal myosin light chain 2) (MLC2B)
Accession number: MLRS_HUMAN
Database: swissProt
Taxonomy: Homo sapiens
MASCOT score: 121
Sequence Coverage: 68%
RMS error: 10 ppm
Sample Name: E082 A (Spot 6544)

Spectrum

MASCOT IDENTIFICATION

Protein name: Mixture 1:


2.- NADH dehydrogenase [ubiquinone] iron-sulfur protein 3, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (NADH-ubiquinone oxidoreductase 30 kDa subunit) (Complex I-30kD) (CI-30kD)
Accession number:
1. **HSPB1** HUMAN
2. **NDUS3** HUMAN

**Database**: SwissProt  
**Taxonomy**: Homo sapiens  
**MASCOT score**: 165  
**Sequence Coverage**:
1. 32%  
2. 19%

**RMS error**:
1. 15 ppm  
2. 14 ppm

**Sample Name**: E082 A plata (Spot 6545)  
**Spectrum**

**MASCOT IDENTIFICATION**

**Accession number**: **HSPB1** HUMAN  
**Database**: SwissProt  
**Taxonomy**: Homo sapiens  
**MASCOT score**: 88  
**Sequence Coverage**: 28%  
**RMS error**: 13 ppm
Sample Name: E082 B plata (Spot 7563)

**Spectrum**

**Voyager Spec #1 MC [BP = 1163.6, 12731]**

**MASCOT IDENTIFICATION**

**Protein name:** Heat-shock protein beta-1 (HspB1) (Heat shock 27 kDa protein) (HSP 27) (Stress-responsive protein 27) (SRP27) (Estrogen-regulated 24 kDa protein) (28 kDa heat shock protein)

**Accession number:** HSPB1_HUMAN

**Database:** SwissProt

**Taxonomy:** Homo sapiens

**MASCOT score:** 91

**Sequence Coverage:** 28%

**RMS error:** 8 ppm
**Analysis MS/MS to improve the score identification of proteins**

*User Name:* Carolina de la Torre (E082)

**Proteomics Facility-Universitat Pompeu Fabra**

*Operator:* Cristina Chiva

**Mass spectrometer:** QStar Pulsar i (Applied Biosystems, 2001)

**Calibration type:** External calibration: CSI sex feromon inhibitor (MW 829)

**Estimated Accuracy:** 100 ppm

**Supply Type:** Fed

**Solvent Flow rate:** 200nL/min

**Solvent composition:** A: 5%ACN 0.1% Formic Acid/B: 95%ACN 0.1% Formic Acid

**Gradient:** 100-50% A (30 min)

**Interface:** Protana nanospray source

**Sprayer Type:** New Objective, Uncoated SilicaTips™ (N) (#FS-360-20-10-N)

**Tip voltages:** 2100-2500V

**Sample Name:** E082 10 (spot 7624)

**Protein name:** slow skeletal muscle troponin T

**Accession number:** gi|339783

**Database:** NCBInr

**Taxonomy:** Homo sapiens

**MASCOT score:** 87

**Sequence Coverage:** 12%

**RMS error:** 107 ppm

**Sample Name:** E082 11 (spot 7625)

**Protein name:** slow skeletal muscle troponin T

**Accession number:** gi|339783

**Database:** NCBInr

**Taxonomy:** Homo sapiens
MASCOT score: 146
Sequence Coverage: 18%
RMS error: 105 ppm

Sample Name: E082 17 (spot 7571)
Protein name: slow skeletal muscle troponin T
Accession number: gi|339783
Database: NCBInr
Taxonomy: Homo sapiens
MASCOT score: 105
Sequence Coverage: 15%
RMS error: 83 ppm
Annotated mass spectra for proteins listed in Table 1. Peaks labeled in red are the peaks included in the peak list for database search, after removing commonly observed matrix clusters, trypsin autolysis and keratin peaks. The resulting filtered peak lists are provided in the corresponding "Peak Lists" excel file. Database search results are attached for each identified protein. Mascot 2.0 program (Matrix Science Ltd, London UK) was used to search the MSDB database, 20050227 release (Imperial College, London), limiting the search to human proteins (130630 sequences). Search parameters were as follows: trypsin cleavages excluding N-terminal to P, 1 or 2 missed cleavages allowed, carbamidomethylation set as fixed modification, methionine oxidation as variable modification, mass tolerance less than 50 ppm.
Spot 22669 Fructose – bisphosphate aldolase A (EC 1.1.2.13)
Spot 22056 Hypothetical protein, similarity heat shock protein

[Abs. Int. * 1000]
Spot 22522  Acyl-CoA dehydrogenase (EC 1.3.99.3)
Spot 22761 Myosin light chain 1, skeletal muscle isoform (MLC1F)

[Table of m/z values and corresponding peptides]

- 1249.592 141-152
- 1242.646 80-91
- 1233.614 141-152
- 1200.701 69-79
- 1384.710 93-105
- 1370.745 80-92
- 1512.801 93-106
- 1527.735 44-55
- 1542.715 124-136
- 1527.735 44-55
- 1512.801 93-106
- 1722.829 137-152
- 1738.823 137-152
- 1914.909 49-63
Spot 22054 Myosin regulatory light chain 2

[Abs. Int. * 1000]

m/z

1080.484
64-72

1173.627
42-51

1192.609
32-41

1319.662
93-105

1524.784
119-130

1560.859
91-105

1762.869
155-169

1880.918
138-154

15 m/z units
Spot 23355 Myosin light polypeptide 3

[Graph showing mass-to-charge (m/z) values with peaks labeled with corresponding masses and ranges.]

- 995.646 (154-162)
- 1233.587 (142-153)
- 1281.610 (70-80)
- 1281.610 (70-80)
- 1370.719 (55-65)
- 1396.743 (81-93)
- 1524.779 (18-32)
- 1722.862 (138-153)
Spot 22016 Myosin light polypeptide 3

[Abs. Int. * 1000]
Spot 22166 Actin alpha, skeletal muscle

[Chart with m/z values and their corresponding absolute intensities]

- 1198.665 31-41
- 1187.522 42-52
- 1130.511 199-208
- 1790.887 241-256
- 1627.825 199-212
- 1623.820 180-193
- 1515.740 87-97
- 1500.689 362-374
- 1354.635 53-64
- 1639.813 180-193
- 1956.048 98-115
- 2262.049 294-314
- 2374.190 293-314
- 2390.164 293-314
- 2278.075 294-314
- 2390.013 294-314
- 2390.164 293-314
- 2278.075 294-314
- 3212.753 150-179
Spot 22271 Actin alpha, skeletal muscle

[Abs. Int. * 1000]

- 1187.516 42-52
- 1627.823 199-212
- 1500.688 362-374
- 1639.866 180-193
- 1790.873 241-256
- 1956.041 98-115
- 2278.047 294-314
- 2406.125 293-314
- 2552.198 218-240
- 3212.604 150-179

m/z
Spot N 22772 Actin gamma, smooth muscle

[Abs. Int. *1000]

m/z

1198.690
30-40

1130.550
198-207

1354.623
52-63

1627.828
198-211

1639.796
179-192

1956.020
97-114

3212.560
149-178

198-211

m/z

1000 1500 2000 2500 3000 3500
Spot 23360 Actin, alpha 1

[Abs. Int. * 1000]
Spot 22113-1 Alpha-crystallin chain B

[Graph showing mass-to-charge (m/z) ratios and corresponding intensities.

- m/z 1088.529, Int. 12-22
- m/z 1192.623, Int. 73-82
- m/z 1213.646, Int. 83-92
- m/z 1222.037, Int. 158-174
- m/z 1374.701, Int. 12-22
- m/z 1562.868, Int. 104-116
- m/z 1639.753, Int. 104-116
- m/z 1822.037, Int. 158-174
- m/z 2786.367, Int. 93-116

Abs. Int. * 1000]
Spot 22000 Myosin alkali light chain, slow skeletal muscle

[Abs. Int. × 1000]
Annotated mass spectra for proteins listed in Table 2. Peaks labeled in red are the peaks included in the peak list for database search, after removing commonly observed matrix clusters, trypsin autolysis and keratin peaks. The resulting filtered peak lists are provided in the corresponding "Peak Lists" excel file. Database search results are attached for each identified protein. Mascot 2.0 program (Matrix Science Ltd, London UK) was used to search the MSDB database, 20050227 release (Imperial College, London), limiting the search to human proteins (130630 sequences). Search parameters were as follows: trypsin cleavages excluding N-terminal to P, 1 or 2 missed cleavages allowed, carbamidomethylation set as fixed modification, methionine oxidation as variable modification, mass tolerance less than 50 ppm.
Spot 21970 OTTHUMP00000059423 (Ankyrin repeat domain 2)

Abs. Int. $\times 1000$
Spot 23241  Actinin-associated LIM Protein

[Graph showing mass/charge ratio (m/z) vs. absolute intensity (Abs. Int. * 1000) with peaks at m/z values and corresponding abundance for the indicated peptides.]

- m/z 1629.888 at 17-31
- m/z 1919.913 at 103-118
- m/z 1876.826 at 314-328
- m/z 1790.859 at 291-307
- m/z 2196.029 at 312-328
- m/z 2439.225 at 310-328
- m/z 1991.950 at 331-346
Spot N 22029 Transferrin Precursor

[Abs. Int. * 1000]
Spot 23345 Fatty acid binding protein

[Abs. Int. × 1000]
Spot 22036 Myosin regulatory light 2, ventricular / cardiac muscle isoform

[Abs. Int. * 1000]
Spot 21940 Myosin regulatory light chain 2

[Abs. Int. * 1000]
Spot 21949 Hypothetical protein FLJ1664 / TRIM 72

[Abs. Int. * 1000]